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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE
EXPRESSION IN HUMAN FETAL LIVER

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene
expression in a sample derived from human Fetal liver is described. Also described are single exon nucleic acid probes expressed in
the Fetal liver and their use in methods for detecting gene expression.

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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER

CROSS REFERENCE TO RELATED APPLICATIONS

5 The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20 The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_FETAL_LIVER.txt,
25 created 24 January 2001, having 25,630,231 bytes. The
Sequence Listing contained in said file on said disc is
incorporated herein by reference in its entirety.

Field of the Invention

30 The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

Fetal liver and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches - and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species - there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al.,
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 . The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition,
20 onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies. There is a need for methods and apparatus that permit prediction of
25 diseases of the liver, particularly those diseases with polygenic etiology, from diagnosis of fetal liver.

Summary of the Invention

30 The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the
35 expression of putative genes identified within genomic

sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human Fetal liver, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,673 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid

probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,129 or a complimentary sequence, or a portion of such a sequence.

5 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

10 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
15 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

 In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
20 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

 Preferably, a spatially-addressable set of single
25 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

 Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
30 nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride,
35 polytetrafluoroethylene, polystyrene, polycarbonate,

polyacetal, polysulfone, celluloseacetate,
cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is
provided a microarray comprising a spatially addressable
5 set of single exon nucleic acid probes in accordance with
the first aspect of the invention.

In one embodiment, a genome-derived single-exon
microarray is packaged together with such an ordered set of
amplifiable probes corresponding to the probes, or one or
10 more subsets of probes, thereon. In alternative
embodiments, the ordered set of amplifiable probes is
packaged separately from the genome-derived single exon
microarray.

In another aspect, the invention provides genome-
15 derived single exon nucleic acid probes useful for gene
expression analysis, and particularly for gene expression
analysis by microarray. In particular embodiments of this
aspect, the present invention provides human single-exon
probes that include specifically-hybridizable fragments of
20 SEQ ID Nos. 12,674 - 25,129, wherein the fragment
hybridizes at high stringency to an expressed human gene.
In particular embodiments, the invention provides single
exon probes comprising SEQ ID Nos. 1 - 12,673.

Accordingly, in a third aspect of the invention,
25 there is provided a single exon nucleic acid probe for
measuring human gene expression in a sample derived from
human Fetal liver which is a nucleic acid molecule
comprising a nucleotide sequence as set out in any of SEQ
ID NOS.: 1 - 12,673 or a complementary sequence or a
30 fragment thereof wherein said probe hybridizes at high
stringency to a nucleic acid expressed in the human Fetal
liver.

In one embodiment, a single exon nucleic acid
probe in accordance with the third aspect comprises a
35 nucleotide sequence as set out in any of SEQ ID NOS.:

12,674 - 25,129 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring
5 human gene expression in a sample derived from human Fetal liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,130 - 37,156 or a complementary sequence or a fragment thereof wherein said probe
10 hybridizes at high stringency to a nucleic acid expressed in the human Fetal liver.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous
15 nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

20 In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb,
25 preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or
30 PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first
35 member of a specific binding pair. Suitable fluorescent

labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single
5 exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks
10 homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance
15 with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is
20 provided a method of measuring gene expression in a sample derived from human Fetal liver, comprising:

contacting the single exon microarray in
accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said
25 first collection of nucleic acids derived from mRNA of human Fetal liver; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is
30 provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably
35 labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the Fetal liver of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 25,129 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 12,674 - 25,129, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -12,673.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ

ID NOS.: 25,130 - 37,156.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 25,130 - 37,156, or fragment
5 thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display
10 can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

15 Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound
20 collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase
25 "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and
30 Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably
35 disposed on a plurality of beads, rather than on a unitary

planar substrate, as is described, *inter alia*, in Brenner
et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000);
in such case, the term "microarray" and phrase "nucleic
acid microarray" refer to the plurality of beads in
5 aggregate.

As used herein with respect to a nucleic acid
microarray, the term "probe" refers to the nucleic acid
that is, or is intended to be, bound to the substrate; in
such context, the term "target" thus refers to nucleic acid
10 intended to be bound thereto by Watson-Crick
complementarity. As used herein with respect to solution
phase hybridization, the term "probe" refers to the nucleic
acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising
15 SEQ ID NO.", and variants thereof, intends a nucleic acid
probe, at least a portion of which probe has either (i) the
sequence directly as given in the referenced SEQ ID NO., or
(ii) a sequence complementary to the sequence as given in
the referenced SEQ ID NO., the choice as between sequence
20 directly as given and complement thereof dictated by the
requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and
the equivalent acronym "ORF" refer to that portion of an
exon that can be translated in its entirety into a sequence
25 of contiguous amino acids i.e. a nucleic acid sequence
that, in at least one reading frame, does not possess stop
codons; the term does not require that the ORF encode the
entirety of a natural protein.

As used herein, the term "amplicon" refers to a
30 PCR product amplified from human genomic DNA, containing
the predicted exon.

As used herein the term "exon" refers to the
consensus prediction of the various exon and gene
predicting algorithms i.e. a nucleic acid sequence
35 bioinformatically predicted to encode a portion of a

natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual

object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional
5 information.

Brief Description of the Drawings

10 The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the
15 functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the
20 process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

25 FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution,
30 among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or
35 more but not all tested tissues ("1" - "9"), or expressed

in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained

in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100
5 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger
10 contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was
15 erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession,
20 species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will
25 be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

30 Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the
35 National Institutes of Health and is maintained by the

National Center for Biotechnology Information (NCBI).
Databases of genomic sequence from species other than
human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*
briggsii, *Drosophila*, zebra fish, and other higher
5 eukaryotic organisms will also prove useful as genomic
sequence database 100.

Genomic sequence obtained by query of genomic
sequence database 100 is then input into one or more
processes 200 for identification of regions therein that
10 are predicted to have a biological function as specified by
the user. Such functions include, but are not limited to,
encoding protein, regulating transcription, regulating
message transport after transcription into mRNA, regulating
message splicing after transcription into mRNA, of
15 regulating message degradation after transcription into
mRNA, and the like. Other functions include directing
somatic recombination events, contributing to chromosomal
stability or movement, contributing to allelic exclusion or
X chromosome inactivation, and the like.

20 The particular genomic sequence to be input into
process 200 will depend upon the function for which
relevant sequence is to be identified as well as upon the
approach chosen for such identification. Process step 200
can be iterated to identify different functions within a
25 given genomic region. In such case, the input often will
be different for the several iterations.

Sequences predicted to have the requisite
function by process 200 are then input into process 300,
where a subset of the input sequences suitable for
30 experimental confirmation is identified. Experimental
confirmation can involve physical and/or bioinformatic
assay. Where the subsequent experimental assay is
bioinformatic, rather than physical, there are fewer
constraints on the sequences that can be tested, and in
35 this latter case therefore process 300 can output the

entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in
5 process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can
10 be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a
15 combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation
20 can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the
25 like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an
30 experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly
35 to the succeeding process, or stored in permanent or

interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

5 FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

10 The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene
15 prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding
20 regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences
25 and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be
30 determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements
35 of the subsequent analytical method. Alternatively, or in

addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate
5 criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

10 Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any
15 given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

20 Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given
25 BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated
30 into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are
35 typically updated on a frequent, even hourly, basis. Thus,

as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods
5 and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the
10 presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for
15 sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery
20 can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query,
25 depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by
30 process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

35 When query 20 returns sequence meeting the query

criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

5 Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

 Preprocessing 24 suitable for most approaches and
10 methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like.
15 Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

 Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence,
20 vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

25 Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies
30 a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

35 Once identified, undesired sequence can be

removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X".

- 5 Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of
10 highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can
15 also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25.
20 Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion
25 from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the
30 informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include,
35 but are not limited to, encoding protein, regulating

transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic
5 recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for
10 identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the
15 novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative
20 coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more
25 software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

30 As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region,
35 2% of the data analyzed; GENEFINDER was second, calling 1%;

and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although
5 discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be
10 repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as
15 well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated
20 and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene
25 prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way,
30 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be
35 identified is coding of protein sequence, and a first used

approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative
5 sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

10 Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

 Predicted functional sequence, optionally representing a consensus among a plurality of methods and
15 approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

 In the preferred embodiment of the methods of the present invention, wherein the function sought to be
20 identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

 For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into
25 putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-
30 specific ORFs can be chosen for subsequent use in gene expression assay.

 Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative
35 exon length, sequence GC content, existence of possible

secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using
5 amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance
10 of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested
15 experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for
20 experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred
25 embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention
30 provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of
35 nucleic acid microarray, the genome-derived single exon

nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by
5 process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture
10 the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying
15 length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the
20 methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can
25 alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or
30 intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about
35 300, 400 or 500 bp in length, can be amplified. However, it

has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for

amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see

above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include

5 polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can

10 also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as

15 described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by

20 presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version

25 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using

30 ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of

35 the present invention, a plurality of *E. coli* genes can

readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified
5 product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as
10 complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

15 Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined,
20 including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon,
25 and positively-charged derivatized nylon membranes.

Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No.
30 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however,
35 provide certain useful advantages, including high

throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of
5 discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For...
10 purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide
15 redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by
20 deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized
25 probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*,
30 or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas *et al.*, *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

35 Such EST microarrays by definition can measure

expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse

transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector

sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence.

10 With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater

15 specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain

20 artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific

25 primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such

30 "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon

35 microarray of the present invention can be made without

such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, 5 in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved 10 using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of 15 differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used 20 for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome- 25 derived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the 30 exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides 35 the additional opportunity to assay prespliced RNA, and

thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely
5 constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be
10 performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered
15 (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the
20 genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the
25 microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed
30 on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the
35 melting temperature of probes hybridized to their

complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the
5 microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ*
10 synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

15 The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari *et al.*, *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

20 Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez *et al.*, *Nucl. Acids Res.* 28:85-86 (2000); Spingola *et al.*, *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome
25 has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

30 Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as
35 *Saccharomyces cerevisiae*, particularly in genomic sequence

drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of
5 novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is
10 performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the
15 putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed
20 for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the
25 reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

30 mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be
35 measured) is reverse transcribed in the presence of

nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically
5 fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to
10 standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage,
15 to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it
20 is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally
25 as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially
30 identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well
35 of a microtiter dish. Although a 96 well microtiter plate

can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions
5 (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of
10 individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific
5' primers used for genomic amplification can have a first
15 common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the
20 amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of
25 agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of
30 probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable
35 media that provide probe identification and addressing

information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

5 If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not
10 required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived
15 microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

20 Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be
25 identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases,
30 such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any
35 sequence query algorithm, such as BLAST ("basic local

alignment search tool"). The results of such query -
including information on identical sequences and
information on nonidentical sequences that have diffuse or
focal regions of sequence homology to the query sequence -
5 can then be passed directly to process 500, or used to
inform analyses subsequently undertaken in process 200,
process 300, or process 400.

Experimental data, whether obtained by physical
or bioinformatic assay in process 400, is passed to process
10 500 where it is usefully related to the sequence data
itself, a process colloquially termed "annotation". Such
annotation can be done using any technique that usefully
relates the functional information to the sequence, as, for
example, by incorporating the functional data into the
15 record itself, by linking records in a hierarchical or
relational database, by linking to external databases, or
by a combination thereof. Such database techniques are
well within the skill in the art.

The annotated sequence data can be stored
20 locally, uploaded to genomic sequence database 100, and/or
displayed 800.

The methods and apparatus of the present
invention rapidly produce functional information from
genomic sequence. Coupled with the escalating pace at
25 which sequence now accumulates, the rapid pace of sequence
annotation produces a need for methods of displaying the
information in meaningful ways.

FIG. 3 shows visual display 80 presenting a
single genomic sequence annotated according to the present
30 invention. Because of its nominal resemblance to artistic
works of Piet Mondrian, visual display 80 is alternatively
described herein as a "Mondrian".

Each of the visual elements of display 80 is
aligned with respect to the genomic sequence being
35 annotated (hereinafter, the "annotated sequence"). Given

the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence
5 is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the
10 sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored
15 electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of
20 a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user
25 specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or
30 alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene
35 name, or even a sequence returned by query for similarity

or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

5 Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

10 Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction.
15 Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be
20 made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

 As earlier described, increased predictive reliability can be achieved by requiring consensus among
25 methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

 Although FIG. 3 shows three series of
30 horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

35 Furthermore, field 81 can be used to show

predictions of a plurality of different functions.

However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the

probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity

has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to

indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

5 Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized
10 mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*.
15 BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by
20 DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates
25 unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of
30 such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present
35 invention rapidly produce functional information from

genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode
5 protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in
10 one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

15 Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray
20 hybridization analysis, the expression of 12,673 of these ORFs in Fetal liver.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in Fetal liver is currently
25 available for use in measuring the level of its ORF's expression in Fetal liver.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition,
30 onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies.

For example, cirrhosis is a major public health
35 problem. In the industrialized world, it is among the top

ten causes of death; among patients aged 45 to 65, it is the third leading cause of death. The high prevalence is largely the result of alcohol abuse, but other major contributors include chronic hepatitis, biliary disease and iron overload. Approximately 10-15% are cryptogenic.

Cirrhosis is a broad description encompassing the common end stage of many forms of liver injury. Many patients with cirrhosis will remain asymptomatic for years, while others show generalized weakness, anorexia, malaise, and weight loss or, occasionally, more severe symptoms.

The progression from fibrosis, an early consequence of liver disease, to cirrhosis, and the specific histologic morphology that characterizes cirrhosis depend on the extent of injury, the presence of continuing damage, and the response of the liver to damage. The liver may be injured acutely and severely (e.g. necrosis with hepatitis), moderately over months or years (e.g. biliary tract obstruction and chronic active hepatitis), or modestly but continuously (e.g. alcohol abuse).

During the repair process, new vessels connecting the hepatic artery and portal vein to the hepatic venules form within the fibrous sheath that surrounds the surviving nodules of liver cells. These vessels restore the intrahepatic circulatory pathway, but provide relatively low-volume, high-pressure drainage that is less efficient than normal and results in increased portal vein pressure (portal hypertension). Thus, cirrhosis is not static and its features depend on the disease activity and stage.

As cirrhosis is the end stage of many forms of liver disease, many genes have been identified that can contribute to the development of cirrhosis. These include, e.g., the genes responsible for Wilson disease (Online Mendelian Inheritance of Man ("OMIM") 277900), type IV glycogen storage disease (OMIM 232500), galactosemia (OMIM

230400), and a deficiency of alpha-1-antitrypsin (OMIM 107400). There is substantial evidence, however, for as yet uncharacterized loci which cause cirrhosis.

For example, Iber and Maddrey, Prog. Liver Dis. 2: 290-302 (1965), reviewed 13 previously reported families and 8 new to this study, each with 2 or more affected members. They pointed out that, with a single exception, the multiple cases were in the same generation. Within a given family, the age of onset, clinical course, and biopsy findings were very similar, but there were wide differences between families.

Kalra et al., Hum. Hered. 32:170-175 (1982) studied the families of 220 cases of Indian childhood cirrhosis and 70 families of age-matched controls. The hypotheses of autosomal recessive, partial sex-linkage, and doubly recessive inheritance were found untenable and the authors concluded that multifactorial inheritance was most plausible. Lefkowitz et al., New Eng. J. Med. 307:271-277 (1982) described 4 white American sibs who died between ages 4.5 and 6 years of cirrhosis that closely resembled that of the childhood cirrhosis of Asiatic Indians.

Another example of uncharacterized loci which cause cirrhosis are those related to the risk of alcoholism.

Cloninger, Science 236:410-416 (1987), defined two separate types of alcoholism. According to these definitions, type 1 alcohol abuse has its usual onset after the age of 25 years and is characterized by severe psychological dependence and guilt. Type 1 occurs in both men and women and requires both genetic and environmental factors to become manifest. By contrast, type 2 alcohol abuse has its onset before the age of 25; persons with this type of alcoholism are characterized by their inability to abstain from alcohol and by frequent aggressive and antisocial behavior. Type 2 alcoholism is rarely found in

women and is much more heritable.

Despite considerable effort to identify genes related to the risk of alcoholism, relatively few genes have been identified. Some of this work has suggested a relationship between the metabolism of dopamine and alcoholism. Blum et al., J.A.M.A. 263:2055-2060 (1990) and Bolos et al., J.A.M.A. 264:3156-3160 (1990) investigated the relationship of the dopamine D2 receptor (DRD2; OMIM 126450) to alcoholism, but the sample size was small and their results were inconclusive. However, Tiihonen et al., Molec. Psychiat. 4, 286-289 (1999), found a markedly higher frequency in a population of type 1 alcoholics of the low activity allele of the enzyme catechol-O-methyltransferase (COMT, OMIM 116790), which has a crucial role in the metabolism of dopamine, suggesting a role for dopamine metabolism in increased risk of alcoholism. For a brief review of recent progress toward the identification of genes related to risk for alcoholism see Buck, Genome 9:927-928 (1998).

As another example, multiple genes have been shown to predispose to hyperlipoproteinemia or hyperlipidemia. Much attention has been focused on these disorders because there is a strong association of hyperlipidemia, especially hypercholesterolemia, with development of coronary artery disease. Coronary artery disease accounts for at least 25% of all deaths in the United States. Coronary artery disease results when the arteries supplying the heart muscle become occluded by plaques composed of lipids like cholesterol, blood clotting components and blood cells.

The major plasma lipids circulate bound to proteins as macromolecular complexes called lipoproteins. Although closely interrelated, the major lipoprotein classes - chylomicron, very-low-density lipoprotein (VLDL), low-density lipoprotein (LDL), and high-density lipoprotein

(HDL) - are usually classified in terms of physicochemical properties (e.g., density after centrifugation). Chylomicrons, the largest lipoproteins, carry exogenous triglyceride from the intestine via the thoracic duct to the venous system and into peripheral sites. VLDL carries endogenous triglyceride primarily from the liver to the same peripheral sites for storage or use. Lipases quickly degrade the triglyceride in VLDL to produce intermediate density lipoproteins (IDL) and within 2 to 6 h, IDL is degraded further to generate LDL, which has a plasma half-life of 2 to 3 days. While the overall fate of LDL is unclear, the liver is responsible for removing approximately 70% and active receptor sites have been found on the surfaces of hepatocytes.

Several monogenic conditions that lead to elevated levels of one or more serum lipoproteins have been defined and the responsible gene identified, including, e.g., hyperlipoproteinemia type I (OMIM 238600), familial hypercholesterolemia (OMIM 143890), and familial defective apolipoprotein B (OMIM 107730). However, in many cases the etiology is unknown and there is strong evidence for additional uncharacterized loci.

For example, Zuliani et al., *Arterioscler. Thromb. Vasc. Biol.* 19:802-809 (1999) identified a Sardinian family with a recessive form of hypercholesterolemia with the clinical features of familial hypercholesterolemia (OMIM 603813), and found that previously identified genes were not responsible for this disorder. They proposed that in this new lipid disorder, a recessive defect causes a selective impairment of the LDL receptor function in the liver. Ciccarese et al., *Am. J. Hum. Genet.* 66:453-460 (2000) recently mapped this novel disease locus.

Another example is designated familial combined hyperlipidemia (OMIM 144250) which affects approximately 1-

2% of the population in the Western world. This disorder can have its basis in mutation in several novel genes, two of which have been mapped to chromosome 1 (Pajukanta et al., Nature Genet. 18:369-373 (1998)) and chromosome 11 (Aouizerat et al., Am. J. Hum. Genet. 65, 397-412 (1999)). The high frequency of this disorder suggests that most, if not all, hyperlipidemias are of multifactorial genetic etiology.

As yet a further example, primary sclerosing cholangitis (PSC) is a disorder characterized by a patchy obliterative inflammatory fibrosis of the large bile ducts. Chronic inflammation leads to extensive bile duct strictures, cholestasis, and gradual progression to biliary cirrhosis. PSC occurs most often in young men and is commonly associated with inflammatory bowel disease, especially ulcerative colitis. The onset is usually insidious, with gradual, progressive fatigue, pruritus, and jaundice. There is no specific therapy for sclerosing cholangitis, and liver transplantation is the only apparent cure.

The etiology of PSC is not known, but both genetic and immunologic abnormalities have been implicated. However, the frequency of HLA-B8 and HLA-DT2, which are associated with a number of autoimmune diseases, is higher in PSC than normal individuals. Prochazka et al., New Eng. J. Med. 322:1842-1844 (1990) found that 100% of 29 patients with primary sclerosing cholangitis carried the HLA-DRw52a antigen, which is normally present in 35% of the population.

As a still further example, sarcoidosis is a disease of unknown cause characterized by non-caseating granulomas in one or more organ systems. These granulomas may resolve completely or proceed to fibrosis. The disorder is systemic, but the liver is affected in approximately 75% of cases. Sarcoidosis occurs mainly in persons aged 20 to

40 yr and is most common in Northern Europeans and American blacks. The lifetime risk of developing sarcoidosis is particularly high among Swedish men (1.15%), Swedish women (1.6%), and African Americans (2.4%).

5 The much greater frequency in African Americans relative to the United States population overall suggests a genetic contribution to etiology. Early research studying familial aggregation indicated that the disease may have a nongenetic basis because the family pattern did not conform
10 to a simple Mendelian mode of inheritance (Allison, Sth. Med. J. 57: 27-32 (1964)). However, Headings et al., Ann. N.Y. Acad. Sci. 278:377-385 (1976) favored multifactorial genetic inheritance of susceptibility. Nowack et al., Arch. Intern. Med. 147:481-483 (1987), found an unusually
15 high frequency of HLA-DR5 in a study of 440 patients with sarcoidosis in Marburg, Germany. They also concluded that the role of an environmental or infectious agent triggering sarcoidosis cannot be envisaged without considering genetically linked cofactors.

20 Other significant diseases of liver are also believed to have a genetic, typically polygenic, etiologic component. These diseases include, e.g., primary biliary cirrhosis, Zellweger syndrome, cholestasis-lymphedema syndrome, Alstrom syndrome, primary pulmonary
25 hypertension, Berardinelli-Seip congenital lipodystrophy, iron overload in Africa, neonatal cholestatic hepatitis, autosomal recessive KID syndrome, familial hypotransferrinemia, type I congenital dyserythropoietic anemia, porphyria variegata, Finnish lactic acidosis with
30 hepatic hemosiderosis, Rotor syndrome, essential hypertension, ARC syndrome, type II conjugated hyperbilirubinemia, Lambert syndrome, ichthyosis congenita with biliary atresia, Kabuki make-up syndrome, Meckel syndrome, cerebral aneurysm-cirrhosis syndrome, glycogen
35 storage diseases, polycystic kidney and hepatic disease,

isolated Caroli disease, trisomy 18-like syndrome, Osler-Rendu-Weber syndrome 3, fatal intrahepatic cholestasis, Coach syndrome, type C Niemann-Pick disease, hereditary persistence of fetal hemoglobin and hepatocellular cancer.

5 Altered responses to a variety of infectious agents that target the liver, especially acute viral hepatitis, have also been shown or are suspected to have genetic bases or contributions. In addition to differential susceptibility to primary infectious agents, 10 these altered responses include predisposition to complicating conditions following contact with particular infectious agents. These include, e.g., development of hepatocellular carcinoma 2 correlated with Hepatitis B infection, and severe hepatic fibrosis following 15 *Schistosoma mansoni* infection.

The central role of the liver in drug metabolism results in exposure of this organ to a large variety of potentially toxic chemical agents and metabolites. These include naturally occurring plant alkaloids and mycotoxins, 20 industrial chemicals, and, additionally, pharmacologic agents used in treating disease. The range of manifestations of toxin- and drug-induced liver disease are virtually as broad as the range of acute and chronic disorders and have also been shown or suspected to have 25 genetic bases or contributions.

Such interactions between drugs and genotype have been shown in the response, e.g., to the anticonvulsant phenytoin, which can cause severe hepatitis-like disease in individuals who are impaired in the ability to detoxify a 30 metabolite of phenytoin in the liver, and in the response to the drug sodium valproate, which can produce severe hepatotoxicity in certain individuals. The abnormal responses to both of these drugs are believed to be influenced by underlying genetic factors.

35 The human genome-derived single exon nucleic acid

probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human liver, particularly those diseases with polygenic etiology. With each of the single
5 exon probes described herein shown to be expressed at detectable levels in human liver, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

10 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders, such as cirrhosis), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression
15 profiles known to be characteristic of a given liver disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the
20 patient's liver to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly, using nucleic acids obtained directly or indirectly from transcripts expressed by liver of individuals with known liver disease. Methods for
25 quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single
30 exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of liver disease to be assessed through the massively parallel determination of
35 altered copy number, deletion, or mutation in the patient's

genome of exons known to be expressed in human liver. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

5 The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art - see Ausubel et al. and Maniatis et al. - each probe reports the level of expression of message specifically containing that ORF.

10 It should be appreciated, however, that the probes of the present invention, for which expression in the Fetal liver has been demonstrated are useful for both measurement in the Fetal liver and for survey of expression in other tissues.

15 Significant among such advantages is the presence of probes for novel genes.

 As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be
20 identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were
25 represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence
30 databases.

 Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes
35 that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and
5 for surveying gene expression in the human.

Gene expression analysis using microarrays - conventionally using microarrays having probes derived from expressed message - is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405,
10 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct
15 Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for
20 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of
25 Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

30 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,
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"Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile

and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in Fetal liver. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to

PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are
5 to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form
10 suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be
15 packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific
20 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3'
25 primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present
30 invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived
35 single exon microarray of the present invention, the

genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a
5 hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

10 In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable
15 of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

20 Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 12,674 – 25,129, respectively, for probe SEQ ID NOS. 1 – 12,673. The minimum amount of ORF required to be
25 included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 12,674 – 25,129 individually by routine experimentation using standard high stringency
30 conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl
35 poly(dA), 0.2 µg/µl human c_ot1 DNA, and 0.5 % SDS, in a

humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in

both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have
5 sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or
10 both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution
15 hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

20 Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or
25 enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for
30 hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

35 When provided as a collection of plural

individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human Fetal liver.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a

plurality of probes known to be expressed in human Fetal liver. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group
5 consisting of SEQ ID NOS.: 1 - 12,673.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of
10 probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the
15 same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with
20 a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to
25 their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 12,673 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 12,674 - 25,129, that encodes
30 a protein domain. Thus, each of SEQ ID NOS. 1 - 12,673 can be used, or that portion thereof in SEQ ID NOS. 12,674 - 25,129 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

35 Additionally, kits are available commercially

that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT™ Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 12,674 - 25,129. Such amino acid sequences are set out in SEQ ID NOS: 25,130 - 37,156. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

... The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted

in Human Genomic Sequence

Bioinformatics Results

5 All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

10 After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden
15 Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

20 The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of
25 genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed.
30 That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two
35 criteria: (1) any 7 consecutive exons within a 25 kb window

were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon

to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR[®] green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular

Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1×10^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1×10^{-5} to 1×10^{-99}). The remaining 45% of

the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

10

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

15

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single

5 Exon Microarrays

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 10 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message 15 pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial 20 sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 25 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II 30 enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. 35 Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 μ l hybridization solution
5 containing 50% formamide, 5X SSC, 0.2 μ g/ μ l poly(dA), 0.2 μ g/ μ l human c₀t1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC,
10 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics
15 Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference
20 permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact,
25 both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when
30 signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is
35 presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all
5 tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue
10 or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class
15 (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

20 FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative
25 expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results
30 returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant
35 homology (white: E values < 1e-100; gray: E values from 1e-

05 to $1e-99$; black: E values $> 1e-05$).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective
5 tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

10 It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested
15 tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence
20 databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

25 Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The
30 data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for "all" sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and
35 shows in blue the normalized Cy3 signal intensity for all

sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

5 As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

10 However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes
15 will not have been detected in an end-sequenced cDNA library.

 The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and
20 further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

 To ascertain the validity of the approach
25 described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

 Two microarray probes were selected on the basis
30 of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene
35 expression panel 24 human cDNAs) (OriGene Technologies,

Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normal Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin

AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
 5 important in the central nervous system or brain. The exon

giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
5 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
10 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
15 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
20 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to
25 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often
30 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et
35 al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result

duplicated with the array. Other highly expressed chip
 sequences included a translation elongation factor 1 α
 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
 chromosome RNA-binding motif (Chai et al., *Genomics*
 5 49(2):283-89 (1998)) (AC007320-3). A low homology analog
 (AP00123-1/2) to a gene, DSCR1, thought to be involved in
 trisomy 21 (Down's syndrome), showed high expression in
 both brain and heart, in agreement with the literature
 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).
 10 As a further validation of the approach, we
 selected the BAC AC006064 to be included on the array.
 This BAC was known to contain the GAPDH gene, and thus
 could be used as a control for the ORF selection process.
 The gene finding and exon selection algorithms resulted in
 15 choosing 25 exons from BAC AC006064 for spotting onto the
 array, of which four were drawn from the GAPDH gene. Table
 3 shows the comparison of the average expression ratio for
 the 4 exons from BAC006064 compared with the average
 expression ratio for 5 different dilutions of a
 20 commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm

Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

30 FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION
5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene
10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the
15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease
20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb,
25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
30 red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

35

EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

5

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be
10 expressed at significant levels in Fetal liver tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical
15 structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification
20 from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 12,673 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

25 The structures of the 12,673 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 12,673. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the
30 exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 12,674 - 25,129, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

35 As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are

presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human Fetal liver and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human Fetal liver tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 12,674 to 25,129 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS... The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8).

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ - which is probative evidence that the query sequence has previously been shown to be expressed - the top hit is highly unlikely
5 exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present
10 identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached
15 sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 12,673) and probe exon (SEQ ID NOs.: 12,674 - 25,129, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which
20 the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST
25 E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX
30 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

Expression of Genes in Human Fetal liver

Table 4 (526 pages) presents expression, homology, and functional information for the genome-derived single exon
5 probes that are expressed significantly in human Fetal liver.

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human Fetal liver comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,673 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 12,674 - 25,129.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single-exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Fetal liver comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,673 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human Fetal liver.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 12,674 - 25,129 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Fetal liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any
10 of SEQ ID NOs.: 25,130 - 37,156, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Fetal liver.

15 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

20 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one
25 of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30

20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

35 21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample
5 derived from human Fetal liver, comprising:
 contacting the microarray of claim 12, with a first
 collection of detectably labeled nucleic acids,
 said first collection of nucleic acids derived
 from mRNA of human Fetal liver; and then
10 measuring the label detectably bound to each probe of
 said microarray.

23. A method of identifying exons in a eukaryotic genome,
comprising:
15 algorithmically predicting at least one exon from
 genomic sequence of said eukaryote; and then
 detecting specific hybridization of detectably labeled
 nucleic acids to a single exon probe,
wherein said detectably labeled nucleic acids are derived
20 from mRNA from the Fetal liver of said eukaryote, said
probe is a single exon probe having a fragment identical in
sequence to, or complementary in sequence to, said
predicted exon, said probe is included within a microarray
according to claim 12, and said fragment is selectively
25 hybridizable at high stringency.

24. A method of assigning exons to a single gene,
comprising:
 identifying a plurality of exons from genomic
30 sequence according to the method of claim 23; and
 then
 measuring the expression of each of said exons in a
 plurality of tissues and/or cell types using
 hybridization to single exon microarrays having a
35 probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

5 25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 25,129 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 25,129.

10

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 25,130 - 37,156.

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
476	13108	25600	4.41			
822	13535	26053	9.9			
1083	13688		2.9			
1345	13940	28462	10.32			
1656	14248	26782	2.59			
1678	14270	26803	5.03			
1763	14353	26899	1.73			
1765	14375	26919	0.99			
1792	14382	26927	9.24			
1935	14519	27075	1.21			
2021	14603	27168	3.24			
2210	14786	27360	4.38			
2318	14890	27465	2.04			
2607	15169	27735	0.89			
2607	15169	27736	0.89			
3220	15832	28311	1.65			
3498	16101	28576	1.22			
3568	16170	28652	10.28			
3617	16220		0.8			
3718	16319	28787	0.97			
4020	16618		0.94			
4275	16861	29310	1.53			
4348	16835	29376	8.4			
4368	16955	29396	0.74			
4368	16955	29397	0.74			
4430	17016		1.3			
4962	17537	29979	1.04			
5007	17580		0.59			
5054	17627	30071	0.61			
5197	17762	30187	5.95			
5212	17777	30198	1.32			
5462	18097	30415	2.1			
5462	18097	30416	2.1			
5615	18244		5.64			

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5783	18408		9.03				
5859	18244		4.85				
5910	18532	31257	0.84				
5915	18537	31262	3.16				
6173	24759	31552	1.41				
6200	18810	31578	1.65				
6548	18148		1.28				
6668	19264	32067	1				
6688	19264	32068	1				
7178	19711	32559	1.13				
7179	19711	32560	1.13				
7441	19965	32831	1.4				
7441	19965	32832	1.4				
8005	20547	33451	1.65				
8422	20962	33878	1.45				
8784	21333	34257	0.57				
8794	21333	34258	0.57				
9453	21878	34931	4.84				
9681	22180	35155	0.78				
9796	22294	35277	1.19				
9938	22431	35406	1.03				
10214	22709	35702	0.48				
10214	22709	35703	0.48				
10326	22820	35815	0.65				
10326	22820	35816	0.65				
10563	23099		3.08				
10725	24789	36268	2.46				
10906	23425		2.99				
11238	23769	36827	2.73				
11338	23034	36043	1.87				
11338	23034	36044	1.87				
11374	23826		2.59				
12117	24376		2.18				
12439	24576	30914	1.6				

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6203	18813	31583	14.37	9.8E+00	AJ238028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
7948	20480	33400	1.65	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
9658	22157	35128	0.47	9.8E+00	Y18930.1	NT	Sulfobus solfataricus 281 kb genomic DNA fragment, strain P2
9658	22157	35129	0.47	9.8E+00	Y18930.1	NT	Sulfobus solfataricus 281 kb genomic DNA fragment, strain P2
7073	18645	32483	0.8	9.8E+00	AF085630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
7073	18645	32484	0.8	9.8E+00	AF085630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10319	22813	35808	1.22	9.8E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds
10319	22813	35809	1.22	9.8E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds
2889	15247	27814	1.14	8.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2889	15247	27815	1.14	8.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2950	15568	28040	3.19	9.4E+00	AB043785.1	NT	Mus musculus A T3 gene for antithrombin, complete cds
8042	20584	33491	0.99	9.3E+00	AF130980.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
8933	21471	34390	3.48	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5500	18134	30543	2.82	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5500	18134	30544	2.82	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9351	21865		0.9	9.0E+00	P09241	SWISSPROT	RHODOPSIN
6186	18786	31584	5.12	8.9E+00	BE971806.1	EST_HUMAN	601631038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'
6517	19117	31807	1.9	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Cptbx3 premature mRNA, partial cds
6517	19117	31808	1.9	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Cptbx3 premature mRNA, partial cds
465	13099	26590	1.68	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9376	20315	33217	3.8	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
11048	23561		2.47	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8092	20933		0.76	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7384	19810		1.85	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8302	20843	33784	1.54	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8302	20843	33785	1.54	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5988	18589	31324	3.35	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285506 5'
8988	21227	34147	2.63	7.4E+00	P04928	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8688	21227	34148	2.63	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3006	15622	28099	3.19	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
3006	15622	28100	3.19	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
7097	19668	32507	0.7	7.2E+00	BE179080.1	EST_HUMAN	RCO-H10613-200300-031-a07 HT0613 Homo sapiens cDNA
7203	19734	32585	1.22	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7203	19734	32586	1.22	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
9516	22016		7.96	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11263	23791	36848	3.2	7.1E+00	P03850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
9892	22389	35367	3.35	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
11129	23637	36679	1.87	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MSI3
8225	20766	33684	4.06	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10253	22748	35736	1.2	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
7849	20391	33293	1.38	6.8E+00	W03412.1	EST_HUMAN	za07c11.1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:291860 5'
7849	20391	33294	1.38	6.8E+00	W03412.1	EST_HUMAN	za07c11.1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:291860 5'
9060	21597		1.13	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VPS AND VP8]
10110	22605	35595	3.85	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
5488	18122		0.99	6.6E+00	Q89028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
9886	22481	35465	1.89	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
9886	22481	35466	1.89	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
11008	23522		2.13	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C6C3.05C
9108	21644	34584	7.21	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
10206	22701	35695	0.49	6.5E+00	BE866001.1	EST_HUMAN	601678435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3980969 5'
9657	22156	35127	1.11	6.2E+00	AY010901.1	NT	Schizosaccharomyces commune unknown mRNA
10455	22949	35658	0.53	6.2E+00	8754621	NT	Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA
7102	19672	32511	1.34	6.0E+00	BE780163.1	EST_HUMAN	601488031F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3871303 5'
9730	22228	35205	0.46	6.0E+00	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt, position (677)
10407	22901	35696	0.6	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10407	22901	35697	0.6	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
6643	19239	32042	6.67	5.8E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlx3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
3578	18180		1.18	5.8E+00	7661557	NT	Homo sapiens DESCI1 protein (DESCI1), mRNA
7215	19748	32801	0.87	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7215	19748	32802	0.87	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7570	20087		1.31	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11349	23047	36059	2.66	5.6E+00	Q55276	SWISSPROT	LYCOPENE BETA CYCLASE
6399	19002	31780	0.73	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
10858	23190		1.54	5.5E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11348	23046	36058	3.79	5.5E+00	P11890	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
11578	24024		2.08	5.5E+00	AL161571.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 67
7009	19507	32328	1.2	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7009	19507	32327	1.2	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7389	19895		0.72	5.4E+00	Q99435	SWISSPROT	NEL PROTEIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; VITELLOGENIN PRECURSOR (VTG)]
7811	20354		1.58	5.4E+00	Q91062	SWISSPROT	LIPOVITELLIN LV-2
8734	21273	34193	0.78	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
8734	21273	34194	0.78	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
9949	22444	35423	1.33	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
9949	22444	35424	1.33	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4899	17474	29930	1.52	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6814	19211		0.67	5.3E+00	P41779	SWISSPROT	HOMEBOX PROTEIN CEH-20
8024	20566		3.71	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
8914	21452		0.62	5.3E+00	AB034990.1	NT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
5655	18282		1.04	5.2E+00	BE184840.1	EST_HUMAN	Homo sapiens HT0691-270400-186-069 HT0691 Homo sapiens cDNA
10274	22769		0.78	5.2E+00	AF248070.1	NT	Drosophila orientacea R1B retrotransposable element reverse transcriptase gene, partial cds
11074	23586		2.1	5.2E+00	Q10136	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME 1
8892	21430	34354	0.88	5.1E+00	Q16005	SWISSPROT	RHODOPSIN
9739	22237	35217	0.97	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROICIN N IMMUNITY PROTEIN)
6430	19033	31817	0.85	5.0E+00	BF310443.1	EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
10098	22591		0.69	5.0E+00	BF308561.1	EST_HUMAN	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'
10327	22821	35817	3.37	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
11170	23677	36723	13.54	5.0E+00	Z83660.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
10131	22626		0.71	4.9E+00	U01328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4135	16727		12.06	4.8E+00	AF185255.1	NT	Emu australis histone H3 (H3) gene, partial cds
8095	20636	33547	0.65	4.8E+00	BF367809.1	EST_HUMAN	RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA
8478	21017		4.95	4.8E+00	AW750067.1	EST_HUMAN	PM0-BT0547-310100-002-b04 BT0547 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
311	12966	25454	1.88	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4098716 5'
312	12968	25454	1.68	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4098716 5'
3312	15923	28389	1.08	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
9124	21659	34601	1.09	4.6E+00	BE648437.1	EST_HUMAN	7e88g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140 KIAA0645 PROTEIN.; contains element PTR5 repetitive element;
9124	21659	34602	1.09	4.6E+00	BE646437.1	EST_HUMAN	7e88g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140 KIAA0645 PROTEIN.; contains element PTR5 repetitive element;
10280	22785		0.77	4.6E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11474	23924	36984	1.99	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
11595	24039	37108	1.67	4.5E+00	BF688841.1	EST_HUMAN	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
3078	15691	28164	1.53	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4215284 5'
3078	15691	28165	1.53	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4215284 5'
6349	18954		1.8	4.4E+00	X13414.1	NT	Murine Ig gene for MHC class II (Ia) associated invariant chain
6268	18874		0.82	4.3E+00	AF059679.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
7484	19986	32851	2.38	4.3E+00	Y13402.1	NT	Plasmodium falciparum R28R+var1 gene, exon 1
7611	20124	33001	0.84	4.3E+00	AE001222.1	NT	Treponema pallidum section 38 of 87 of the complete genome
10741	23268	36282	8.92	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5708	18334		3.21	4.2E+00	P18444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-1) (RENAL DIPEPTIDASE) (RDP)
5780	18405	31121	1.46	4.2E+00	P51826	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
6869	19003	32435	1.86	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6869	19003	32436	1.86	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
8890	21428	34353	4.95	4.2E+00	AI809013.1	EST_HUMAN	wf67g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360692 3'
8832	22330	35312	2.07	4.2E+00	P31368	SWISSPROT	NUBBIN PROTEIN (TWININ PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
7166	19698	32545	0.81	4.1E+00	BE253668.1	EST_HUMAN	601110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5'
7264	19792	32648	1.7	4.1E+00	BF247839.1	EST_HUMAN	601859030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4069758 5'
7657	20169	33056	8.1	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
7759	20267	33163	4.03	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
7759	20267	33164	4.03	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
7657	20399	33306	2.78	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
9459	21985	34939	0.63	4.1E+00	P11253	SWISSPROT	50S RIBOSOMAL PROTEIN L4
9590	22080	35054	2.26	4.1E+00	BF692425.1	EST_HUMAN	602247898F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10208	22703		0.5	4.1E+00	P46414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27) (P27KIP1)
10489	22893	36003	0.82	4.1E+00	O84242	SWISSPROT	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III)
10765	23289		2.97	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVLF1
10851	23372		13.84	4.1E+00	BE885880.1	EST_HUMAN	601607510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909031 5'
3599	18203		0.82	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5650	18515	32336	0.74	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE; INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
5650	18515	32337	0.74	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE; INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7017	18515	32336	0.95	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE; INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7017	18515	32337	0.95	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE; INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7240	19769	32625	1.34	4.0E+00	Q33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
10070	22565	35560	0.6	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
10158	22653	35647	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
10158	22653	35648	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
11423	23874	36937	3.99	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11423	23874	36938	3.99	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3550	16154	28636	4.79	3.9E+00	X84518.1	NT	N. tabacum chitinase gene 50 for class I chitinase C
4413	16998		0.74	3.9E+00	AF055488.1	NT	Mus musculus seminal vesicle secretory protein 89 (MSVSP89) gene, promoter region
5839	18463	31188	3.08	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
5839	18463	31187	3.08	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
6746	18339	32145	0.71	3.9E+00	AF288208.1	NT	Dictyostelium discoideum non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
6792	18383	32198	0.72	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6955	18532	32357	4.12	3.9E+00	P39299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION
7398	18923	32787	6.09	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.:	Exon SEQ ID NO.:	ORF SEQ ID NO.:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8259	20800	33718	2.15	3.9E+00	X68885.1	NT	X.laavis mRNA for M4 muscarinic receptor
11269	23007	36014	3.27	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
11291	23743	36800	1.62	3.9E+00	AA661489.1	EST_HUMAN	nt18a12.s1 NC1_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1188318 similar to gb:A10416
2658	15217		1.1	3.8E+00	AE001562.1	NT	METALLOPROTEINASE INHIBITOR.1 PRECURSOR (HUMAN);
6525	18125	31918	0.78	3.8E+00	Q57830	SWISSPROT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
8371	20911	33831	1.06	3.8E+00	D44725.1	EST_HUMAN	HYPOTHETICAL PROTEIN MJ0385
9710	22208		0.55	3.8E+00	AJ390961.1	NT	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
4092	16887	28144	13.56	3.7E+00	AL161539.2	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7864
7218	19749		0.79	3.7E+00	AL445065.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
							Thermoplasma acidophilum complete genome; segment 3/5
							Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene encoding mitochondrial protein, mRNA
8842	21181		0.53	3.7E+00	4503950	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
8105	21641	34581	0.68	3.7E+00	U43541.1	NT	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11308	23801	36861	3.11	3.7E+00	BF669278.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11308	23801	36862	3.11	3.7E+00	BF669278.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11767	24158		1.28	3.7E+00	AB013746.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
619	13246	25719	2.6	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
4917	17492		0.99	3.6E+00	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
8487	21026	33942	0.76	3.6E+00	D12367.1	EST_HUMAN	HUM000TB08 Liver HepG2 cell line, Homo sapiens cDNA clone tb08
8487	21026	33943	0.76	3.6E+00	D12367.1	EST_HUMAN	HUM000TB08 Liver HepG2 cell line, Homo sapiens cDNA clone tb08
8579	21118	34038	4.02	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
8579	21118	34039	4.02	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
							Escherichia coli glycerophosphate dehydrogenase (glpD) gene, partial cds, and the translation start site has been verified (glpE), the translation start site has been verified (glpG), and repressor protein (glpR) genes, complete cds
10733	23259		4.32	3.6E+00	M96795.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
3284	15895	28373	1.08	3.5E+00	AF221538.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
8151	18784		1.08	3.5E+00	L42898.1	NT	Y940C08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34940 5'
6360	18984	31742	0.92	3.5E+00	R19745.1	EST_HUMAN	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
8421	20961		0.55	3.5E+00	P24657	SWISSPROT	z88b04.s1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element;contains element MSR1 repetitive element ;
8962	21500	34421	0.88	3.5E+00	AA190998.1	EST_HUMAN	z88b04.s1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element;contains element MSR1 repetitive element ;
8962	21500	34422	0.88	3.5E+00	AA190998.1	EST_HUMAN	z88b04.s1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element;contains element MSR1 repetitive element ;
9414	21623	34872	1.12	3.5E+00	AL161553.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1559	14151	26883	4.49	3.4E+00	AF254577.1	NT	Brassica napus RP85d mRNA, complete cds
2612	15174	27742	1.02	3.4E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7397	19922	32786	2.95	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7690	20199	33086	0.86	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8611	21150		0.89	3.4E+00	U65406.1	NT	Human alternatively spliced poliovirus channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNJ1) gene, complete cds
9003	21540	34470	0.7	3.4E+00	AJ228042.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6
9040	21577	34506	0.5	3.4E+00	AJ250567.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
10165	22660	35655	3.61	3.4E+00	AF013167.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
11406	23857	36922	1.98	3.4E+00	L77570.1	NT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
6218	18828	31601	0.9	3.3E+00	Q09869	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
6218	18828	31602	0.9	3.3E+00	Q09869	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
7634	20376	33281	0.88	3.3E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10361	22855	35847	0.87	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
10361	22855	35848	0.87	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
528	13158	25840	1.72	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
4098	13158	25840	0.7	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
4835	17413	29866	1.24	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5757	18383	31085	1.34	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5757	18383	31096	1.34	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5787	18412	31128	2.45	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5787	18412	31129	2.45	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6448	19049	31834	1.86	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6448	19049	31835	1.86	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7601	20114	32981	0.84	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7750	20258	33154	2.22	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7750	20258	33155	2.22	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
8960	21498		4.84	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
9449	21975	34927	1.52	3.2E+00	M36383.1	NT	S. cerevisiae threonine deaminase (ILV1) gene, complete cds
10047	22542	35539	1.91	3.2E+00	AB016081.2	NT	Oryzias latipes OIGC6 gene for guanylyl cyclase C, complete cds
11727	24133		4.08	3.2E+00	L33838.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
8035	18654	31396	2.24	3.1E+00	Q10135	SWISSPROT	HYPOTHEICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7421	18945	32810	0.97	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7711	20220		1.09	3.1E+00	AF303225.1	NT	Bacillus alcalophilus peckate lyase (pelE) gene, complete cds
8538	21077	33995	4.27	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5DEIODINASE) (DIOI) (TYPE 1 DIO) (5DI)
8538	21077	33996	4.27	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5DEIODINASE) (DIOI) (TYPE 1 DIO) (5DI)
9183	21760		3.77	3.1E+00	Q14957	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9249	21775	34728	0.52	3.1E+00	Q01149	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9810	22308	35292	0.75	3.1E+00	7524759	NT	Chlorelia vulgaris chloroplast, complete genome
9899	22396		0.56	3.1E+00	Q10125	SWISSPROT	HYPOTHETICAL 58.3 KD PROTEIN F52C9.5 IN CHROMOSOME III
10239	22734	35728	4.7	3.1E+00	P49365	SWISSPROT	DEOXYHYPOSINE SYNTHASE (DHS)
11338	23036		2.91	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN[CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11355	23809		7.48	3.1E+00	S66860.1	NT	retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]
12490	24619		1.38	3.1E+00	U77666.1	NT	Brassica rapa pollen coat protein homodog (BAN103) gene, complete cds
5541	18173	30588	1.68	3.0E+00	X53096.1	NT	S aureus genes encoding Sau961 DNA methyltransferase and Sau961 restriction endonuclease
6873	19269	32073	0.72	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6873	19269	32074	0.72	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7209	19740		10.44	3.0E+00	P18408	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7247	19776		0.77	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
8838	21377		1.33	3.0E+00	X87838.1	NT	B.napus DNA for myosinase
10185	22690	35683	0.53	3.0E+00	Q58605	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYL TRANSFERASE) (ADOMET SYNTHETASE)
10927	23064	36075	1.62	3.0E+00	Q16181	SWISSPROT	ODC10 PROTEIN HOMOLOG
10888	23409	36428	7.04	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
10888	23409	36427	7.04	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
2055	14636	27207	2.32	2.9E+00	AE002225.2	NT	Chlamydomonas reinhardtii AR39, section 53 of 94 of the complete genome
6224	18833		0.68	2.9E+00	AB028033.1	NT	Bonaparitia pedicellata mitochondrial DNA for 16S ribosomal RNA
6989	19487	32309	3.74	2.9E+00	Z36879.1	NT	F.pringlei gdsP A gene for P-protein of the glycine cleavage system
7262	19790	32644	4.37	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR

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7262	19790	32845	4.37	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7479	20001	32866	6.04	2.8E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
7809	20352	33260	0.67	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
7809	20352	33261	0.67	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8041	20583	33490	0.89	2.8E+00	BF344171.1	EST_HUMAN	602017413F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4153059 5'
1504	14096	28634	4.87	2.8E+00	AF186398.1	NT	Buxus harlandii maturase K (matK) gene, partial cds; chloroplast gene for chloroplast product
1875	14287		3.45	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7348	19874	32740	4.88	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
9531	22031		0.57	2.8E+00	BE565182.1	EST_HUMAN	601342758F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5'
10569	19874	32740	1.68	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
251	12811	25394	9.31	2.7E+00	8676306	NT	Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA
251	12911	25395	9.31	2.7E+00	8676306	NT	Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA
5740	18366	31073	1.2	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
8088	20828		0.8	2.7E+00	U15947.1	NT	Iponoea purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
8898	21436		1.68	2.7E+00	AL116459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9353	20292	33191	0.63	2.7E+00	AW088191.1	EST_HUMAN	xc88e12.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb:M17733
10394	22868		1.48	2.7E+00	BE063527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4781	17362	29812	4.97	2.6E+00	AF068749.1	NT	CMO-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
5736	18362	31068	1.94	2.6E+00	6755601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5736	18362	31069	1.94	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5892	18812		2.42	2.6E+00	Y17062.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7689	20198		5.98	2.6E+00	AF235502.1	NT	Mycobacterium fortuitum furA II gene
8003	20545	33447	1.08	2.6E+00	AJ132180.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
8003	20545	33448	1.08	2.6E+00	AJ132180.1	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
9576	22756	35039	3.02	2.6E+00	AL161540.2	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
10257	22072		1.51	2.6E+00	8955193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10607	23426	38443	1.69	2.6E+00	AF143675.1	NT	Arabidopsis cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12390	24988		2.78	2.6E+00	11419220	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1513	14105	26640	2.28	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1513	14105	26641	2.28	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
1513	14105	26641	2.28	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

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5981	18601	31334	1.71	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5981	18601	31335	1.71	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5986	18601	31334	1.39	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5986	18601	31335	1.39	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6828	19418	32234	0.73	2.5E+00	D30052.1	NT	Vibrio cholerae cbaA gene and cbaB gene for cholera toxins, complete cds
7736	20244	33135	1.05	2.5E+00	AW949158.1	EST_HUMAN	QV4-FT0005-110500-205-g07 FT0003 Homo sapiens cDNA
9032	21569	34488	1.75	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
9766	22264	35247	0.88	2.5E+00	BE297758.1	EST_HUMAN	601175770F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531090 5'
11724	24131		1.68	2.5E+00	AF289665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
3047	15663	28144	0.9	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
5033	17607	30052	6.78	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
6161	18774	31538	4.02	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
8082	20624	33536	1.99	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8082	20624	33537	1.99	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8153	20694		2.33	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8585	21124		1.62	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA
8762	21301	34222	8.16	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
9951	22446	35427	2.59	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
9951	22448	35428	2.59	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10017	22512	35504	1.62	2.4E+00	X92511.1	NT	H. sapiens CTGF gene and promoter region
10141	22636		7.38	2.4E+00	P09099	SWISSPROT	XYLULOSE KINASE (XYLUKINASE)
10225	22720	35710	1.63	2.4E+00	BE326702.1	EST_HUMAN	hr63f08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10225	22720	35711	1.63	2.4E+00	BE326702.1	EST_HUMAN	hr63f08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10483	22977	35988	1.27	2.4E+00	Q31481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ
10958	23473	36498	1.68	2.4E+00	Y14079.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: gfpPKD operon and downstream
11237	23768	36828	2.27	2.4E+00	AF158652.2	NT	Frederia x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1296	13890	26413	11.15	2.3E+00	Z46724.1	NT	G domesticus artificial single chain antibody gene (L3)
4199	18788		1.65	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b
6000	18620		0.81	2.3E+00	N86245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYLCARBOXYPEPTIDASE
7477	19999	32864	2.54	2.3E+00	6978554	NT	Rattus norvegicus ATPase, Cav+ transporting, ubiquitous (Atp2a3), mRNA
7593	25120		4.61	2.3E+00	P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
7758	20284	33159	1.06	2.3E+00	X60265.1	NT	M.mazei dnaK and dnaJ genes homologues coding for DnaK and DnaJ

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9038	21575	34505	0.53	2.3E+00	5835317	NT	Polypterus ornatipinnis mitochondrion, complete genome
9097	21633	34572	1.79	2.3E+00	Q11127	SWISSPROT	ALPHA(1.3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)
10681	23213	36224	2	2.3E+00	Q07076	SWISSPROT	ANNEXIN VII (SYNEXIN)
11612	24055	37119	2.92	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
11612	24055	37120	2.92	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
11950	24278	31020	7.31	2.3E+00	BE895237.1	EST_HUMAN	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918843 5'
4089	16685	29143	91.07	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4403	16988	29432	4.5	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4403	16988	29433	4.5	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
5545	18177	30591	12.27	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5545	18177	30592	12.27	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
6016	18635	31373	0.95	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-008 CT0254 Homo sapiens cDNA
6016	18635	31374	0.95	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-008 CT0254 Homo sapiens cDNA
6212	18622	31593	9.1	2.2E+00	BE250383.1	EST_HUMAN	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
8495	19096	31880	4.32	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6709	18303	32107	3.04	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7037	18057		3.58	2.2E+00	AA594574.1	EST_HUMAN	n195b02.s1 NCL_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1058379 3'
7358	19884	32747	0.9	2.2E+00	AA137027.1	EST_HUMAN	zn9704.r1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:566143 5'
7602	20115	32982	25.23	2.2E+00	AA449012.1	EST_HUMAN	z05g10.r1 Soares_t041 Fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785634 5'
8046	20588	33494	0.65	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
8046	20588	33495	0.65	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
9265	21791		12.17	2.2E+00	BE741678.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
9488	24783		2.57	2.2E+00	Q04708	SWISSPROT	TRANSPONOSON TY1 PROTEIN A
9966	22461	35443	1.96	2.2E+00	AI280373.1	EST_HUMAN	qm56b03.x1 Soares_placenta_8to8weeks_2NBHP8t9w Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9866	22481	35444	1.96	2.2E+00	AI290373.1	EST_HUMAN	qim6b03.x1 Soares_placenta_8to9weeks_2nbHP8to9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10008	22503	35494	3.7	2.2E+00	BF248782.1	EST_HUMAN	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
10353	22847	35841	2.99	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
11316	23014	36023	4.01	2.2E+00	P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
11482	23832	37003	4.23	2.2E+00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
595	15419	25699	6.28	2.1E+00	AF132612.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3648	16251		0.65	2.1E+00	AW449366.1	EST_HUMAN	UIH-B13-aki-e08-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6281	18889		0.85	2.1E+00	P78357	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6898	19633	32471	3.38	2.1E+00	O70159	SWISSPROT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
7110	19450	32268	5.13	2.1E+00	N29575.1	EST_HUMAN	yw08a10.s1 Soares_melanocyte_2nbHM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654
8434	20974		2.27	2.1E+00	AU123630.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
10454	22848		0.58	2.1E+00	Y10284.1	NT	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000871 5'
1238	13836	26352	1.3	2.0E+00	AF180527.1	NT	H. sapiens TRAF1 gene, putative promoter region
1238	13836	26353	1.3	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1380	13973	26501	0.92	2.0E+00	AF204927.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1618	14212		2.89	2.0E+00	P25582	SWISSPROT	Oryctolagus cuniculus Na ⁺ K ⁺ -ATPase beta 1 subunit mRNA, complete cds
2194	14770	27343	3.69	2.0E+00	Z78278.1	NT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2194	14770	27344	3.69	2.0E+00	Z78278.1	NT	R. norvegicus mRNA for collagen alpha1 type I
4176	16767	29215	1.9	2.0E+00	AW684496.1	EST_HUMAN	R. norvegicus mRNA for collagen alpha1 type I
4176	16767	29216	1.9	2.0E+00	AW684496.1	EST_HUMAN	hi13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
7552	20071		0.77	2.0E+00	P07566	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7987	20509	33415	3.56	2.0E+00	AB008876.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7987	20509	33416	3.56	2.0E+00	AB008876.1	NT	hi13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
7987	20509	33417	3.56	2.0E+00	AB008876.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8853	21392	34314	3.62	2.0E+00	F31500.1	EST_HUMAN	STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
12295	24946	30622	7.77	2.0E+00		NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
5784	18409	31124	6.89	1.9E+00	6754389	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
5784	18409	31125	6.89	1.9E+00	6754389	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6249	18858	31630	1.2	1.9E+00	BE869695.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117808
						NT	Gallus gallus mitochondrion, complete genome
						NT	Mus musculus inositol 1,4,5-trisphosphate receptor 1 (ltp1), mRNA
						NT	Mus musculus inositol 1,4,5-trisphosphate receptor 1 (ltp1), mRNA
						EST_HUMAN	601878636F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6760	19353		1.02	1.9E+00	AW845689.1	EST_HUMAN	MR0-CT0063-071099-002-g02 CT0063 Homo sapiens cDNA
6845	19435		2.31	1.9E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN R44
8396	20836	33858	2.16	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8396	20836	33859	2.16	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8593	21132		2.45	1.9E+00	BF360206.1	EST_HUMAN	CM3-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA
8825	21364		1.35	1.9E+00	O51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
9548	22048	35009	0.6	1.9E+00	AA689125.1	EST_HUMAN	ab94a04.s1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element; contains element L1 L1 repetitive element;
10458	22950	35959	0.52	1.9E+00	AF248269.1	NT	Homo sapiens gag-pro-poi precursor protein gene, partial cds
3128	15742	28211	1.98	1.9E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3154	15768	28234	2.42	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3154	15768	28235	2.42	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
6027	18648		2.02	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
8253	18802	31634	2.02	1.8E+00	BF311989.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
8532	19132		1.53	1.8E+00	BF683327.1	EST_HUMAN	602139470F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4298272 5'
6838	19428	32244	1.35	1.8E+00	BF305652.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7119	19459	32274	1.08	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
8060	20602	33512	0.81	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8060	20602	33513	0.81	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8788	21327	34252	2.12	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9102	21638	34577	0.63	1.8E+00	R31042.1	EST_HUMAN	y7208.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
9186	21703	34845	0.8	1.8E+00	AW880004.1	EST_HUMAN	QV0-O10030-070300-148-a03 OT0030 Homo sapiens cDNA
9763	22811	35244	0.87	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10183	22878		3.78	1.8E+00	AF111849.1	NT	Homo sapiens PRO0530 mRNA, complete cds
10447	22941		0.85	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE [CYTIDINE AMINOHYDROLASE] (CDA)
12075	24915		8.85	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12163	24403		4.86	1.8E+00	9506404	NT	Rattus norvegicus Actin-related protein complex 1b (Apc1b), mRNA
12476	24815	30790	1.38	1.8E+00	BF212412.1	EST_HUMAN	601813714F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048251 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1147	13750	26259	2.08	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2311	14883	27458	2.37	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2411	14879	27554	1.29	1.7E+00	AI141067.1	EST_HUMAN	oz43H05.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4558	17141	29589	0.74	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5797	18422	31137	1.65	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
5797	18422	31138	1.65	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
6188	18780	31545	3.35	1.7E+00	Q81TR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)
7270	18786	32654	1.33	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7270	18786	32655	1.33	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7306	19834	32693	1.63	1.7E+00	P20393	SWISSPROT	ORPHAN NUCLEAR RECEPTOR NR1D1 (V-ERBA RELATED PROTEIN EAR-1) (REV-ERBA-ALPHA)
7796	20339	33247	0.96	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
7976	20518	33425	1.34	1.7E+00	8755715	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Tall), mRNA
8006	20548	33452	0.57	1.7E+00	BF530630.1	EST_HUMAN	602071817F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4214669 5'
8479	21018	33933	0.61	1.7E+00	AF245513.1	NT	Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete cds
8582	21101		2.08	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
8638	21177	34086	0.49	1.7E+00	X69063.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
8638	21177	34087	0.49	1.7E+00	X69063.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
9076	24782	34545	2.25	1.7E+00	O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9076	24782	34546	2.25	1.7E+00	O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9524	22024		1.65	1.7E+00	AF161380.1	NT	Homo sapiens HSPC262 mRNA, partial cds
11467	23917	36985	2.16	1.7E+00	W22424.1	EST_HUMAN	87B7 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
12030	24320	30993	1.52	1.7E+00	A1678443.1	EST_HUMAN	tu82d07.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.11
12558	24659	30873	1.79	1.7E+00	A1198573.1	EST_HUMAN	MSR1 repetitive element
2078	14658	27228	21.82	1.6E+00	AF199338.1	NT	qf50b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.11 L1 repetitive element
2087	14688	27238	4.3	1.6E+00	AF077374.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2093	14673	27243	1.04	1.6E+00	Y11344.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2323	14894		1.13	1.6E+00	X98373.1	NT	Mus musculus ST6GalNAcII gene, exon 2
2888	15604	28084	1.5	1.6E+00	W58426.1	EST_HUMAN	B. napus gene encoding endo-polygalacturonase
4104	16698		7.23	1.6E+00	BF570077.1	EST_HUMAN	zid5f01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D29805 N-ACETYL-LACTOSAMINE SYNTHASE (HUMAN);
							602186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'

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4444	17030	29470	1.11	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4444	17030	29471	1.11	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5145	17715	30145	0.6	1.6E+00	AF075394.1	NT	Uroteuthis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5145	17715	30146	0.6	1.6E+00	AF075394.1	NT	Uroteuthis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5243	17807	30228	2.2	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5243	17807	30229	2.2	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5993	18613	31347	1.95	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2*01 gene, 3' end
6072	18613	31434	0.92	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (TgaseI) gene, promoter region
6596	19193	31998	0.83	1.6E+00	BF380703.1	EST_HUMAN	IL2UT0073-060900-145-E02 UT0073 Homo sapiens cDNA
6811	19402	32218	1.07	1.6E+00	AW284881.1	EST_HUMAN	U1-H-512-ahr-b-04-0-U1.s1 NCL CGAP Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7293	19821	32880	2.32	1.6E+00	BE697287.1	EST_HUMAN	RQ9-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA
7973	20515		1.09	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
8320	20861	33786	3.24	1.6E+00	AJ287131.1	NT	Mus musculus SIL, MAP 17, CYP_a, SCL & CYP_b genes
8831	21370	34284	0.95	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
8831	21370	34285	0.95	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9381	24790	33221	3.16	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-1
9381	24790	33222	3.16	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-1
9649	22148	35119	1.34	1.6E+00	T41280.1	EST_HUMAN	ph6b6_19/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph6b6_19/1TV
10052	22547	35541	0.52	1.6E+00	AF121381.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Ial (IAL), and zinc finger protein (DNZ1) genes, complete cds
10088	22583	35575	0.92	1.6E+00	AW835644.1	EST_HUMAN	QV4LT0018-090200-100-d07 LT0018 Homo sapiens cDNA
10088	22583	35576	0.92	1.6E+00	AW835644.1	EST_HUMAN	QV4LT0018-090200-100-d07 LT0018 Homo sapiens cDNA
10248	22741	35731	0.49	1.6E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
10650	23182	36198	1.59	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
10886	23216	36228	1.56	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
10723	18689	31434	6.41	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (TgaseI) gene, promoter region
11552	24000	37072	2.92	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
35	12714	25173	4.02	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
252	12912	25396	2.17	1.5E+00	AE002201.2	NT	Chlamydomonas reinhardtii AR39, section 32 of 94 of the complete genome
649	13272		1.98	1.5E+00	6752981	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metagardlin) (Adam15), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1960	14544	27101	2.55	1.5E+00	AF275265.1	NT	Mus musculus receptor protein tyrosine phosphatase-rho (Ptpn) gene, exons 10 and 11 and partial cds
2454	15021	27592	2.13	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2558	15120	27690	1.83	1.5E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3172	15021	27592	1.54	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3421	16028	28510	0.7	1.5E+00	AE001945.1	NT	Dainococcus radiodurans R1 section 8.2 of 229 of the complete chromosome 1
5903	18525	31250	0.94	1.5E+00	AI855301.1	EST_HUMAN	HKF-1.1
5903	18525	31251	0.94	1.5E+00	AI855301.1	EST_HUMAN	HKF-1.1
6538	19137	31630	2.68	1.5E+00	R17879.1	EST_HUMAN	Y910602.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
7182	19714		1.37	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
7214	19745	32599	20.84	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7214	19745	32600	20.84	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7383	19809	32774	1.02	1.5E+00	AA889259.1	EST_HUMAN	ak2610.s1 Soares testis NIH_MGC_71 Homo sapiens cDNA clone IMAGE:14071153
8095	20607	33519	0.85	1.5E+00	BE887446.1	EST_HUMAN	601509586F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8578	21117	34037	1.1	1.5E+00	K02138.1	NT	Mouse germline IgM chain gene, mu-delta region
8946	21494		0.53	1.5E+00	AB038516.1	NT	Homo sapiens hGPIb alpha gene for platelet glycoprotein Ib alpha, complete cds
9081	21598	34528	0.54	1.5E+00	BF217818.1	EST_HUMAN	601882682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095135 5'
9404	21813	34862	0.9	1.5E+00	R81928.1	EST_HUMAN	y03h01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147697 5'
9553	22053	35016	1.12	1.5E+00	AW375697.1	EST_HUMAN	QV3-CT0192-281099-008-d09 CT0192 Homo sapiens cDNA
9774	22272	35257	5.97	1.5E+00	BF376754.1	EST_HUMAN	RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
9865	22460		1.47	1.5E+00	BF37944.1	EST_HUMAN	602035771F1 NCL_CGAP_Brm84 Homo sapiens cDNA clone IMAGE:4183865 5'
10098	22593	35585	2.95	1.5E+00	AA017689.1	EST_HUMAN	z638g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381306 5'
10098	22593	35586	2.95	1.5E+00	AA017689.1	EST_HUMAN	z638g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381306 5'
11277	23730	36785	4.1	1.5E+00	AL134197.1	EST_HUMAN	DKFZ547P243_s1 547 (synonym: hfor1) Homo sapiens cDNA clone DKFZ547P243 3'
11416	23867		9.57	1.5E+00	X07380.1	NT	Maize mitochondrial RNA-Sar gene and RNA-Phe pseudogene
12022	25010	30615	1.59	1.5E+00	D63480.1	NT	Human mRNA for KIAA0146 gene, partial cds
12255	24465		4.99	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
32	12711	25169	1.8	1.4E+00	7661885	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
32	12711	25170	1.8	1.4E+00	7661885	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1774	14384	26809	1.32	1.4E+00	H19859.1	EST_HUMAN	y057e03.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172540 5'
2316	14888		0.98	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds
2372	14942		7.8	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2693	15250	27820	1.45	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2802	15354	27822	2.79	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2802	15354	27823	2.79	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3376	15985		0.68	1.4E+00	5453733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4342	16929	29369	1.14	1.4E+00	AW900455.1	EST_HUMAN	CMO-NN1005-140300-288-h08 NN1005 Homo sapiens cDNA
4342	16929	29370	1.14	1.4E+00	AW900455.1	EST_HUMAN	CMO-NN1005-140300-288-h08 NN1005 Homo sapiens cDNA
4685	17267		1.78	1.4E+00	BF681547.1	EST_HUMAN	602156687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'
5575	18206	30657	1.78	1.4E+00	AW054976.1	EST_HUMAN	w45g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5719	18345		5.04	1.4E+00	AB032883.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6425	19028	31811	2.73	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6437	25118		4.4	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
6544	19143	31936	2.32	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6544	19143	31937	2.32	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6583	19181	31981	0.67	1.4E+00	11086333	NT	Mus musculus WW domain binding protein 11 (Wbp11-pending), mRNA
6911	19570	32398	0.77	1.4E+00	AW893057.1	EST_HUMAN	CM3-NN0006-300300-132-512 NN0006 Homo sapiens cDNA
7330	19857	32720	2.31	1.4E+00	AJ133269.1	NT	Homo sapiens cavedin-1/-2 locus, Contig 1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7343	19870	32735	1.1	1.4E+00	AW467760.1	EST_HUMAN	he23f05.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918873 3' similar to contains Alu repetitive element;
8277	20818		0.68	1.4E+00	P07683	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE)(1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8729	21288		4.01	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
9023	21560	34487	2.13	1.4E+00	R20459.1	EST_HUMAN	y933f12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5'
9125	21660	34803	3.72	1.4E+00	BE084687.1	EST_HUMAN	RC1-BT0313-301299-012-05 BT0313 Homo sapiens cDNA
9158	21693	34837	0.58	1.4E+00	AF134844.1	NT	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds
10109	22604	35594	0.77	1.4E+00	BE157545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10150	22645	35637	0.67	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291039-008-C04 HT0198 Homo sapiens cDNA
10150	22645	35638	0.67	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291039-008-C04 HT0198 Homo sapiens cDNA
10418	22912	35912	1.11	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10418	22912	35913	1.11	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10948	23463	36485	2.16	1.4E+00	AA195528.1	EST_HUMAN	z36a09.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:665512 5' similar to contains element MER22 repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11104	23614	36654	6.28	1.4E+00	AB006882.1	NT	Homo sapiens APECED mRNA for AIRE-1, complete cds
11263	23736	36781	3.92	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11283	23736	36782	3.92	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11304	23797	36855	3.18	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11304	23797	36858	3.19	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11865	24935		2.43	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
12287	25108		2.38	1.4E+00	11645838	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen sa70-2 (SE70-2), mRNA
596	13225		1.38	1.3E+00	Z73640.1	NT	M.mucedo gene encoding 4-Dihydropyrimidin-trisporate dehydrogenase
935	13548	26065	2.33	1.3E+00	AJ271182.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1168	13770		22.19	1.3E+00	Y19213.1	NT	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
1340	13835	26458	13.67	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1340	13835	26457	13.67	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1400	13994		1.05	1.3E+00	U61730.2	NT	Cod lacrymae-jodi dihydrolipicolinate synthase (dapA) gene, complete cds
1653	14245		2.35	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 85 of the complete genome
2285	14859		1.1	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2586	15149		0.97	1.3E+00	BE966735.2	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
2966	15581	28060	0.66	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA
3657	16260	28732	0.81	1.3E+00	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete cs
4713	15581	28060	1.31	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA
5184	17749	30178	0.92	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5184	17749	30178	0.92	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5705	18331	30835	1.06	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOXYGENASE P3 COMPONENT)
6169	18781	31546	7.47	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291189-004-f08 CT0289 Homo sapiens cDNA
6169	18781	31547	7.47	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291189-004-f08 CT0289 Homo sapiens cDNA
6549	19147		1.24	1.3E+00	M33496.1	NT	D.melanogaster no-on-transient A gene product, complete cds
6847	19437		0.71	1.3E+00	Q00156	SWISSPROT	HYPOTHETICAL GENE 84 PROTEIN
6928	19585	32415	0.85	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds
7033	19587	32394	1.01	1.3E+00	BE536819.1	EST_HUMAN	601081420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447965 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7157	19689	32533		0.79	BE243571.1	EST_HUMAN	TCBAP1D0959 Pediatric pre-B cell acute lymphoblastic leukemia BAYLOR-HCSC project=TCBA Homo sapiens cDNA clone TCBAP0959
7481	20003	32888		3.97	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8239	20780	33701		2.06	AJ009912.1	NT	Sus scrofa plp gene
8394	20924	33844		2.54	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866195 3'
8496	21035	33956		0.89	BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
8644	21183			1.57	6910247	NT	Homo sapiens GL004 protein (GL004), mRNA
8725	21264	34184		0.88	A1927629.1	EST_HUMAN	wo85a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9073	21610	34540		0.48	H42881.1	EST_HUMAN	yo68c03.s1 Soares breast 3NHBst Homo sapiens cDNA clone IMAGE:183076 3'
9073	21610	34541		0.48	H42881.1	EST_HUMAN	yo68c03.s1 Soares breast 3NHBst Homo sapiens cDNA clone IMAGE:183076 3'
9434	21860			4.54	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
9443	21969	34917		2.12	X72018.1	NT	S. alba phr-1 mRNA for photolyase
9443	21969	34918		2.12	X72019.1	NT	S. alba phr-1 mRNA for photolyase
9542	22042	35003		1.1	AF059250.1	NT	Homo sapiens lipoxigenase (ALOX12B) mRNA, complete cds
9588	22088	35052		1.62	O00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
9665	22164	35137		1.21	A1927629.1	EST_HUMAN	wo85a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9740	22238	35218		0.83	AJ223862.1	NT	Lactococcus lactis cremoris NCDO-inv1 chromosomal inversion junction DNA
9740	22238	35219		0.83	AJ223862.1	NT	Lactococcus lactis cremoris NCDO-inv1 chromosomal inversion junction DNA
9780	22278	35263		3.85	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866195 3'
10114	22609	35600		1.25	AE004392.1	NT	Vibrio cholerae chromosome II, section 49 of 83 of the complete chromosome
10130	22625	35615		2.41	M29853.1	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10476	22970			0.65	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10504	22998			0.52	8923637	NT	Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA
10507	23001	36008		0.48	H42881.1	EST_HUMAN	yo68c03.s1 Soares breast 3NHBst Homo sapiens cDNA clone IMAGE:183076 3'
10507	23001	36009		0.48	H42881.1	EST_HUMAN	yo68c03.s1 Soares breast 3NHBst Homo sapiens cDNA clone IMAGE:183076 3'
10573	23108			4.66	Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE)(HYDANTOINASE) (DHP)
10785	23309	36316		2.3	P25289	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
10807	23330	36342		2.17	Z18892.2	NT	Mus musculus desmin gene
11215	23718			1.87	A1927629.1	EST_HUMAN	wo85a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2739868 3'
11414	23865	36928		3.09	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11488	23937	37007		3.09	Z98882.1	NT	Bacillus subtilis genomic DNA 23.9kB fragment
12011	24312			3.63	AF187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds

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12182	24423	30948	3.47	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCI_COAP_Bm67 Homo sapiens cDNA clone IMAGE:4158452 5'
12204	24826		1.78	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12303	24500		2.08	1.3E+00	AF187035.1	NT	Sturnira lilium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
12673	24904		1.25	1.3E+00	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
678	13302	25784	9.75	1.2E+00	AA676246.1	EST_HUMAN	Z122408.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
858	13472	25983	1.04	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
858	13472	25984	1.04	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
858	13472	25985	1.04	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
911	13524		1.9	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1203	13803	26316	4.97	1.2E+00	AF080245.2	NT	Elais oleifera sesquiterpene synthase mRNA, complete cds
1247	13844	26361	1.3	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1247	13844	26362	1.3	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2054	14635	27208	53.59	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
2417	14985	27559	1.53	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
3144	15758	28224	1.16	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3201	15813	28287	7.17	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3201	15813	28288	7.17	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3326	15935		3.43	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3399	16007	28489	0.57	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3774	16374	28839	8.66	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4058	16555	29121	1.87	1.2E+00	BF373570.1	EST_HUMAN	MRO-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA
4386	16007	28489	1.12	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4570	17153		2.09	1.2E+00	M87060.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4821	17204	29653	1.08	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4859	17241	29695	1.5	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4890	17272		9.41	1.2E+00	Y09200.1	NT	T. pinnaeum chloroplast rbcL gene, partial
4791	18008		0.77	1.2E+00	M81778.1	NT	G.gallus T-cadherin mRNA, complete cds
5629	18258	30729	1.06	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5743	18369	31077	2.27	1.2E+00	AW813278.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
6034	18653	31395	0.72	1.2E+00	AF016032.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6300	18908	31679	2.17	1.2E+00	X74885.1	NT	D.hydrel ayl repeat cluster DNA, fragment D
6361	18965	31743	3.98	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA
6433	19036	31822	1.43	1.2E+00	X89084.1	NT	C-glutamicum pla gene and ackA gene
6433	19036	31823	1.43	1.2E+00	X89084.1	NT	C-glutamicum pla gene and ackA gene

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6475	19076	31859	34.96	1.2E+00	AA759254.1	EST_HUMAN	ah94g12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374 3'
6628	19225	32030	2.25	1.2E+00	AW813278.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
6995	19493	32314	1.18	1.2E+00	AB029010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7007	19505	32324	2.8	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
7300	19828		0.8	1.2E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
7417	24782	32808	1.59	1.2E+00	AV734585.1	EST_HUMAN	AV734585 cda Homo sapiens cDNA clone cdaAFH03 5'
7648	20158	33045	2.84	1.2E+00	X74207.1	NT	L.lactis pyD and pyrF genes
8504	21043	33964	3.05	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
							ALPHA-ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE GLUCOSYLTRANSFERASE)
8597	21136	34051	0.69	1.2E+00	P38427	SWISSPROT	Homo sapiens CGI-30 protein (LOC51811), mRNA
8809	21348		0.53	1.2E+00	7706271	NT	MR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA
8855	21493	34416	2.03	1.2E+00	AW377210.1	EST_HUMAN	R. communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
9319	21833	34783	2.92	1.2E+00	Z32850.1	NT	HUMHM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01
9523	22023	34981	1.88	1.2E+00	D11745.1	EST_HUMAN	H.sapiens ENO3 gene for muscle specific endase
9844	22342	35324	3.47	1.2E+00	X58832.1	NT	Homo sapiens kioho gene, exon 1
10228	22724		0.67	1.2E+00	AB009668.1	NT	PM0-ST0284-161199-001-d01 ST0284 Homo sapiens cDNA
11224	23755	36813	2.19	1.2E+00	AW817817.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
11282	23780		6.64	1.2E+00	BE160761.1	EST_HUMAN	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
11331	23029	36038	3.76	1.2E+00	U50147.1	NT	Homo sapiens chromosome 21 segment HS21C003
11976	24807	30712	32.4	1.2E+00	AL163203.2	NT	Bacillus halodurans genomic DNA, section 9/14
11998	24304		2.11	1.2E+00	AP001515.1	NT	Human mRNA for KIAA0227 gene, partial cds
489	13122	25608	1.19	1.1E+00	D89880.1	NT	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1799	14389	26934	1.48	1.1E+00	AW998393.1	EST_HUMAN	Wheat yellow mosaic virus RNA1 270 kDa precursor protein gene, complete cds
2617	15179	27746	1.09	1.1E+00	AF067124.1	NT	Homo sapiens chromosome 21 segment HS21C013
3373	15981	28458	9.32	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3373	15981	28459	9.32	1.1E+00	AL163213.2	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3533	16136	28620	0.84	1.1E+00	8922841	NT	wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW:P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ;
3639	16242	28718	1.06	1.1E+00	A1808360.1	EST_HUMAN	Xyella fastidiosa, section 32 of 229 of the complete genome
3781	16381	28845	1.41	1.1E+00	AE003886.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3781	16381	28846	1.41	1.1E+00	AE003886.1	NT	H. parahaemolyticus hphIM(A), hphIM(C), hphIR and menB genes
3889	16488		0.61	1.1E+00	X85374.1	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4016	16614	29087	0.67	1.1E+00	8922841	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4093	16688	29145	0.65	1.1E+00	6755205	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Pamb7), mRNA
4295	16881		7.81	1.1E+00	5835331	NT	R.unicornis complete mitochondrial genome
5131	17703	30137	3.54	1.1E+00	U18488.1	NT	African swine fever virus, complete genome
5132	17704	30138	0.98	1.1E+00	AJ271740.1	NT	Drosophila melanogaster D-Titin gene, exons 1-37
5201	17766	30180	1	1.1E+00	U34740.1	NT	Emricella nidulans sterigmatocystin biosynthetic gene cluster: (stcA), (stcB), (stcC), (stcD), (stcE), (stcF), (stcI), (stcJ), (stcK), (stcL), (stcO), (stcQ), (stcS), (stcT), (stcU), (stcV) and (stcW) genes, complete cds
5230	17794	30213	0.98	1.1E+00	X78425.1	NT	E.faecalis pbp5 gene
5409	17968		1.04	1.1E+00	AE003859.1	NT	Xylella fastidiosa, section 15 of 229 of the complete genome
5510	18143	30555	1.52	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5798	18423	31139	19.88	1.1E+00	BE960184.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'
5815	18439	31161	3.23	1.1E+00	AI136582.1	EST_HUMAN	q85c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736260 3'
6242	18851	31621	1.25	1.1E+00	11419739	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA
6420	18023	31807	0.71	1.1E+00	AF197861.1	NT	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6539	19138	31831	0.71	1.1E+00	R06037.1	EST_HUMAN	ye89e03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124924 5'
6817	19408	32225	0.7	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 58 (EP58 gene)
7338	19865	32729	0.78	1.1E+00	X55981.1	NT	Maize mRNA for endase (2-phospho-D-glycerate hydrolase)
7501	20023	32886	2.08	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7501	20023	32887	2.08	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7521	20041	32910	0.72	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7580	24787	32973	0.89	1.1E+00	11967960	NT	Mus musculus silent mating type information regulation 2, (S.cerevisiae, homolog-like (Sir2)), mRNA
8074	20616	33530	2.8	1.1E+00	BF693996.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246628 5'
8163	20704	33620	0.75	1.1E+00	AI478339.1	EST_HUMAN	bm39h11.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160549 3'
8672	21211	34130	0.75	1.1E+00	AB003088.1	NT	Acetabularia caliculus mitochondrial COXI-like gene
8749	21288	34208	0.78	1.1E+00	S60750.1	NT	VH-anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt]
8958	20287		0.68	1.1E+00	BE384876.1	EST_HUMAN	601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9546	22046	35007	0.68	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene)
9599	22099		0.81	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9687	22186	35160	0.84	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9747	22245	35228	1.59	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0934 protein, partial cds
9850	22348	35330	4.82	1.1E+00	AL181515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9909	22408	35381	19.39	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10395	22889	35883	1	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10530	23067	36079	2.93	1.1E+00	11087364	NT	Homo sapiens KIAA0928 gene product (KIAA0928), mRNA
10588	23121		4.06	1.1E+00	AF068942.1	NT	Klebsorridium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
10978	18026		5.28	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
10983	23497	36526	3.76	1.1E+00	AF012882.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
10983	23497	36527	3.76	1.1E+00	AF012882.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11234	23765	36822	6.02	1.1E+00	AB090699.1	EST_HUMAN	wf76811 x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
11946	24275		1.82	1.1E+00	P07868	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12051	24335	30987	2.25	1.1E+00	AF216696.1	NT	Taenla solium immunogenic protein T578 mRNA, partial cds
12184	24903		1.64	1.1E+00	AF234169.1	NT	Dichostelium discoidium isopentenyl pyrophosphate isomerase (DipI) mRNA, complete cds
103	12779		3.22	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
118	12789	25271	3.48	1.0E+00	D98425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
443	13078		2.14	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
602	13231	25704	1.53	1.0E+00	AJ251680.1	NT	Girardia tigrina mRNA for homeodomain transcription factor (so gene)
705	13326	25813	7.12	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
707	13328		0.89	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1429	15441		1.73	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
1794	14384	26929	0.91	1.0E+00	AB006531.1	NT	Plautia stali Intestine Virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2526	15090	27692	1.2	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2526	15090	27693	1.2	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2900	15517	27866	4.47	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2900	15517	27867	4.47	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2894	15610		0.83	1.0E+00	O14228	SWISSPROT	HYPOHETICAL 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME 1
3232	15844	28324	0.91	1.0E+00	AA628453.1	EST_HUMAN	af2608.st Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:C42D8.3 CE04204; contains element MER22 MER22 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3659	12779		0.78	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3744	16345	28813	1.55	1.0E+00	AJ223818.1	NT	Agaricus bisporus mRNA for tyrosinase
4144	18736	29189	1.5	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4362	19949		0.64	1.0E+00	8922245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
5165	17734		17.2	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
5339	17900		0.6	1.0E+00	AF200817.1	NT	Pilot whale morbillivirus phosphoprotein (P) gene, partial cds
5432	18010	30394	1	1.0E+00	AB039022.1	NT	Oncorhynchus mykiss sht1 mRNA for rhamnose binding lectin STL1, complete cds
5486	18120	30527	2.56	1.0E+00	Z97022.1	NT	Hardycore vulgare gene encoding cysteine proteinase
6013	18633	31368	4.54	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6013	18633	31369	4.54	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6111	18727	31480	1.22	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
6263	18871	31641	4.41	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
6269	18877	31645	1.56	1.0E+00	AW452782.1	EST_HUMAN	U-H-B13-alk-d-09-0-UI.s1 NC1_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088989 3'
6615	19212	32018	1.79	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6682	19258	32082	0.83	1.0E+00	AF104689.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5
6742	19338		1.5	1.0E+00	P46506	SWISSPROT	SRB-11 PROTEIN
6874	19608	32442	1.27	1.0E+00	Y11204.1	NT	V. carteri gene encoding volvoxopsin
7192	19724	32573	1.22	1.0E+00	S52770.1	NT	insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7493	20016		8.58	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
7697	20206	33093	1.36	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7710	20219	33107	7.92	1.0E+00	AA775191.1	EST_HUMAN	ac79008.s1 Stratagene lung (4937210) Homo sapiens cDNA clone IMAGE:888791 3'
7902	20444	33349	1.49	1.0E+00	BE888287.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
7902	20444	33350	1.49	1.0E+00	BE888287.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8084	17734		1.28	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
							PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
8291	20832	33753	2.1	1.0E+00	Q02207	SWISSPROT	

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8281	20832	33754	2.1	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
8413	20863		0.85	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8447	20987	33902	0.48	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN-PROCESSING PROTEASE UBP-M)
8447	20987	33903	0.48	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN-PROCESSING PROTEASE UBP-M)
8475	24791		2.17	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT0228-181098-011-406 HT0228 Homo sapiens cDNA
8513	21052	33974	1.06	1.0E+00	U42720.2	NT	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds, and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
8659	21198	34116	1.07	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33,
9195	21712	34855	2.05	1.0E+00	BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'
9402	21911	34860	1.34	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9402	21911	34861	1.34	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9528	22028	34987	2.08	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GKC Homo sapiens cDNA clone GKCCYA11 5'
9534	22034	34993	1.33	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds
9534	22034	34994	1.33	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds
9767	22265	35248	0.5	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
9767	22265	35249	0.5	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10021	22516	35510	0.62	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10021	22516	35511	0.62	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10105	22600	35592	0.75	1.0E+00	A077920.1	EST_HUMAN	cy15407.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665901 3'
10230	22725	35716	4.17	1.0E+00	AV759825.1	EST_HUMAN	AV759825 BM Homo sapiens cDNA clone BMFAW C04 5'
10372	22868	35859	19.78	1.0E+00	AA004982.1	EST_HUMAN	zh94602.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10372	22868	35860	19.78	1.0E+00	AA004982.1	EST_HUMAN	zh94602.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10404	22868	35893	0.93	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
10953	23374	36393	1.87	1.0E+00	S90825.1	NT	PBR1=proline-rich protein (intron 3) [human, Genomic, 898 nt]
11587	18120	30527	1.57	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
11837	24201		4.85	1.0E+00	P15308	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12171	24410		3.08	1.0E+00	AW976184.1	EST_HUMAN	EST388293 MAGE resequences, MAGN Homo sapiens cDNA
1816	14209	26742	0.97	9.9E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
1616	14209	26743	0.97	9.9E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
2664	15222	27794	1.17	9.9E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3665	16267		0.94	9.9E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5816	18440	31182	14.59	9.9E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
6029	18648	31389	0.83	9.9E-01	Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9185	21702		1.39	9.9E-01	U05667.1	NT	Lycopodium obscurum putative Mt1 copy 1 nematode-resistance gene
9474	21873		2.61	9.9E-01	Q28642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
10593	23128	38142	1.68	9.9E-01	AJ005029.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase ritk8
549	13180	25658	1.77	9.9E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2336	14907		0.89	9.9E-01	AJ003108.1	NT	Callithrix jacchus UBE1 gene derived retroposon on the Y chromosome
2827	15379		2.05	9.9E-01	AF174644.1	NT	Xenopus laevis rec GTPase mRNA, complete cds
3869	16467	28930	0.95	9.9E-01	O67551	SWISSPROT	PROBABLE ENDONUCLEASE IV (ENDONUCLEOTRIBONUCLEASE IV)
3872	16470	28933	0.61	9.9E-01	BE957439.2	EST_HUMAN	601655583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
3872	16470	28934	0.61	9.9E-01	BE957439.2	EST_HUMAN	601655583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
7250	19779	32634	4.86	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7250	19779	32635	4.86	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7641	20153	33038	1.13	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3860049 5'
7641	20153	33039	1.13	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3860049 5'
8653	21192	34110	0.77	9.8E-01	P38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10334	22828		0.56	9.8E-01	AA875565.1	EST_HUMAN	cd55d04.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3'
10874	23395	38410	4.86	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
10874	23395	38411	4.86	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
11597	24040	37109	1.78	9.8E-01	A1690876.1	EST_HUMAN	b42c10.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2272242 3'
12058	24341		1.39	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CTR), CDM protein (CDM), adrenolectomydystrophy protein >
7212	19743	32597	2.51	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
8440	20980	33895	1.7	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8446	20986	33901	1.28	9.7E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11049	23562		5.23	9.7E-01	BF511209.1	EST_HUMAN	UI-H-B14-e01-e-07-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
12658	24728		2.92	9.7E-01	AL114281.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
4531	17115	29559	0.58	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4531	17115	29560	0.58	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4557	17140	29593	1.71	9.6E-01	AF1769674.1	EST_HUMAN	PM2-UM0053-240300-005-12 UM0053 Homo sapiens cDNA
5928	18550	31276	3.9	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2994
5928	18550	31277	3.9	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2994
8331	20872		1.23	9.6E-01	X95275.1	NT	P.falciparum complete gene map of plastid-like DNA (IR-A)
8785	21324	34248	0.47	9.6E-01	L81138.1	NT	Rattus norvegicus (strain R21) Rps2r gene, complete cds
9020	21557	34485	0.62	9.6E-01	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
10666	23481	36507	1.81	9.6E-01	AF041427.1	NT	Homo sapiens ribosomal protein s4 Y isoform gene, complete cds
11395	23847	36912	5.18	9.6E-01	AV752805.1	EST_HUMAN	AV752805 NP0 Homo sapiens cDNA clone NPDBAG06 5'
11395	23847	36913	5.18	9.6E-01	AV752805.1	EST_HUMAN	AV752805 NP0 Homo sapiens cDNA clone NPDBAG06 5'
11733	24139		2.36	9.6E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
12388	24983	30609	2.8	9.6E-01	U91423.1	NT	Sphyma tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2515	15079	27651	1.02	9.5E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
2691	15248	27817	1.2	9.5E-01	Q02834	SWISSPROT	ENDOGLUCANASE I PRECURSOR (EGI) (ENDO-1,4-BETA-GLUCANASE) (CELLULOSE 1)
3850	16448	28909	1.89	9.5E-01	BE902340.1	EST_HUMAN	601875639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3850	16448	28910	1.89	9.5E-01	BE902340.1	EST_HUMAN	601875639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
8931	21469	34387	0.63	9.5E-01	AI190162.1	EST_HUMAN	gd57d07.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1733581 3'
9034	21571	34500	1.07	9.5E-01	AW881102.1	EST_HUMAN	RC1-CT0295-241199-011-B02 CT0295 Homo sapiens cDNA
11123	23631	36674	1.71	9.5E-01	BF218771.1	EST_HUMAN	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'
11326	23024	36033	1.59	9.5E-01	AW293799.1	EST_HUMAN	UI-H-B12-ahp-f03-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
3235	15847		1.8	9.4E-01	AF165990.1	NT	Bartonella claridgeae RNA polymerase beta subunit (poB) gene, partial cds
3254	15866		2.47	9.4E-01	AF080595.1	NT	Pimplipella brachycarpa zinc finger protein (ZFPI) mRNA, complete cds
8789	21338	34265	0.98	9.4E-01	M80724.1	NT	Human Fe-gamma-receptorIIA (FCGR2A) gene, exon 4
1768	14358		0.95	9.3E-01	AF242382.1	NT	Homo sapiens phyenoyl-CoA hydroxylase (PHYH) gene, exon 5
2662	15220	27782	1.09	9.3E-01	BE071172.1	EST_HUMAN	RCS-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
4107	18701	29154	0.92	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4107	18701	29155	0.92	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5778	18403	31119	1.41	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5858	18481	31204	3.99	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
8011	20563	33456	1.62	9.3E-01	AA847040.1	EST_HUMAN	ce08b03.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385357
8748	21287		1.13	9.3E-01	AF061981.1	NT	Xenopus laevis COCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
8887	21408	34330	1.01	9.3E-01	AL161534.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
12508	24628	30893	1.87	9.3E-01	11440298	NT	Homo sapiens incositol 1,4,5-triphosphate receptor, type 2 (ITPR2), mRNA
12515	24634		2	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl34 mRNA, complete cds
3278	15887	28369	3.99	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
5004	17577		0.92	9.2E-01	BF128973.1	EST_HUMAN	601817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041363 5'
5894	18518		1.41	9.2E-01	7108410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
6140	18754	31512	4.4	9.2E-01	BF037586.1	EST_HUMAN	601461153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864661 5'
9578	22078	35042	1.31	9.2E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9683	22162	35135	1.15	9.2E-01	6871877	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10168	22661	35658	3.47	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10314	22808	35800	1.58	9.2E-01	BF593251.1	EST_HUMAN	7658e08.x1 NCI_CGAP_Kld11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW:NU5M_TRYBB
10528	23063	36074	1.75	9.2E-01	BE563811.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5;
11569	24018	37085	2.27	9.2E-01	BF132402.1	EST_HUMAN	601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688714 5'
1666	14259	26793	4.89	9.1E-01	T86675.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
2169	14746		2.38	9.1E-01	8923056	NT	ye5201.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains Alu repetitive element.
3239	15851	28331	0.93	9.1E-01	T26418.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3239	15851	28332	0.93	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
6315	18922	31699	1.42	9.1E-01	L36033.1	NT	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
6630	19226	32031	2.82	9.1E-01	D61704	SWISSPROT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
7577	20093	32970	15.95	9.1E-01	AA806623.1	EST_HUMAN	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7719	20227	33115	3.12	9.1E-01	U72895.1	NT	cb71g08.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1336862 3'
12093	24976		33.14	9.1E-01	AF050113.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
3241	15853	28335	0.81	9.0E-01	7681825	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3401	18010		0.64	9.0E-01	AL161515.2	NT	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
4468	17054	29498	1.44	9.0E-01	AF098810.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
							Homo sapiens neurexin III-alpha gene, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7424	19948	32814	0.78	9.0E-01	L4257.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
7450	19974		1.64	9.0E-01	D38621.1	NT	Xenopus laevis gene for aldolase, complete cds
9271	21787	34746	0.54	9.0E-01	AF086761.1	NT	Danio rerio semaphorin Z1a mRNA, complete cds
9744	22242	35223	0.47	9.0E-01	U39702.1	NT	Mycoplasma genitalium section 24 of 51 of the complete genome
5875	18497	31222	2.49	8.9E-01	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 hr_molog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
6398	18988		1.27	8.9E-01	X60986.1	NT	Rabbit MHC fragment RLA-DF DNA
8152	20693		0.47	8.9E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8365	20905	33824	1.04	8.9E-01	AF259887.1	NT	Oithona nana cytochrome-c oxidase subunit I (cox) gene, partial cds, mitochondrial gene for mitochondrial product
11616	24058	37122	2.59	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
11927	24282		5.33	8.9E-01	AE002186.2	NT	Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome
4640	17222	28678	2.1	8.8E-01	O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5576	18207	30658	0.7	8.8E-01	AF310817.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
10960	23475	36500	3.82	8.8E-01	Z28337.1	NT	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
11749	25067		2.27	8.8E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
480	13123	25609	1.48	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2446	15013	27585	1.13	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2898	15515	27984	5.67	8.7E-01	AA595883.1	EST_HUMAN	nn05f11.s1 NCI_CGAP_Pt4.1 Homo sapiens cDNA clone IMAGE:1076877
4845	17423	28875	0.61	8.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
4845	17423	28878	0.61	8.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
5151	17721		3.08	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome
7983	20525	33431	0.66	8.7E-01	AW697335.1	EST_HUMAN	halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put>
8860	21399	34322	0.75	8.7E-01	AI239456.1	EST_HUMAN	dioxigenase alpha-ISP protein OhbB (ohbB), and put>
8860	21399	34323	0.75	8.7E-01	AI239456.1	EST_HUMAN	RC4-NN0057-120500-013-c07 NN0057 Homo sapiens cDNA
9653	22152	35122	1.7	8.7E-01	AE004963.1	NT	qh36e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846788 3'
10205	22700	35683	0.56	8.7E-01	BF570169.1	EST_HUMAN	qh36e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
10205	22700	35684	0.56	8.7E-01	BF570169.1	EST_HUMAN	qh36e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
10711	23239	36254	5.79	8.7E-01	BF363970.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome
11582	24028	37097	4.31	8.7E-01	BF107694.1	EST_HUMAN	60218554111 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'
11582	24028	37098	4.31	8.7E-01	BF107694.1	EST_HUMAN	60218554111 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'
11582	24028	37098	4.31	8.7E-01	BF107694.1	EST_HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
11582	24028	37098	4.31	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
11582	24028	37098	4.31	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12148	24881		4.44	8.7E-01	AV661898.1	EST_HUMAN	AV661898 GLC Homo sapiens cDNA clone GLCGYG07.3
500	13132		1.55	8.6E-01	X17012.1	NT	Rat IGFI gene for insulin-like growth factor II
891	13505	28024	8.72	8.6E-01	W69089.1	EST_HUMAN	zd44e03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343516.5
2310	14882	27457	1.08	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3681	10282	28750	0.78	8.6E-01	AL161585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3870	16468	28931	1.38	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
6057	18674	31415	9.06	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6057	18674	31418	9.08	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6810	19401	32216	1.88	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6810	19401	32217	1.88	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7868	20410		1.33	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
7986	20528	33434	0.54	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapse response mediator protein (CRMP) mRNA, complete cds
9603	22103		0.48	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12338	24812		1.73	8.6E-01	AL112162.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
6826	19416	32232	1.32	8.5E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7533	20053	32028	2.38	8.5E-01	BE542812.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505.5
7932	20474	33383	0.51	8.5E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8357	20897	33817	0.94	8.5E-01	P08601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8357	20897	33818	0.84	8.5E-01	P08601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8441	20981	33888	0.51	8.5E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10252	22747	35734	1.38	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
10252	22747	35735	1.38	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
12077	24978		3.12	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA
12084	24355		7.92	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4882	17440	29880	0.62	8.4E-01	AF083975.2	NT	Fowl adenovirus 8, complete genome
5685	24747	30807	3.15	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5685	24747	30808	3.15	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
9868	22365		2.68	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
771	13390	25889	2.48	8.3E-01	M83437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3129	15743	28212	3.26	8.3E-01	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3883	16481	28943	0.66	8.3E-01	AB1010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4084	16680	28140	3.24	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5473	18107	30426	2.15	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9587	22087		3.14	8.3E-01	A1791952.1	EST_HUMAN	nm01f12.y5 NCL_CGAP_C08 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.11 THR repetitive element:
10019	22514	35507	1.11	8.3E-01	AF098070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
10119	22614	35604	3.5	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
10553	23089	36103	2.92	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270310 to 1283409 (section 109 of 148) of the complete genome
10571	23106		2.52	8.3E-01	7212472	NT	Phylophthora infestans mitochondrion, complete genome
11183	23688	36735	2.45	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2096	14675	27244	3.23	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2137	14715		1.45	8.2E-01	AF145589.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
3969	16567	29036	1.12	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0674 protein, partial cds
4209	16798	29248	0.81	8.2E-01	Z72584.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL062w
4209	16798	29247	0.81	8.2E-01	Z72584.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL062w
5270	17832	30258	1.08	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
5420	17977	30385	2.11	8.2E-01	AB028957.1	NT	Homo sapiens mRNA for KIAA1034 protein, partial cds
6871	18605	32439	0.8	8.2E-01	AJ010142.1	NT	Amanita muscaria mRNA for SC1125 protein
6978	18554	32379	3.18	8.2E-01	AW379433.1	EST_HUMAN	CM4-HT0243-081199-037-401 HT0243 Homo sapiens cDNA
7313	24779	32700	4.21	8.2E-01	Z12126.1	NT	S.cerevisiae MET, LEU4, and POL1 genes encoding MET14 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
9938	22433	35409	0.63	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
9971	22466	35450	1.67	8.2E-01	AF052659.1	NT	Homo sapiens thioredoxin-related protein mRNA, complete cds
10123	22618	35609	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10123	22618	35610	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10286	22781	35772	3.52	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10286	22781	35773	3.52	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11498	23847	37017	3.33	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
11576	24022	37091	8.05	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
11583	24029	37099	5.68	8.2E-01	H87398.1	EST_HUMAN	yw14d02.11 Scores_placenta_81cdweeks_2NHP81cd9W Homo sapiens cDNA clone IMAGE:252195 5' similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
12102	24364	30970	1.86	8.2E-01	AJ001261.1	NT	Mus musculus mRNA for NIPSNAP2 protein
2787	15340		1.79	8.1E-01	AF191839.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3504	18109	28585	2.89	8.1E-01	AF055066.1	NT	Homo sapiens MHC class 1 region
3504	18109	28586	2.89	8.1E-01	AF055066.1	NT	Homo sapiens MHC class 1 region

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5048	17619		0.88	8.1E-01	AF202834.1	NT	Drosophila melanogaster NaK-ATPase beta subunit isoform 4 (JYbeta2) mRNA, complete cds
6457	19058	31843	0.88	8.1E-01	U16780.1	NT	Mus musculus putative collagen alpha-2(XI) chain (COL11A2) gene, partial cds
6735	19329	32134	2.54	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
6735	19329	32135	2.54	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
7852	20394	33288	0.84	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cd>
7852	20394	33289	0.84	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cd>
8545	21084	34006	0.92	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8545	21084	34007	0.92	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8705	21244	34167	1.08	8.1E-01	AW242647.1	EST_HUMAN	xc01h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2692469 3' similar to SW1LYAR_MOUSE Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN ; contains MER22.b1 PTR5 repetitive element ;
10032	22527	35522	0.54	8.1E-01	P08425	SWISSPROT	PROBABLE E4 PROTEIN
11356	23810	36869	2.87	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11356	23810	36870	2.87	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11811	24183	31031	3.32	8.1E-01	AE001711.1	NT	Thermotoga maritima section 23 of 136 of the complete genome
188	12849		4.99	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pta gene for phosphate acetyltransferase allele 15
310	12985	25453	7.95	8.0E-01	AJ132772.1	NT	Bos taurus tub and rlf genes
2080	14881		1.47	8.0E-01	BF550982.1	EST_HUMAN	602072473f1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4215091 5'
3113	15728	28199	1.24	8.0E-01	AF127897.1	NT	Salmonella enteritidis offcary receptor (SBO27) gene, partial cds
3354	15962	28439	1.13	8.0E-01	AB006183.1	NT	Mus musculus gene for oviductal glycoprotein, complete cds
3765	16368		1.05	8.0E-01	AL162758.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 7/7
4630	17213	28664	5.65	8.0E-01	X63739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
5117	17689	30127	1.09	8.0E-01	7657352	NT	Mus musculus myosin IXb (Myo9b), mRNA
7931	20473		2.32	8.0E-01	AW901489.1	EST_HUMAN	RCO-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA
8462	21002	33919	1.17	8.0E-01	Y11065.1	NT	Rice stripe virus RNA 3
479	13112	25602	1.37	7.9E-01	D11478.1	NT	Lynanthia dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
744	13364		1.05	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1648	14240		28.9	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1695	14288		1.11	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2303	14876	27452	6.76	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin28, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2304	14877	27453	5.48	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3587	18171	28653	2.33	7.9E-01	AF228664.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4389	19875		0.76	7.9E-01	BE263912.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4717	17298	29743	1.04	7.9E-01	6753745	NT	Mus musculus embigin (Emb) mRNA
4717	17298	29744	1.04	7.9E-01	6753745	NT	Mus musculus embigin (Emb) mRNA
5315	17877		5.8	7.9E-01	M28830.1	NT	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17
6485	19086	31868	0.69	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8053	20595	33502	2.52	7.9E-01	X90986.1	NT	P. sativum GR gene
9468	21991	34948	4.57	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
9982	22457	35440	4.27	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
10003	22498	35487	0.75	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GKC Homo sapiens cDNA clone GKCDRE12 3'
10405	22899	35894	0.71	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds
10886	23407		2.28	7.9E-01	7862471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11089	23601	36639	2.72	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
909	13522		1.4	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1k04
2314	14888	27461	1.4	7.8E-01	AW959587.1	EST_HUMAN	EST371637 MAGE resequences, MAGF Homo sapiens cDNA
4811	17389	20840	0.81	7.8E-01	U67305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5189	17754		0.81	7.8E-01	AW753353.1	EST_HUMAN	RC3-CT0254-130100-023-c02 CT0254 Homo sapiens cDNA
6219	18829	31603	2.33	7.8E-01	AF115856.1	NT	Sphenodon punctatus alpha endase mRNA, partial cds
6367	18971	31750	1.05	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6589	19186	31988	0.75	7.8E-01	AL445066.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
8428	20968	33881	1.04	7.8E-01	BF108927.1	EST_HUMAN	7154d05.x1 Soares NSF_F8_gW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525176 3'
9160	21895	34639	1.02	7.8E-01	Y10159.1	NT	D discoideum racGAP gene
9255	21781	34733	0.53	7.8E-01	4826873	NT	Homo sapiens nucleoporin 214kD (CAIN) (NUP214), mRNA
10031	22528		0.78	7.8E-01	Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12071	24957		2.33	7.8E-01	L28260.1	NT	Arabidopsis thaliana L-aminio-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
150	12813	25300	4.65	7.7E-01	AF184345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
755	13374		1.44	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IiAlpha) and major histocompatibility protein class II beta chain (IiBeta) genes, complete cds;
2737	16292	27860	2.33	7.7E-01	O33915	SWISSPROT	butyrophilin-like (NG9), butyrophilin-like CITRATE SYNTHASE

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3400	16009		0.62	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNAc-T7) (GALNAc-T7), mRNA
3660	16262	28734	4.78	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4488	17071	29521	3.17	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4486	17071	29522	3.17	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5749	18376	31084	1.33	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5749	18375	31085	1.33	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6110	18726	31479	0.8	7.7E-01	R08800.1	EST_HUMAN	y24b02.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:127755 3'
9758	22256	36239	0.82	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
11957	24280		15.01	7.7E-01	11497921	NT	Archaeoglobus fulgidus, complete genome
4780	17370	28822	19.73	7.6E-01	L27316.1	NT	Oryctolagus cuniculus immunoglobulin VDJ region gene
4780	17370	28823	19.73	7.6E-01	L27316.1	NT	Oryctolagus cuniculus immunoglobulin VDJ region gene
6248	18857	31628	4.81	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6248	18857	31629	4.81	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6641	19237	32039	0.7	7.6E-01	P37938	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA 24
6935	18043	30465	0.95	7.6E-01	AI253399.1	EST_HUMAN	ac14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
6935	18043	30488	0.95	7.6E-01	AI253399.1	EST_HUMAN	ac14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7113	19453	32269	0.98	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds
8009	20551	33455	1.34	7.6E-01	AF148783.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8068	20610	33522	1.76	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
8068	20610	33523	1.76	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
8267	20608	33727	0.55	7.6E-01	Q01098	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8267	20608	33728	0.55	7.6E-01	Q01098	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8897	21435	34359	0.91	7.6E-01	P30372	SWISSPROT	Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA
9203	21720	34664	3.33	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9203	21720	34665	3.33	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11236	23767	36824	2.74	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11236	23767	36825	2.74	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11556	24004		5.74	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
11711	24121		6.31	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
539	13170		1.32	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
610	13238	25712	1.13	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
7530	20050	32923	0.74	7.5E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
12027	24318		5.28	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
12522	24638	30897	1.91	7.5E-01	D90907.1	NT	Synechocystis sp. PCC6803 complete genome, 9/27, 1058467-1188885
1169	13771	28279	1.36	7.4E-01	AI598146.1	EST_HUMAN	bt14b09.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element ;
3789	16389	28854	0.93	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
4400	16985	29430	7.7	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21G046
7785	20328	33234	1.03	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
7785	20328	33235	1.03	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8568	21107	34026	0.93	7.4E-01	BF346266.1	EST_HUMAN	602018456F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154340 5'
8647	21186		0.84	7.4E-01	U87960.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9028	21563	34492	7.17	7.4E-01	BE747503.1	EST_HUMAN	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9083	21619	34554	1.19	7.4E-01	AA187886.1	EST_HUMAN	zp67h01.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625297 3' similar to SW:TCPO_MOUSE P42932 T-COMPLEX PROTEIN 1, THETA SUBUNIT ;
10301	22795	35786	0.59	7.4E-01	11424933	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
11516	23684	37034	1.68	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11516	23684	37035	1.68	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11677	24086		4.11	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
11794	24175		1.28	7.4E-01	AI472641.1	EST_HUMAN	tat13m01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4723	17304	28748	0.72	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4910	17388	28839	2.63	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5260	17823	30248	0.98	7.3E-01	CA3103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
6720	19314	32116	5.86	7.3E-01	U35772.1	NT	Mus musculus antigen (CD72) gene
6720	19314	32117	5.86	7.3E-01	U35772.1	NT	Mus musculus antigen (CD72) gene
7151	24777	32525	0.82	7.3E-01	AJ011418.1	NT	Lycopodium obscurum mRNA for ubiquitin activating enzyme
7549	20068	32942	7.77	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
7549	20068	32943	7.77	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
11307	23800	36859	3.86	7.3E-01	AA678019.1	EST_HUMAN	z125b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11307	23800	36860	3.86	7.3E-01	AA678019.1	EST_HUMAN	z25b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
884	13479		1.66	7.2E-01	U29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
2000	14582	27141	3.04	7.2E-01	X78140.1	NT	N.tubercum NeIF-4A13 mRNA
2501	15065	27639	1.36	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3103	15718	28188	1.29	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3500	16105	28580	2.97	7.2E-01	AF065608.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-J) allele, complete cds
3940	16538	29005	1.81	7.2E-01	BF338350.1	EST_HUMAN	602035589F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183222 5'
4185	16775	29222	0.6	7.2E-01	U02568.1	NT	Dictyocaulus viviparus nematode polyprotein antigen precursor (DVA) mRNA, complete cds
4884	17459	29811	2.54	7.2E-01	D90314.1	NT	L.mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5348	17908	30323	0.9	7.2E-01	AF158600.2	NT	Streptococcus thermophilus bacteriophage Sfi11, complete genome
5386	17945	30358	0.69	7.2E-01	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
7265	19783	32648	0.82	7.2E-01	U69633.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8391	20631	33851	1.15	7.2E-01	AF236081.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
8893	21431		0.53	7.2E-01	AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD06 5'
10243	22738	35729	2.14	7.2E-01	BF670081.1	EST_HUMAN	602118381F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381 5'
10818	23150	35162	5.23	7.2E-01	U82823.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
12037	16775	29222	1.66	7.2E-01	U02568.1	NT	Dictyocaulus viviparus nematode polyprotein antigen precursor (DVA) mRNA, complete cds
12233	24449		4.42	7.2E-01	AF000063.1	NT	Aeropyrum pernix genomic DNA, section 87
12266	24995		1.67	7.2E-01	Y10168.1	NT	B.thuringiensis PK1 & cap genes, putative
721	13341	25831	10.56	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3098	15713	28185	18.71	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4287	16873	29321	4.11	7.1E-01	7305360	NT	Mus sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4287	16873	29322	4.11	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
6103	18719	31471	1.81	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
6103	18719	31472	1.81	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
7028	19563	32360	6.04	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvyltetrahydropterin synthase (pr) gene, complete cds
8132	20673	33594	0.53	7.1E-01	H54244.1	EST_HUMAN	y489409.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202961 3'
8871	21210	34128	0.78	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-409 BT0567 Homo sapiens cDNA
8871	21210	34129	0.78	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-409 BT0567 Homo sapiens cDNA
9769	22267	35252	1.46	7.1E-01	BE604405.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3893495 5'
10308	22803	35795	1.06	7.1E-01	M12961.1	NT	Human T-cell receptor gamma-chain J2 gene
12012	24878		2.58	7.1E-01	AA421492.1	EST_HUMAN	zu06h11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1272	13668	26387	1.3	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1272	13668	26388	1.3	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2492	15057	27630	1.22	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NbHMSF Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
2492	15057	27631	1.22	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NbHMSF Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
5213	17778		1.98	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5362	17922	30336	2.99	7.0E-01	AE003921.1	NT	Xylella fastidiosa, section 87 of 229 of the complete genome
6107	18723		1.03	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8319	20860		11.92	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
9240	21766	34714	0.61	7.0E-01	U53968.1	NT	Clostridium acetabutylicum mannitol-specific phosphotransferase system (PTS) system, mltA, mltR, mltF, and mltD genes, complete cds
9240	21768	34715	0.61	7.0E-01	U53968.1	NT	Clostridium acetabutylicum mannitol-specific phosphotransferase system (PTS) system, mltA, mltR, mltF, and mltD genes, complete cds
10999	23513	36546	1.99	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
10998	23513	36547	1.99	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
12594	24918	30715	1.35	7.0E-01	9630484	NT	Bacteriophage N15 vlon, complete genome
1005	13616	26130	10.2	6.9E-01	U69874.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1005	13616	26131	10.2	6.9E-01	U69874.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1353	13948	26472	2.8	6.9E-01	AA593530.1	EST_HUMAN	nm28a09.st.NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3256	15968	28348	1.7	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5954	18578	31310	0.8	6.9E-01	AB035682.1	NT	Branchiostoma belcheri BbNA3 mRNA for notochord actin, complete cds
6508	19108	31893	1.31	6.9E-01	BE296188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
7921	20463	33369	3.4	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
7921	20463	33370	3.4	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
9098	21634		0.83	6.9E-01	AF118046.1	NT	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds
9611	22111	35073	0.62	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
9611	22111	35074	0.62	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
10307	22801	35793	0.66	6.9E-01	BF242367.1	EST_HUMAN	601880580F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109419 5'
11138	23646	36687	1.94	6.9E-01	D88013.1	NT	Homo sapiens DAN gene, complete cds
11138	23646	36688	1.94	6.9E-01	D88013.1	NT	Homo sapiens DAN gene, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11651	24870		2.36	6.9E-01	Q99958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK
12670	25003	30811	1.33	6.9E-01	AI889312.1	EST_HUMAN	HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)
992	13604	28118	1.28	6.8E-01	AF017784.1	NT	wn31102.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2447087 3'
2698	15255		1.25	6.8E-01	D00917.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2856	14249	26783	1.62	6.8E-01	AA854475.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
4672	17254	29708	1.45	6.8E-01	J00762.1	NT	aj75a05.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to
9556	22056	35017	2.11	6.8E-01	AB037786.1	NT	gb:X56411.ma1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN); Rat(hooded) prolactin gene : exon iii and flanks
10281	22758		0.48	6.8E-01	AA687936.1	EST_HUMAN	Homo sapiens mRNA for KIAA1345 protein, partial cds
10965	23480	36505	2.06	6.8E-01	AJ276675.1	NT	nv13e07.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1220100 3' similar to gb:X13546_ma1
10965	23480	36506	2.96	6.8E-01	AJ276675.1	NT	Human HMG-17 gene for non-histone chromosomal protein (HUMAN);
10993	23507	36540	2.16	6.8E-01	AF038939.1	NT	Stagonospora avenae bg11 gene for beta-glucosidase, exons 1-4
10993	23507	36541	2.16	6.8E-01	AF038939.1	NT	Stagonospora avenae bg11 gene for beta-glucosidase, exons 1-4
11178	23684	36730	2.2	6.8E-01	AF164151.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11475	23925	36985	1.77	6.8E-01	AF110520.1	NT	Anopheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds
11475	23925	36986	1.77	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RaiGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds: Sacm21 gene, partial>
320	12974	25463	27.63	6.7E-01	AF213884.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RaiGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds: Sacm21 gene, partial>
361	13010	25493	26.51	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1955	14539		0.97	6.7E-01	M12132.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2192	14768	27340	1.65	6.7E-01	AA451884.1	EST_HUMAN	Quail fast skeletal muscle troponin I gene, complete cds zx12g12.s1 Soares_totat_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element;
2211	15460	27361	2.68	6.7E-01	AF186075.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
3026	15642	28120	4.28	6.7E-01	6678560	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4550	17133	28581	0.64	6.7E-01	X74421.1	NT	S.tuberosum mRNA for glucose-6-phosphate dehydrogenase

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5100	17672	30111	0.96	6.7E-01	AW079110.1	EST_HUMAN	xa95g12.x1 NCL_CGAP_Col17 Homo sapiens cDNA clone IMAGE:2574598 3'
5700	18326	30829	0.8	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5700	18326	30830	0.8	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6118	18732	31485	0.83	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6405	19066	31851	1.55	6.7E-01	9635035	NT	Galid herpesvirus 2, complete genome
6485	19066	31852	1.55	6.7E-01	9635035	NT	Galid herpesvirus 2, complete genome
7358	19882		4.12	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7378	19904	32768	0.9	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10049	22544		0.87	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
10832	23353	36368	2.52	6.7E-01	BF354649.1	EST_HUMAN	GM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA
11333	23031	36040	3.45	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLOSITOL BIOSYNTHETIC PROTEIN GP1
2546	15110	27682	2.66	6.6E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2724	15279	27646	1.01	6.6E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3336	16141	28623	1.35	6.6E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaforin) 5A (SEMA5A) mRNA
3719	16320	28788	3.42	6.6E-01	Y07669.1	NT	C.albicans random DNA marker, 282bp
4187	16777		0.67	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5227	17791	30210	0.97	6.6E-01	AI218230.1	EST_HUMAN	qh23a10.x1 Scarses_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845498 3' similar to contains PTR5.b2 MER28 repetitive element ;
6474	19075	31858	4.22	6.6E-01	6680577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7875	20186	33074	3.61	6.6E-01	AY660506.1	EST_HUMAN	AV660506 GLG Homo sapiens cDNA clone GLCGID04 3'
8501	21040	33961	0.64	6.6E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
9582	22082		1.73	6.6E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9915	22411		0.68	6.6E-01	AU18108.1	EST_HUMAN	AU118198 HEMBA1 Homo sapiens cDNA clone HEMBA1003079 5'
12118	24377	30973	1.27	6.6E-01	AF110001.1	NT	Homo sapiens guanylate cyclase activating protein 3 (GCAP3) gene, exon 4 and complete cds
651	13274	25751	1.12	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
651	13274	25752	1.12	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3480	16086	28560	5.04	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4110	16704	29157	1.1	6.5E-01	4504632	NT	Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA
4369	16956	29398	3.29	6.5E-01	AJ27285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
4699	17281	28728	1.28	6.5E-01	D00584.1	NT	Oryza sativa gene for prepro-glutelin, exons 1, 2, 3, 4, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5219	17784	30202	2.39	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5336	17897	30312	1.02	6.5E-01	Z70928.1	NT	H sapiens mRNA for immunoglobulin heavy chain variable region (9D4-A6, VH4, 4-59/DP-71)
6825	19415	32231	1.26	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
7663	20175	33062	0.86	6.5E-01	A1798882.1	EST_HUMAN	wc46802.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2321842 3'
9751	22249		1.25	6.5E-01	T78904.1	EST_HUMAN	y421b04.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108847 3'
10238	22733	35725	2.49	6.5E-01	AF119876.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10512	23050	36061	3.35	6.5E-01	H87583.1	EST_HUMAN	yw1708.r1 Soares placenta_8tc8weeks_2NblHP8to9W Homo sapiens cDNA clone IMAGE:252515 5'
10568	23102	36116	4.35	6.5E-01	AA601287.1	EST_HUMAN	nc15c07.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
10669	23201		4.29	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
11470	23920	36989	2.7	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12067	24348		8.24	6.5E-01	BE468050.1	EST_HUMAN	h74410.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
12321	24817		3.04	6.5E-01	Z74145.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL097c
273	12930	25417	9.34	6.4E-01	U48948.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3502	16107	28583	3.78	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3928	16526	28963	1.33	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4591	17174	29819	0.86	6.4E-01	Y12488.1	NT	M. musculus whn gene
4591	17174	29820	0.66	6.4E-01	Y12488.1	NT	M. musculus whn gene
6402	17960	30371	0.97	6.4E-01	AE002551.2	NT	Neisseria meningitidis serogroup B strain MC58 section 193 of 208 of the complete genome
8549	21088	34010	1.76	6.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 87 of the complete genome
10001	22496	35486	8.26	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10015	22510	35501	1.16	6.4E-01	BF670405.1	EST_HUMAN	602150289FT NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291128 5'
12188	24420		29.97	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGCG09 5'
459	13093	25587	3.75	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
560	13191	25669	56.3	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2207	14783	27356	3.24	6.3E-01	U81136.1	NT	Shigella flexneri multi-antigen resistance locus
2614	15178	27744	2.78	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2614	15178	27745	2.78	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
3050	15668		0.75	6.3E-01	Y17275.1	NT	Lycopodium obscurum p69a gene, complete CDS
6214	18824	31595	0.78	6.3E-01	BE093906.1	EST_HUMAN	PMO-BT0757-010500-002-a05 BT0757 Homo sapiens cDNA
6712	18308	32110	1	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (msg) gene, complete cds
6712	18308	32111	1	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (msg) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8458	20998		3.32	6.3E-01	BE902044.1	EST_HUMAN	601876889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5'
8819	21358	34284	0.81	6.3E-01	S62927.1	NT	glycoprotein Ila (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
8147	21682	34827	1.15	6.3E-01	BF216984.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102586 5'
9341	21855	34804	2.9	6.3E-01	9827521	NT	Varicella virus, complete genome
9341	21855	34805	2.9	6.3E-01	9827521	NT	Varicella virus, complete genome
9851	22349		0.87	6.3E-01	AE002329.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10324	22818	35814	1.52	6.3E-01	Z73003.1	NT	S cerevisiae chromosome VII reading frame ORF YGR218w
10421	22915	35915	0.87	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
10839	23458	36479	2.45	6.3E-01	AA877715.1	EST_HUMAN	nr0906.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:O02916 O02916 HLARK ;
11216	23719	36773	15.21	6.3E-01	AI904160.1	EST_HUMAN	CM-BT043-080299-048 BT043 Homo sapiens cDNA
11302	23795	36853	1.94	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11458	23908	36975	2.02	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
11769	25042	30505	30.63	6.3E-01	9910293	NT	Mus musculus keratin complex 2, gene 8g (Krl2-6g), mRNA
11864	24219		1.85	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPS) mRNA, complete cds
12082	24953		3.2	6.3E-01	X83528.1	NT	C. limicola pscD gene
5175	17742	30171	0.71	6.2E-01	AF157898.1	NT	Spermophilus suslicus isolate S47 cytochrome b (cytb) gene, complete cds; mitochondrial gene for mitochondrial product
6030	18648	31390	2.03	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7508	20028		3.14	6.2E-01	AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
7548	24786	32941	1.08	6.2E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
8243	20784	33703	5.85	6.2E-01	H72255.1	EST_HUMAN	ys01e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213542 3'
8780	21329	34254	0.54	6.2E-01	AF034411.1	NT	Lycopodium obscurum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinase dehydratase/shikimate:NADP oxidoreductase gene, complete cds
9370	20308	33212	1.75	6.2E-01	BE562687.1	EST_HUMAN	601339146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3660010 5'
9428	21938		2.35	6.2E-01	M24481.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
9980	22485	35472	5.85	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10429	22923	35927	3.76	8.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL
10429	22923	35928	3.76	8.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL
2438	15005		4.95	6.1E-01	6678076	NT	PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
4632	17215	26656	1.05	6.1E-01	4557538	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
							Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2) mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6141	17712	30142	1.09	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxypolyprenylbenzoate methyltransferase mRNA, complete cds
5141	17712	30143	1.09	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxypolyprenylbenzoate methyltransferase mRNA, complete cds
5727	18353	31057	1.34	6.1E-01	M59940.1	NT	Caenorhabditis elegans N2 CcmYd (hlt-1) alternatively spliced genes, complete cds
6951	19528	32351	3.55	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6951	19528	32352	3.55	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
8175	20716	33632	3.57	6.1E-01	AF033535.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8730	21269	34187	1.23	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8730	21269	34188	1.23	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9336	21850	34788	19.4	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9336	21850	34789	19.4	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9756	22254	35238	1.15	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PAO1, section 13 of 529 of the complete genome
9959	22454	35438	1.8	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
10837	23358		8.53	6.1E-01	X74507.1	NT	P. sativum mdh mRNA for chloroplast malate dehydrogenase (NADP+)
11581	24027	37095	2.19	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
11581	24027	37098	2.19	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12530	24643		1.91	6.1E-01	X95287.1	NT	M.maza orfA, orfB, and orfC of archaeal ABC-transporter system
520	13152	25635	1.46	6.0E-01	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
587	13217		3.41	6.0E-01	5802988	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (GLA20), mRNA
1406	13999	26528	1.93	6.0E-01	AF085253.1	NT	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds
3887	18485	28946	0.86	6.0E-01	AJ233386.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4287	18853		1.16	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
5485	18118	30526	1.93	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5631	18260	30732	2.28	6.0E-01	AW139713.1	EST_HUMAN	U1H-B1-aab-a-10-Q-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
6660	19256	32059	3.73	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6767	19360	32169	0.79	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
7391	19918	32780	5.29	6.0E-01	AJ277861.1	NT	(CDW136) (CD136 ANTIGEN)
8068	20608	33520	4.72	6.0E-01	P02835	SWISSPROT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8066	20608	33521	4.72	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
9737	22235	35214	2.22	6.0E-01	AB008163.1	NT	SEGMENTATION PROTEIN FUSHI TARAZU
							Homo sapiens genes for leukotriene B4 receptor BL T2, leukotriene B4 receptor BL T1, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10174	22669		1.61	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)
10936	23453	38476	2.14	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
10938	23453	38477	2.14	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11426	23877	38842	2.84	6.0E-01	AI420623.1	EST_HUMAN	U08107.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2095621 3'
12158	24308	30878	1.82	6.0E-01	11421663	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12285	24475		1.99	6.0E-01	AA706087.1	EST_HUMAN	218805.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462776 3'
12426	24879		1.28	6.0E-01	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
12469	24885	30709	2.49	6.0E-01	9055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
12489	24910		6.92	6.0E-01	BE157817.1	EST_HUMAN	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
1038	13648	26160	1.09	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
1447	14039	26568	1.06	5.9E-01	6880232	NT	Mus musculus 3-hydroxy-3-methylglutaryl-Coenzyme A lyase (Hmgcl), mRNA
3308	15919	28395	5.12	5.9E-01	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
3308	15919	28396	5.12	5.9E-01	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4304	16890		4.32	5.9E-01	AF162756.1	NT	Rattus norvegicus cenech 2 mRNA, partial cds
6591	19188	31991	1.48	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7310	19838	32696	5.58	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7941	20483	33395	0.57	5.9E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719843
9482	21987	34943	0.93	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain K/UW31/Cx major outer membrane protein (omp1) gene, complete cds
9827	22325		0.68	5.9E-01	P06483	SWISSPROT	E8 PROTEIN
10091	22566	35579	1.15	5.9E-01	P65284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
10551	23087	36102	3.24	5.9E-01	Q9X013	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
10557	23093	36105	1.75	5.9E-01	AF197944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
10840	23361	36376	3	5.9E-01	AW693715.1	EST_HUMAN	PM1-DT0041-190100-002-h03 DT0041 Homo sapiens cDNA
11073	23585	36626	2.25	5.9E-01	AF084626.1	NT	Mus gretus strain SPRET/EI CD48 antigen (Cd48) gene, partial cds
11810	24182	31030	1.92	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12053	24336		2.88	5.9E-01	AB011705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5-phosphate decarboxylase, complete cds
12280	24483		7.56	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1952	14536	27092	1.8	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
4058	16653	29119	1.22	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4612	17195	29641	3.73	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4914	17489		1.18	5.8E-01	AF110846.1	NT	Megascalia scalaris sex-lethal homolog (Magsxl) gene, partial cds, alternatively spliced products
5577	16208		0.75	5.8E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5722	18348	31051	2.52	5.8E-01	Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6331	18937	31713	2.37	5.8E-01	D78659.1	EST_HUMAN	HUM500E06B Human placenta polyA+ (Tfujivara) Homo sapiens cDNA clone GEN-500E06 5'
6454	19055	31840	0.71	5.8E-01	D50601.1	NT	Shigella sonnei DNA for 26 ORFs, complete cds
6903	19637		2.47	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
7828	20370		2.57	5.8E-01	H41571.1	EST_HUMAN	yp91b03.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:175757 3' similar to gb:378187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8031	20573	33477	0.66	5.8E-01	AI280051.1	EST_HUMAN	qh85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1653779 3'
8031	20573	33478	0.66	5.8E-01	AI280051.1	EST_HUMAN	qh85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1653779 3'
8131	20672	33582	2.34	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
8131	20872	33583	2.34	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
8823	21362	34287	9.48	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
8902	21440	34363	0.86	5.8E-01	Q27368	SWISSPROT	TRANSCRIPTION FACTOR E2F
8903	21441	34364	0.56	5.8E-01	Q20471	SWISSPROT	PUTATIVE CASEIN KINASE I F46F2.2 IN CHROMOSOME X
9514	22014		0.89	5.8E-01	BF031606.1	EST_HUMAN	601557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827298 5'
10869	23390	36405	9.44	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10915	23434		3.66	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
11021	23535		2.04	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
3079	15684		0.68	5.7E-01	6755253	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
3260	15972	28352	1.58	5.7E-01	Q9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOV01) (MOV01A)
3552	16156		2.63	5.7E-01	AB033503.1	NT	Populus euramericana peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
3973	16571	29041	3.09	5.7E-01	AF011581.1	NT	Homo sapiens T cell receptor beta chain (BV6S72-BJ1S1) mRNA, partial cds
6498	19097	31881	3.67	5.7E-01	BF035413.1	EST_HUMAN	601454982F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858590 5'
6812	19403	32219	0.72	5.7E-01	AA194201.1	EST_HUMAN	z33c08.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665874 5'
6945	18053	30478	1.28	5.7E-01	AL111440.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
7741	20249	33142	1.97	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
7911	20453		0.57	5.7E-01	AJ251835.1	NT	Mus musculus Kcnq1, Ltrpc5, Mash2, Tapa-1, Tssc4 and Tssc6 genes, alternative transcripts
9715	22213	35186	1.17	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9715	22213	35187	1.17	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10468	22962	35973	0.86	5.7E-01	BF540962.1	EST_HUMAN	602087712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066610 5'
3410	16019	28498	1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3410	16019	28498	1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
4324	16910	28351	0.69	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
8738	21277	34200	4.42	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKc Homo sapiens cDNA clone GKCF505 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8738	21277	34201	4.42	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKCC Homo sapiens cDNA clone GKCF5F05 5'
9297	21897	34844	1.11	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
11658	24085		2.5	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
11779	24166	36775	1.28	5.6E-01	AA493535.1	EST_HUMAN	ng75g10.s1 NCI_CGAP_P16 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element
12156	18028	30490	3.31	5.6E-01	AL181501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12185	24419		2.56	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
12619	24698		3.11	5.6E-01	BF573829.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1253	13850	28367	1.13	5.5E-01	8383912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2725	15280	27847	13.6	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2725	15280	27848	13.6	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2943	15559	28033	0.69	5.5E-01	5902085	NT	Homo sapiens superkiller virulicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3102	15717		1.61	5.5E-01	H46219.1	EST_HUMAN	y018a10.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178286 3'
3271	18983	28365	2.69	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3755	16358	28825	0.97	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
8386	20926	33846	0.66	5.5E-01	A1791768.1	EST_HUMAN	or82c01.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602336 5'
8682	22181		0.74	5.5E-01	U88415.1	NT	Crimean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds
10279	22774	35763	0.84	5.5E-01	T05047.1	EST_HUMAN	EST02835 Fetal brain, Stragelene (cat#936206) Homo sapiens cDNA clone HFBCQ36
151	12814	25301	12.97	5.4E-01	7657286	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
151	12814	25302	12.97	5.4E-01	7657286	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
611	13239	25713	1.6	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
611	13239	25714	1.6	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
1314	13908	26428	2.58	5.4E-01	AW895087.1	EST_HUMAN	QV4-NN0040-0704003-160-c04 NN0040 Homo sapiens cDNA
2154	14731		3.6	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of 84 of the complete genome
2296	14870	27446	2.18	5.4E-01	AJ276682.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
3984	16582	29053	0.62	5.4E-01	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5259	17822		1.04	5.4E-01	AW747972.1	EST_HUMAN	QV0-BT0041-081099-033-e02 BT0041 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5388	13239	25713	0.59	5.4E-01	AF232006.1	NT	<i>Pseudomonas syringae</i> pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsA (gsA) genes, complete cds; and unknown genes
5388	13239	25714	0.59	5.4E-01	AF232006.1	NT	<i>Pseudomonas syringae</i> pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsA (gsA) genes, complete cds; and unknown genes
5838	18462	31185	0.81	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6338	18844	31723	1.49	5.4E-01	AB025017.1	NT	<i>Rattus norvegicus</i> gene for TIS11, complete cds
7094	19665	32504	1.1	5.4E-01	BE86592.2	EST_HUMAN	601660276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906090 3'
7374	19800	32762	0.75	5.4E-01	Z21619.1	NT	<i>S. cerevisiae</i> RIB3 gene encoding DBP synthase
7374	19800	32763	0.75	5.4E-01	Z21619.1	NT	<i>S. cerevisiae</i> RIB3 gene encoding DBP synthase
							MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
7376	19902	32768	1.47	5.4E-01	Q64428	SWISSPROT	602078545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'
9901	22398		1.98	5.4E-01	BF572536.1	EST_HUMAN	
10957	23472	36497	3.25	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11485	23634	37004	5.78	5.4E-01	Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11485	23934	37005	5.78	5.4E-01	Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11586	18944	31723	2.42	5.4E-01	AB025017.1	NT	<i>Rattus norvegicus</i> gene for TIS11, complete cds
11725	24132		2.62	5.4E-01	AI858368.1	EST_HUMAN	w137g04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
							Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (BF), and complement component C2 (C2) genes.2
542	13173	25653	2.26	5.3E-01	AF019413.1	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2811	15363	27931	6.51	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2811	15363	27932	6.51	5.3E-01	4506328	NT	Homo sapiens secreted C-type lectin precursor (LIS1CL) gene, complete cds
3280	15891	28370	3.13	5.3E-01	AF087658.1	NT	
4290	16876		1.39	5.3E-01	U39687.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5049	18277	30753	1.91	5.3E-01	AI820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5840	18277	30754	1.91	5.3E-01	AI820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5742	18368	31075	0.87	5.3E-01	AA193672.1	EST_HUMAN	z42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5742	18368	31076	0.87	5.3E-01	AA193672.1	EST_HUMAN	z42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
							7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
5827	18451	31174	1.84	5.3E-01	BE645620.1	EST_HUMAN	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5827	18451	31175	1.84	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
							PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8835	21374		1.83	5.3E-01	L01950.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
8885	21423	34348	0.63	5.3E-01	BF433958.1	EST_HUMAN	7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER29 repetitive element;
8885	21423	34349	0.63	5.3E-01	BF433958.1	EST_HUMAN	7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER29 repetitive element;
10112	22607	35597	0.48	5.3E-01	AI954210.1	EST_HUMAN	w94b02.x1 NCI_CGAP_Med15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to SW:COXA_HUMAN P20674 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR;
11435	23885	36952	6.92	5.3E-01	BE566291.1	EST_HUMAN	601339887F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682188 5'
11650	24881		4.22	5.3E-01	AA916053.1	EST_HUMAN	qg30e05.s1 NCI_CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441378 3' similar to gb:J02611 APOLIPOPROTEIN D PRECURSOR (HUMAN);
849	13465	25973	19.16	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1206	13808	28319	10.07	5.2E-01	Q9WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-A15)
1233	13832	28346	2.91	5.2E-01	AF22492.1	NT	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1930	14514		4.11	5.2E-01	AL163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
2191	14787	27339	2.97	5.2E-01	AB018283.2	NT	Homo sapiens chromosome 21 segment HS21C085
3153	15767	28233	1.87	5.2E-01	U65942.1	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3274	15886		0.71	5.2E-01	D73443.1	NT	Chlamydomonas reinhardtii lsd gene for isocitrate dehydrogenase, complete cds
3452	16059		1.74	5.2E-01	AL116780.1	NT	Azotobacter vinelandii lsd gene for isocitrate dehydrogenase, complete cds
3492	16097	28572	2.46	5.2E-01	AA984185.1	EST_HUMAN	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3664	16295		0.92	5.2E-01	AF020269.1	NT	am77g05.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
5161	17730		0.87	5.2E-01	7108444	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
5314	17876		0.89	5.2E-01	AL163281.2	NT	Mus musculus vanilloid receptor-like protein 1 (Vrl1), mRNA
5834	18458	31179	0.97	5.2E-01	AA284281.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
9846	24785	35115	1.19	5.2E-01	X02218.1	NT	zc44c08.T7 Soares_senescent_fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:325169 3'
9846	24785	35116	1.19	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9845	22343	35325	0.84	5.2E-01	AA194518.1	EST_HUMAN	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9940	22435	35411	1.65	5.2E-01	AF143952.2	NT	zc05b09.r1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:628793 5'
12590	24882		4.94	5.2E-01	P18516	SWISSPROT	Homo sapiens PELOTA (PELOTA) gene, complete cds
845	13268	25746	2.13	5.1E-01	MS8509.1	NT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
876	13300	25781	3.98	5.1E-01	AJ233944.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
							Polygammaglutathione (strain PI vt) 16S rRNA gene

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
676	13300	25782	3.98	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI v1) 16S rRNA gene
1692	14284		0.88	5.1E-01	X87885.1	NT	R. norvegicus mRNA for mammalian fusca protein
2069	14649		11.33	5.1E-01	BF683095.1	EST_HUMAN	602139319F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298117 5'
4151	16743	29197	4.61	5.1E-01	AI858495.1	EST_HUMAN	wf39b12.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427263 3'
4268	16852	29300	3.03	5.1E-01	P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5229	17783		0.71	5.1E-01	BE091786.1	EST_HUMAN	IL2-BT0731-250400-077-G08 BT0731 Homo sapiens cDNA
6422	19025		0.79	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAAF07 5'
6897	19495	32316	1.42	5.1E-01	R80873.1	EST_HUMAN	y94a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
8507	21046	33966	0.73	5.1E-01	AW809881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
8507	21046	33967	0.73	5.1E-01	AW809881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
8602	22102	35065	4.6	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
9603	22103	35068	3.4	5.1E-01	W22302.1	EST_HUMAN	6581 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
10085	22560	35555	0.95	5.1E-01	M94579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
11874	24805		2.04	5.1E-01	BF030207.1	EST_HUMAN	601556863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826787 5'
12129	24385		2.01	5.1E-01	BF439982.1	EST_HUMAN	nac51f10.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element
2180	14757	27328	1.4	5.0E-01	4885552	NT	TAR1 repetitive element
2180	14757	27327	1.4	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
							Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2189	14765	27335	5.46	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (apCDGAHFEF), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
							Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (apCDGAHFEF), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2189	14765	27336	5.46	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (apCDGAHFEF), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
3740	16341	28909	5.58	5.0E-01	AE001785.1	NT	Thermotoga maritima section 97 of 136 of the complete genome
3811	16410	28875	0.85	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3942	16540	29006	3.11	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
8467	21007		1.78	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8504	21143	34057	0.64	5.0E-01	BF107848.1	EST_HUMAN	601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3'
8379	20318	33219	3.1	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136832 5'
							GLYCOCEN DEBRANCHING ENZYME (GLYCOCEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 8-ALPHA-D-GLUCOSIDASE)]
9543	22043	35004	1.34	5.0E-01	P35573	SWISSPROT	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9543	22043	35005	1.34	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) (INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE))
10281	22788		1.04	5.0E-01	BE869218.1	EST_HUMAN	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849436 5'
11815	24187		3.45	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
12554	24656		2.38	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
12569	24688		4.27	5.0E-01	Q13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
822	13439	25946	2.31	4.9E-01	BF571462.1	EST_HUMAN	602076849F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1689	14282	26827	1.6	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1949	14533	27089	1.35	4.9E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5602	18231	30881	1.32	4.9E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6187	18787	31565	2.35	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6187	18787	31566	2.35	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7475	18997	32862	1.9	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
8920	21458		1.49	4.9E-01	BF209791.1	EST_HUMAN	601874964F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'
9115	21851	34592				EST_HUMAN	hc90c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907266 3' similar to TR:O95714
9220	25126		0.88	4.9E-01	AW339905.1	EST_HUMAN	O95714 HERC2.;
10220	22715	35706	2.2	4.9E-01	10946863	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
11704	24117		0.74	4.9E-01	AF053980.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
12546	25081		2.48	4.9E-01	AF176912.1	NT	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
12555	24857	30872	5.73	4.9E-01	AA613562.1	EST_HUMAN	ng22e11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144652 3'
12930	24708		1.74	4.9E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
3591	16195		1.36	4.9E-01	11431438	NT	Homo sapiens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA
4782	17011		1.05	4.8E-01	AA912842.1	EST_HUMAN	d32a09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1525144 3'
5688	18324	30827	0.62	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
6790	18381		8.6	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
7357	19883		4.22	4.8E-01	AA659878.1	EST_HUMAN	nu86f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513
7682	20174	33081	1.85	4.8E-01	5031650	NT	Homo sapiens reproduction 8 (DRS2298E) mRNA
7738	20246	33138	0.87	4.8E-01	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7738	20246	33138	0.87	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7738	20246	33139	3.72	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7846	20388	33281	1.36	4.8E-01	AI820744.1	EST_HUMAN	y177110_y6 Soares breast 2NbrHst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element
9169	21748		1.13	4.8E-01	BE155148.1	EST_HUMAN	MER6 repetitive element;
9921	22417		0.58	4.8E-01	BF588633.1	EST_HUMAN	PM1-HT0350-201289-004-b04 HT0350 Homo sapiens cDNA
10607	23141		2.02	4.8E-01	X35502.1	NT	602184267F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'
11786	24170		1.29	4.8E-01	AL163227.2	NT	S cerevisiae ORFs from chromosome X
12016	24842		3.04	4.8E-01	AF227565.1	NT	Homo sapiens chromosome 21 segment HS21C027
12646	24895		3.36	4.8E-01	AJ132884.1	NT	Typanosoma cruzi transposon VIP II SIRE repeat region
6638	19234	32036	8.72	4.7E-01	BF217173.1	EST_HUMAN	Chlamydomonas reinhardtii cop gene, exons 1-8
7107	19447	32263	0.78	4.7E-01	AI204374.1	EST_HUMAN	601863860F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
7806	20349	33257	0.52	4.7E-01	T11414.1	EST_HUMAN	q772a09.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:175544 3'
7806	20349	33258	0.52	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5' end
9005	21542	34473	0.5	4.7E-01	6081501	NT	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5' end
10467	22961	35972	0.79	4.7E-01	AW087791.1	EST_HUMAN	Rattus norvegicus Spermine binding protein (Sbp), mRNA
10727	23253		4.94	4.7E-01	AF102873.1	NT	xb69e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581580 3'
10963	23478	36503	2.19	4.7E-01	U41089.1	NT	Influenza A virus isolate hk51897 hemagglutinin (HA) gene, partial cds
11163	23670	36715	11.61	4.7E-01	BF528658.1	EST_HUMAN	Human collagen alpha2(XI)(COL11A2) gene, exons 6 through 16, and partial cds
11254	23784	36840	2.89	4.7E-01	AW889448.1	EST_HUMAN	602043889F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4181303 5'
11904	24243		1.92	4.7E-01	BE887763.1	EST_HUMAN	RC8-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
12036	24325		1.33	4.7E-01	AW341561.1	EST_HUMAN	601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
12666	24736		1.38	4.7E-01	AF000007.1	NT	hd11c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809188 3'
3797	16397	28862	2.23	4.6E-01	AW818638.1	EST_HUMAN	Pyrococcus horikoshii OT3 genomic DNA, 1485001-1738505 nt, position (777)
3808	16406	28870	1.68	4.6E-01	BF693300.1	EST_HUMAN	RC1-ST0278-040400-018-608 ST0278 Homo sapiens cDNA
3808	16406	28871	1.68	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5323	17865		1.03	4.6E-01	M11287.1	NT	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5429	17896	30390	22.08	4.6E-01	AL163248.2	NT	Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds
							Homo sapiens chromosome 21 segment HS21C048
							AMILORIDE-SENSITIVE SODIUM CHANNEL GAMMA-SUBUNIT (EPITHELIAL NA+ CHANNEL GAMMA SUBUNIT) (GAMMA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 GAMMA SUBUNIT) (SCN9G) (GAMMA NACH)
5440	17895	30400	1.37	4.6E-01	P51170	SWISSPROT	
5612	18241	30690	1.12	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5612	18241	30691	1.12	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5693	18290	30768	3.27	4.6E-01	Q80643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5693	18290	30769	3.27	4.6E-01	Q80643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5735	18381	31087	2.39	4.6E-01	BE734781.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5748	18374	31082	4.22	4.6E-01	A1247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN ;
5748	18374	31083	4.22	4.6E-01	A1247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN ;
5756	18382	31084	1.4	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
5828	18432		1.05	4.6E-01	AF212124.1	NT	Andis schwartzi cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
5907	18529		0.86	4.6E-01	BE817247.1	EST_HUMAN	PMD-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
6058	18675	31417	0.75	4.6E-01	D28215.1	NT	Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA
6404	19007	31788	1.05	4.6E-01	AE000894.1	NT	Methanobacterium thermoautotrophicum from bases 1165751 to 1176238 (section 100 of 148) of the complete genome
6865	19599	32429	1.36	4.6E-01	U62332.1	NT	Emricella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6865	19599	32430	1.36	4.6E-01	U62332.1	NT	Emricella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7712	20221	33108	0.88	4.6E-01	AA493577.1	EST_HUMAN	nh04h05.s1 NCI_QGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element/contains element L1 repetitive element ;
8282	20803	33721	13.23	4.6E-01	BF697399.1	EST_HUMAN	602130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
9225	21741	34684	1.04	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9225	21741	34685	1.04	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9583	22083	35046	0.55	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
9583	22083	35047	0.55	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
9886	22383	35358	2.63	4.6E-01	A1915634.1	EST_HUMAN	wg73a12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
9886	22383	35359	2.63	4.6E-01	A1915634.1	EST_HUMAN	wg73a12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
10870	23391		3.09	4.6E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)
10879	23400	36416	4.13	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
10879	23400	36417	4.13	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11346	23044	36054	5.52	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11346	23044	36055	5.52	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
12854	24726		1.28	4.6E-01	M22360.1	NT	Rat plasma proteinase inhibitor alpha-1-inhibitor III group 3 variants 6J, 12J, 13J, and 17J mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1954	14538	27094	1.69	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 228 of the complete chromosome 1
1954	14538	27095	1.69	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 228 of the complete chromosome 1
2895	15512	27682	4.77	4.5E-01	AA877086.1	EST_HUMAN	z55d02.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3346	15966	28431	0.64	4.5E-01	AW083781.1	EST_HUMAN	xc25c08.x1 NCI_CGAP_Cot19 Homo sapiens cDNA clone IMAGE:2585280 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
3346	15956	28432	0.64	4.5E-01	AW083781.1	EST_HUMAN	xc25c08.x1 NCI_CGAP_Cot19 Homo sapiens cDNA clone IMAGE:2585290 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
3359	15967	28444	5.18	4.5E-01	Q05793	SWISSPROT	BASIMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3424	16032	28512	1.15	4.5E-01	AF126378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4100	16694	29195	1.35	4.5E-01	Q28247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pde) gene, exons 2 through 12
4149	16741	29195	0.73	4.5E-01	AI708908.1	EST_HUMAN	COLLAGEN ALPHA 5(V) CHAIN
4255	18015	30092	4.04	4.5E-01	AW873495.1	EST_HUMAN	as96609.x1 Barstead aceta HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'
5078	17651	30092	1.16	4.5E-01	BE863445.2	EST_HUMAN	ho60g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
5427	17984		26.74	4.5E-01	AF060195.1	NT	60165725R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
5737	18363	31070	1.37	4.5E-01	AW608814.1	EST_HUMAN	Mus musculus proteasome regulator PA28 beta subunit gene, complete cds
6719	19313		1.38	4.5E-01	Q00956	SWISSPROT	QV2-PT0012-140100-031-c09 PTO012 Homo sapiens cDNA
7443	19967	32834	1.69	4.5E-01	M37036.1	NT	COAT PROTEIN
7604	20117	32993	2.53	4.5E-01	AI858849.1	EST_HUMAN	Rat nuclear proteins B23.1 and B23.2
8249	20760		0.97	4.5E-01	M92861.1	NT	w32e02.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923 SWISNF COMPLEX 170 KDA SUBUNIT. ;
8342	20883	33804	4.02	4.5E-01	AI648596.1	EST_HUMAN	D melanogaster Shaw2 protein mRNA, complete cds
							t556g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292844 3'
8494	21033	33954	0.69	4.5E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
8716	21255		1.74	4.5E-01	11444786	NT	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
8928	21467	34395	0.69	4.5E-01	AE000218.1	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
9853	22351		1.02	4.5E-01	9630816	NT	Bombyx mori nuclear polyhedrosis virus, complete genome
10389	22863	35877	23.95	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17
10389	22863	35878	23.95	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17
10744	23268	36285	3.01	4.5E-01	AW591271.1	EST_HUMAN	xc014h01.x1 NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
11131	23639		1.9	4.5E-01	AV719382.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1];
							AV719382 GLC Homo sapiens cDNA clone GLOCED12 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11376	23828	36890	1.68	4.5E-01	BE068472.1	EST_HUMAN	RC3-BT0333-160300-016-e03 BT0333 Homo sapiens cDNA
11671	25070		3.3	4.5E-01	BE971461.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852961 5'
12370	24540		2.13	4.5E-01	BF337531.1	EST_HUMAN	602035275F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183290 5'
12442	24578		6.25	4.5E-01	11422099	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
2081	14682		1.39	4.4E-01	6680503	NT	Mus musculus integral membrane-associated protein 1 (Itmap1), mRNA
2432	14999	27572	3.26	4.4E-01	P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3357	15965	28442	1.27	4.4E-01	AF058780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3357	15965	28443	1.27	4.4E-01	AF058780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3361	15969	28446	2.31	4.4E-01	BF056726.1	EST_HUMAN	7f91d02.Y1 NCL_CGAP_Brn16 Homo sapiens cDNA clone IMAGE:3393795 5'
4318	16804		1.28	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'
5134	17706		2.07	4.4E-01	BE141396.1	EST_HUMAN	MRO-HT0078-131299-007-g05 HT0078 Homo sapiens cDNA
5277	17839	30265	0.94	4.4E-01	U61154.1	NT	Buzura suppressaria nucleopolydnavirus ecdysteroid UDP-glucosyltransferase (egt) gene, complete cds
5417	17974		0.9	4.4E-01	AW814985.1	EST_HUMAN	MR1-ST0206-120400-022-g07 ST0206 Homo sapiens cDNA
5613	18242	30692	4.06	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5613	18242	30693	4.06	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5867	18489	31215	1.72	4.4E-01	S65019.1	NT	mucin [Rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5883	18505	31231	1.9	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCCSC12 5'
6108	18724	31476	1.53	4.4E-01	A1198413.1	EST_HUMAN	q162h11.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
6108	18724	31477	1.53	4.4E-01	A1198413.1	EST_HUMAN	UNKNOWN PROTEIN ;
6387	18990	31771	1.69	4.4E-01	AW080795.1	EST_HUMAN	xc27e08.x1 NCL_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:Q95154 Q95154
6470	19071		1.02	4.4E-01	AA776132.1	EST_HUMAN	AFLATOXIN B1-ALDEHYDE REDUCTASE ;
7428	19953	32818	0.89	4.4E-01	AE009571.1	NT	ae85d11.s1 Stragene echizo brain S11 Homo sapiens cDNA clone IMAGE:970965 3' similar to gb:IM16038
7782	20325		10.05	4.4E-01	Z11678.1	NT	TYROSINE-PROTEIN KINASE LYN (HUMAN);
8698	21237	34160	1.01	4.4E-01	AA056427.1	EST_HUMAN	Helicobacter pylori 26895 section 49 of 134 of the complete genome
9078	21814	34549	0.76	4.4E-01	AF112540.1	NT	S.tuberosum mRNA for induced stolon tip protein (partial)
9111	21847	34587	0.56	4.4E-01	AW612578.1	EST_HUMAN	z162a03.s1 Stragene colon (#837204) Homo sapiens cDNA clone IMAGE:509836 3'
9214	21731	34674	1.13	4.4E-01	O62836	SWISSPROT	HIV-1 isolate 08107v8 from USA, envelope glycoprotein (env) gene, partial cds
							hm05c08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2954222 3' similar to SW:MSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
							ZINC FINGER X-CHROMOSOMAL PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9872	22369	35347	1.69	4.4E-01	AI288650.1	EST_HUMAN	q03909.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
9873	22370		2.12	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10009	22504	35495	4.51	4.4E-01	P35590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10276	22771	35759	1.43	4.4E-01	S76404.1	NT	beta-HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10278	22771	35760	1.43	4.4E-01	S76404.1	NT	beta-HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
11939	24271	31016	4.68	4.4E-01	6877874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
11952	25000		14.98	4.4E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
12517	24635		1.5	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
436	13069	25564	1.77	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
436	13069	25565	1.77	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
3086	15711	28182	0.91	4.3E-01	AW999477.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4231	16819	29298	1.21	4.3E-01	J00306.1	NT	Human somatostatin 1 gene and flanks
4495	13069	25584	3.98	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4495	13069	25585	3.96	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5597	18198	30845	0.76	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5567	18198	30846	0.76	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
6049	18668	31407	1.34	4.3E-01	BE181655.1	EST_HUMAN	QV1-HT0638-070500-191-d08 HT0638 Homo sapiens cDNA
6085	18682	31424	2.06	4.3E-01	AF179825.1	NT	Saimiri sciureus olfactory receptor (SSC188) gene, partial cds
6809	19400	32215	4.28	4.3E-01	AJ001678.1	NT	Columba coturnix japonica fnG gene
6949	19526		0.78	4.3E-01	O33357	SWISSPROT	DNA GYRASE SUBUNIT B
7456	19880		1.76	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4158296 5'
8366	20906		2.66	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-I (flaC-flaI) genes, complete cds
9179	21756	34702	0.7	4.3E-01	Y14604.1	NT	Erwinia amylovora rcsV gene
9842	22142	35109	2.63	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
9842	22142	35110	2.63	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
10128	22623	35614	0.57	4.3E-01	AW170559.1	EST_HUMAN	TR-000189 000189 MU-ADAPTIN-RELATED PROTEIN 2 ;
10811	19616	32451	2.52	4.3E-01	AF075628.1	NT	Equus caballus microsatellite LEX027
11588	24031	37101	1.54	4.3E-01	AB74332.1	EST_HUMAN	t284d04.x1 NCI_CGAP_O35 Homo sapiens cDNA clone IMAGE:2283351 3'
11632	18198	30845	1.55	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
11632	18198	30846	1.55	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
12616	24698		2.81	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor whiH gene
1402	15440	26524	1.39	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
1991	14573		1.04	4.2E-01	AA761653.1	EST_HUMAN	nt24d09.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1288686 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2068	14646		1.37	4.2E-01	AF258325.1	NT	Plasmodium falciparum multidrug resistance protein Pgh1 gene, complete cds
3669	16270	28738	4.81	4.2E-01	AE003947.1	NT	Xylella fastidiosa, section 93 of 229 of the complete genome
3689	16300	28768		4.2E-01	AI280338.1	EST_HUMAN	q94b01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878945 3'
3773	18014		0.6	4.2E-01	N81203.1	EST_HUMAN	788E1 fetal brain cDNA Homo sapiens cDNA clone 788E1-K similar to R07879, Z40498
3948	18546	29014	0.73	4.2E-01	AW835927.1	EST_HUMAN	QV0-L T0015-180200-127-H01 LT0015 Homo sapiens cDNA
4054	16651	29118	0.98	4.2E-01	Q04886	SWISSPROT	SOX-8 PROTEIN
4807	17385	29835	4.3	4.2E-01	AA534093.1	EST_HUMAN	ni69h01.s1 NCL CGAP_P710 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4895	17470	29826	4.04	4.2E-01	R13467.1	EST_HUMAN	yf77e01.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
5232	17796		3.77	4.2E-01	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
5891	18514	31241	1.52	4.2E-01	BF242055.1	EST_HUMAN	601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
5953	18575	31309	2.16	4.2E-01	AW854162.1	EST_HUMAN	RC3-CT0254-060400-029-g04 CT0254 Homo sapiens cDNA
6352	18957	31736	1.08	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7031	19565	32392	10.28	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7031	19565	32393	10.29	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7082	24776	32492	1.97	4.2E-01	S82504.1	NT	Brcat=breast cancer gene (rats, WF, spleen, Genomic, 419 nt, segment 2 of 2)
7150	18683	32524	5.81	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7934	20476	33385	2.61	4.2E-01	AW957448.1	EST_HUMAN	EST369413 IMAGE resequences, MAGE Homo sapiens cDNA
7934	20476	33386	2.61	4.2E-01	AW957448.1	EST_HUMAN	EST369413 IMAGE resequences, MAGE Homo sapiens cDNA
8148	20889	33802	0.55	4.2E-01		NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
9235	21761	34706	0.52	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
9235	21761	34707	0.52	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
9880	22377		0.81	4.2E-01	AA705007.1	EST_HUMAN	z95f01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462849 3'
10083	22578	35571	0.5	4.2E-01	AF181854.1	NT	Lassa virus strain 803213 glycoprotein precursor and nucleoprotein genes, complete cds
10390	22884	35879	1.35	4.2E-01	AW863866.1	EST_HUMAN	MR3-SN0010-280300-103-H07 SN0010 Homo sapiens cDNA
10921	23440	36481	3.69	4.2E-01	AB023489.1	EST_HUMAN	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
11273	23726	36780	2.65	4.2E-01	BE966485.2	EST_HUMAN	601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
12561	24661		1.49	4.2E-01	AV731815.1	EST_HUMAN	AV731815 HTF Homo sapiens cDNA clone HTF8H05 5'
1133	13736	26245	1.59	4.1E-01	A905491.1	EST_HUMAN	RC-BT091-210159-142 BT091 Homo sapiens cDNA
1142	13745	26254	1.54	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1142	13745	26255	1.54	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2735	15290	27858	1.58	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2967	15582	29081	2.11	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2867	15582	28062	2.11	4.1E-01	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3342	15952	28428	0.66	4.1E-01	AA906344.1	EST_HUMAN	094508.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
3839	16438	28859	0.58	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGE resequences, MAGG Homo sapiens cDNA
3839	16438	28800	0.58	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGE resequences, MAGG Homo sapiens cDNA
4381	16948	29390	2.82	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoJ, isoK, isoL, isoM, isoN, isoO and isoP genes
4393	16979		0.76	4.1E-01	AA90257.1	EST_HUMAN	on33402.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4774	17355	29807	1.31	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
6141	18755	31513	3.87	4.1E-01	BF681393.1	EST_HUMAN	602158590F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
7480	19983	32848	2.74	4.1E-01	U67535.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
7978	20521	33427	1.31	4.1E-01	BF574604.1	EST_HUMAN	602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'
9019	21556	34484	1.26	4.1E-01	6755521	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Sitpec-pending), mRNA
9484	21941		0.61	4.1E-01	AF160597.1	NT	Voalevo gymnoceus Vgym560 cytochrome b (cytb) gene, complete cds; mitochondrial gene for
10184	22659		1.26	4.1E-01	AL139076.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 3/6
10310	22804	35766	0.79	4.1E-01	AV649579.1	EST_HUMAN	AV649579 GLC Homo sapiens cDNA clone GLCBVD12 3'
10401	22895	35890	0.51	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10401	22895	35891	0.51	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10471	22965		2.29	4.1E-01	BF346382.1	EST_HUMAN	CM2-HT0137-200999-010-408 HT0137 Homo sapiens cDNA
10719	23247	36262	45.22	4.1E-01	X68700.1	NT	Zea mays ZMIPMS2 gene for 19 kDa zein protein
11270	23008	36015	3.57	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1)
12290	25049		2.6	4.1E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
147	15408		4.55	4.0E-01	AW847123.1	EST_HUMAN	RC2-CT0201-280999-012-010 CT0201 Homo sapiens cDNA
1077	13681	26181	0.82	4.0E-01	8404656	NT	Laqueus rubellus mitochondrion, complete genome
1384	13978	26505	1.51	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
1532	14124		4.1	4.0E-01	6679259	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2049	15456	27200	1.22	4.0E-01	Z96933.1	NT	Ascaris lumbricoides masc2 gene
2049	15456	27201	1.22	4.0E-01	Z96933.1	NT	Ascaris lumbricoides masc2 gene
2204	14780	27352	17.82	4.0E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2204	14780	27353	17.82	4.0E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2831	12811	25299	1.45	4.0E-01	6678490	NT	Mus musculus ubiquitin-protein ligase e3 component n-recognition (Ubr1), mRNA
2895	15811	28090	1.23	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2895	15811	28091	1.23	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3758	16359	28829	2.17	4.0E-01	AF068903.1	NT	Streptococcus pneumoniae Y1C (y1C), Y1D (y1D), penicillin-binding protein 2x (bbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3899	16408	28960	3.04	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3899	16498	28961	3.04	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4942	17517		8.41	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
6069	18686	31429	1.18	4.0E-01	AW070610.1	EST_HUMAN	EST382691 IMAGE resequences, MAGK Homo sapiens cDNA
6567	19165	31981	0.87	4.0E-01	P27285	SWISSPROT	STRUCTURAL POLYPROTEIN (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
7777	20286	33183	0.72	4.0E-01	P27548	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 4
7869	20411	33317	0.46	4.0E-01	BF092634.1	EST_HUMAN	MR4-TN0110-180900-202-g02 TN0110 Homo sapiens cDNA
7954	20498	33408	0.99	4.0E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
8936	21474	34394	0.88	4.0E-01	AA323289.1	EST_HUMAN	EST26066 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
11443	23863		1.65	4.0E-01	BF030262.1	EST_HUMAN	601558283F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828092 5'
11568	24015		3.52	4.0E-01	L76080.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
11958	24901		2.5	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12518	24636		1.42	4.0E-01	P36049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION
1420	14013	26543	1.98	3.9E-01	AF206618.1	NT	Gorilla gorilla carboxyl-ester lipase (GEL) gene, complete cds
2668	15226	27798	3.8	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2730	15285	27851	3.79	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2730	15285	27852	3.79	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3131	15745	28214	3.95	3.9E-01	AJ258896.1	NT	Sinorhizobium meliloti egl, syB2, cya3 genes and orf3
4153	16745	29199	1.49	3.9E-01	BF592611.1	EST_HUMAN	7161d01.x1 NCJ_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339169 3'
5130	17702	30136	1.86	3.9E-01	BE728687.1	EST_HUMAN	601563948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833699 5'
6080	18708	31454	6.44	3.9E-01	BF208036.1	EST_HUMAN	601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
6426	19029	31812	0.68	3.9E-01	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7896	20438	33343	0.78	3.9E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds
8795	21334	34269	0.73	3.9E-01	AW177011.1	EST_HUMAN	CM3-CT0105-170889-004-b08 CT0105 Homo sapiens cDNA
8804	21343		0.7	3.9E-01	BF348534.1	EST_HUMAN	602018944F1 NCJ_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155322 5'
9181	21686	34640	1.24	3.9E-01	AW195888.1	EST_HUMAN	xn86d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:094821

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9484	21989	34945	1.42	3.9E-01	AI937337.1	EST_HUMAN	wp76a02.x1 NCI_QGAP_Bm25 Homo sapiens cDNA clone IMAGE:2407658 3' similar to SW:RFX5_HUMAN P48382 BINDING REGULATORY FACTOR.
9792	22290	35274	3.68	3.9E-01	M19879.1	NT	Human cladinin 27 gene, exons 10 and 11, and L1 and Alu repeats
9856	22354		0.5	3.9E-01	11485820	NT	Porphyra purpurea mitochondrion, complete genome
10071	22566	35561	0.69	3.9E-01	D80722.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10492	22886	35983	0.46	3.9E-01	M18440.1	NT	Human beta-B2-crystallin (B2-1) gene, exon 4, partial cds
10700	23228		1.82	3.9E-01	AV695974.1	EST_HUMAN	AV695974 GKC Homo sapiens cDNA clone GKCBQC11 5'
11728	24977		3.42	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
11854	24214		1.42	3.9E-01	Q61670	SWISSPROT	HOMEOBOX PROTEIN HLX1
11930	24285	31015	1.56	3.9E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
12389	24551		1.37	3.9E-01	11433335	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
171	12834		19.28	3.9E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
531	13182		3.11	3.9E-01	AB029281.1	NT	Mus musculus pcm-1 mRNA for pericentriolar material-1, complete cds
1911	14496		0.99	3.9E-01	AE003870.1	NT	Xylella fastidiosa, section 18 of 229 of the complete genome
2605	15187	27734	1.89	3.9E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2681	15473	27781	3.94	3.9E-01	6878002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
3034	15650		0.89	3.9E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3084	15699	28173	2.2	3.9E-01	AF043383.1	NT	Pleurocetes americanus aminopeptidase N (ampN) gene, partial cds
3530	16135	28815	9.83	3.9E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3592	16196		0.59	3.9E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3609	16196		0.75	3.9E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3820	16420	28882	0.94	3.9E-01	BE154080.1	EST_HUMAN	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
3989	16587	29058	0.8	3.9E-01	8754095	NT	Mus musculus general transcription factor II1 (Gtf2), mRNA
4138	16730	29183	0.69	3.9E-01	AJ271381.2	NT	Takifugu rubripes wnt2 (partial), frank1, cfr and frank2 (partial) genes
5271	17833	30259	0.98	3.9E-01	BE544653.1	EST_HUMAN	601074110F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460154 5'
							y68a11.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:210428 5' similar to gbIM87933JHUMAALU364 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gbIM96956 EPIDERMAL GROWTH FACTOR-LIKE CRIPTO PROTEIN (HUMAN); contains Alu repetitive element; contains MER4 repetitive element
5412	17969	30378	1.07	3.9E-01	H64927.1	EST_HUMAN	TRANSSCRIPTION FACTOR SOX-10
5784	18419	31135	1.11	3.9E-01	Q04888	SWISSPROT	p10n protein [mink, Genomic, 2446 nt]
6481	19082		0.68	3.9E-01	S48825.1	NT	
6737	19331	32137	5.29	3.9E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271299-049-e02 BT0537 Homo sapiens cDNA
6857	19591	32423	3.97	3.9E-01	AI374601.1	EST_HUMAN	hs411.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7019	19517	32339	1.33	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7525	20045		4.75	3.8E-01	X81597.1	NT	M.musculus gene for kallikrein-binding protein
8238	20779	33700	0.49	3.8E-01	M81385.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8492	21031	33951	2.34	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8560	21099	34019	1.14	3.8E-01	11441284	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
8751	21280	34210	1.12	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9480	21879		4.03	3.8E-01	T95413.1	EST_HUMAN	ye43h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains
11408	23859		3.5	3.8E-01	BE719219.1	EST_HUMAN	Alu repetitive element; contains PTR5 repetitive element ;
11541	23989	37080	2.95	3.8E-01	R42550.1	EST_HUMAN	RCO-HT0841-Q40900-032-b12 HT0841 Homo sapiens cDNA
11541	23989	37061	2.95	3.8E-01	R42550.1	EST_HUMAN	y92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
11940	24272		2.91	3.8E-01	AE001124.1	NT	y92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
12069	24888		1.75	3.8E-01	U94788.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12189	24421		1.45	3.8E-01	BE829256.1	EST_HUMAN	Human p53 (TP53) gene, complete cds
12565	24864		2.22	3.8E-01	U78031.1	NT	QV3-ET0063-190700-271-a05 ET0063 Homo sapiens cDNA
12638	24713	30866	1.25	3.8E-01	AF194972.1	NT	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds
2521	19085	27657	15.01	3.7E-01	AB037831.1	NT	Mus musculus developmental control protein mRNA, partial cds
3507	16112	28589	10.84	3.7E-01	AF056336.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3638	16536	29003	0.88	3.7E-01	AA319482.1	EST_HUMAN	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
4313	16899	29344	9.19	3.7E-01	A1218707.1	EST_HUMAN	EST121715 Adrenal gland tumor Homo sapiens cDNA 5' end
4412	16997	29440	1.18	3.7E-01	AW878037.1	EST_HUMAN	ck39c07.x1 Soares NSF F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4479	17064	29514	3.13	3.7E-01	AE002408.1	NT	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
5938	18557	31285	1.27	3.7E-01	AF135187.1	NT	Nassaria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome
6105	18721	31474	0.94	3.7E-01	AL163278.2	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
6633	19229	32033	1	3.7E-01	M10806.1	NT	Homo sapiens chromosome 21 segment HS21C078
6651	19247		0.81	3.7E-01	L10353.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
7187	19728	32579	4.44	3.7E-01	11525843	NT	Mus saxicida haptoglobin mRNA, complete cds
8271	20812	33733	1.88	3.7E-01	11436739	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
8271	20812	33734	1.88	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8306	20847	33770	0.78	3.7E-01	AA902912.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
9129	21664		1.54	3.7E-01	AJ271366.1	NT	ck43b11.s1 NCI_CGAP_La2 Homo sapiens cDNA clone IMAGE:1516701 3'
10074	22569		0.46	3.7E-01	K00891.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCDO gene)
10111	22606	35596	4.17	3.7E-01	A1336411.1	EST_HUMAN	mouse Ig germline alpha membrane exons region
10809	23428	36446	3.47	3.7E-01	AJ297357.1	NT	q146b07.x1 Soares Fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950997 3'
							Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10909	23428	38447	3.47	3.7E-01	AJ297357.1	NT	Homo sapiens partial UMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11341	23039	36048	4.81	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
11549	23997		1.6	3.7E-01	AA973540.1	EST_HUMAN	cc46d03.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569221 3' similar to gb:IM77698 TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN);
11603	24046		2.78	3.7E-01	8677678	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
11640	24601		1.82	3.7E-01	J04982.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
11821	24191		4.15	3.7E-01	AJ243525.1	NT	Chlamydomonas psittaci partial omp1 gene for outer membrane protein 1
11913	24251		4.72	3.7E-01	D86976.1	NT	Human mRNA for KIAA0223 gene, partial cds
12302	24499		2.94	3.7E-01	AL121154.1	EST_HUMAN	DKFZp762K075_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K075 5'
12377	24545	30804	7.01	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
282	12838	25424	1.07	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
1033	13643		8.45	3.6E-01	U89241.1	NT	Human mlbp gene, partial cds
1357	13951	26477	4.32	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1357	13951	26478	4.32	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1859	14543	27099	6.39	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1859	14543	27100	6.39	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1994	14576	27138	7.23	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2098	14877		0.88	3.6E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2309	14881		1.13	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2433	15000		2.49	3.6E-01	X76725.1	NT	P. irregularis (P3804) gene for actin
2528	15082	27665	3.34	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA
2659	15218	27789	1.38	3.6E-01	P24206	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2824	18012		10.38	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (sug3) mRNA, complete cds
3518	18121	28600	2.16	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3516	18121	28601	2.16	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4497	17081	29530	1.97	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150800-014-b12 HT0545 Homo sapiens cDNA
4850	17428	29880	0.94	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
4887	17443	29894	0.65	3.6E-01	Y11526.1	NT	Z. mays mRNA for casein kinase II alpha subunit
5153	17729	30154	2.28	3.6E-01	AW393693.1	EST_HUMAN	ha02g04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872568 3'
5261	17824	30249	0.58	3.6E-01	BE087698.1	EST_HUMAN	MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
6238	18845	31618	1.16	3.6E-01	P16431	SWISSPROT	FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6604	19201	32006	1.68	3.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
7202	19733		4.57	3.6E-01	R94090.1	EST_HUMAN	y74006.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:275987 5'
7327	19854	32717	1.73	3.6E-01	AW027174.1	EST_HUMAN	w72c10.x1 Soares_thymus_NHFTb Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
8166	20707	33623	0.68	3.6E-01	P98167	SWISSPROT	O15117 FYN BINDING PROTEIN. [1];
8221	20782	33678	13.59	3.6E-01	AL161583.2	NT	SCO-SPONDIN
8932	21470	34388	3.06	3.6E-01	4504956	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
8932	21470	34388	3.06	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
8932	21470	34388	3.06	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9120	21656	34597	1.32	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9320	21834	34784	0.92	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9320	21834	34785	0.92	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9390	21813		0.54	3.6E-01	X62825.1	NT	C. perfingens plc gene for phospholipase C upstream region containing bent DNA fragment
9777	22275	35260	16.15	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
9904	22401	35374	0.53	3.6E-01	AW762801.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
9904	22401	35375	0.53	3.6E-01	AW762801.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
10823	23344	36359	2.51	3.6E-01	BE902390.1	EST_HUMAN	601670418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
10987	23501	36531	4.15	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11065	23577	36615	2.02	3.6E-01	L41687.1	NT	Mus musculus T-cell receptor V region delta 1 chain gene, 5' region
11318	23016	36025	4.07	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
11680	25109		2.45	3.6E-01	Y19210.1	NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
11768	24159		5.79	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
11923	24258		4.7	3.6E-01	U66888.1	NT	Mus musculus Emr1 mRNA, complete cds
12308	24502		2.16	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 (AF10), mRNA
120	12791	25273	1.35	3.5E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
223	12884	25369	2.67	3.5E-01	6678933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
706	13327	25814	4.48	3.5E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
754	13373	25868	1.39	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
754	13373	25869	1.39	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
812	13430	25935	3.83	3.5E-01	BF129796.1	EST_HUMAN	901811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1682	14274	28807	1.91	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2322	14893	27469	1.12	3.5E-01	P06798	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)
2637	15472	27770	1.92	3.5E-01	AA223252.1	EST_HUMAN	z08a09.e1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:850872 3'
2729	15284		11.8	3.5E-01	U05897.1	NT	Fibrobacter succinogenes S85 endoglucanase E (celE) and endoglucanase D (celD) gene, complete cds
3030	15646	28124	0.57	3.5E-01	AA057891.1	EST_HUMAN	204703.11 Stratagene corneal stroma (#037222) Homo sapiens cDNA clone IMAGE:512285 5'
3878	16476		1.27	3.5E-01	AA642138.1	EST_HUMAN	nr60d03.s1 NCI_CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4349	16836	29377	2.3	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hox5b) gene, complete cds
5014	17588	30031	0.57	3.5E-01	N81203.1	EST_HUMAN	788E1 fetal brain cDNA Homo sapiens cDNA clone 788E1-K similar to R07879, Z40498
5066	17639	30082	4.33	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5537	18169	30583	0.74	3.5E-01	Q96887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5537	18169	30584	0.74	3.5E-01	Q96887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5738	18384	31071	1.42	3.5E-01	D42045.1	NT	Human mRNA for KIAA0086 gene, complete cds
6384	18988		0.9	3.5E-01	AW663916.1	EST_HUMAN	PM4-SN0012-030400-001-a11 SN0012 Homo sapiens cDNA
6540	19139	31932	0.75	3.5E-01	AA431833.1	EST_HUMAN	zw79f03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR:G1066935
6578	19176	31976	0.72	3.5E-01	U37150.1	NT	G1066935 F10F2.1 ;
6770	19363	32172	0.93	3.5E-01	O24357	SWISSPROT	Bos taurus peptidyl methionine sulfoxide reductase (msrA) mRNA, complete cds
7116	19456		3.51	3.5E-01	X08605.1	NT	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
8016	20558		2.02	3.5E-01	11448042	NT	S. scrofa mRNA for CD31 protein (PECAM-1)
8019	20561	33462	0.65	3.5E-01	BF358871.1	EST_HUMAN	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8403	20943		0.61	3.5E-01	AF051661.1	NT	RC4-E10024-280800-014-d07 ET0024 Homo sapiens cDNA
8857	21396	34319	1.12	3.5E-01	4507610	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
9651	22150	35120	1.93	3.5E-01	Q02284	SWISSPROT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
9801	22269	35284	4.91	3.5E-01	Z28825.1	NT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
9877	22374	35351	1.14	3.5E-01	BE174794.1	EST_HUMAN	X. laevis gene for albumin including HP 1 enhancer
10613	23146	36157	4	3.5E-01	X61084.1	NT	OV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
10902	23422	36440	2.09	3.5E-01	AJ243178.1	NT	C. griseus rhodopsin gene for opsin protein
10902	23422	36441	2.09	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11462	23912	36879	1.93	3.5E-01	N77597.1	EST_HUMAN	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11532	23980	37050	1.71	3.5E-01	U05145.1	NT	y290h12.r1 Soares_multiple sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:290375 5'
							Human glucokinase (GCK) gene, repeat polymorphism

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11778	25112		1.51	3.5E-01	AF297468.1	NT	Schistosoma mansoni strain NMRI chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds
11851	24211		7.56	3.5E-01	X64565.1	NT	B. taurus alpA1 gene for F(0)F(1) ATP synthase alpha-subunit
12014	24313		2.03	3.5E-01	AE001774.1	NT	Thermotoga maritima section 86 of 136 of the complete genome
12209	24433		2.21	3.5E-01	AE001891.1	NT	Thermotoga maritima section 3 of 136 of the complete genome
12643	24950	30625	2.64	3.5E-01	H80814.1	EST_HUMAN	ys64f1.1.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:218597 5'
12643	24950	30626	2.64	3.5E-01	H80814.1	EST_HUMAN	ys64f1.1.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:218597 5'
736	13356		1.5	3.4E-01	AJ242856.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
1011	13821	26136	7.62	3.4E-01	Y08798.2	NT	Pseudomonas fluorescens colR, colS genes, orf222 and partial inaA gene
1013	13823	26138	8.97	3.4E-01	AW380120.1	EST_HUMAN	QV3-HT0261-241189-019-g10 HT0261 Homo sapiens cDNA
1371	13965	26491	1.86	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2445	15012	27584	2.6	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3032	15648	28126	0.73	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3032	15648	28127	0.73	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3183	15796	28268	0.96	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3197	15809	28282	6.78	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3387	15996	28473	0.84	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3584	16188	28671	4.84	3.4E-01	AF108835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3858	16456		1.32	3.4E-01	BF449010.1	EST_HUMAN	7n94a01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q8UJ15
4108	16702		1.23	3.4E-01	AF184614.1	NT	Q9UJ15 DJ18C9.1 ;
4126	16718		1.56	3.4E-01	AA584186.1	EST_HUMAN	Homo sapiens p47-phox (NCF1) gene, complete cds
4594	17177	28624	0.7	3.4E-01	AF166341.1	NT	no11b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4749	17330	28773	2	3.4E-01	BE069912.1	EST_HUMAN	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4765	17346	28795	1.01	3.4E-01	BF314689.1	EST_HUMAN	MIR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
5087	17660		4.2	3.4E-01	A1240973.1	EST_HUMAN	601901632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130935 5'
5884	18488	31210	2.9	3.4E-01	AL161594.2	NT	q95c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element;
5979	18599		5.68	3.4E-01	AA085313.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6158	18771		2.44	3.4E-01	L02871.1	NT	zn12d11.s1 Sitalagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:547221 3'
							Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6181	18781	31560	0.69	3.4E-01	BE748912.1	EST_HUMAN	60157181T1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3838826 3'
6258	18865	31635	2.45	3.4E-01	AW204505.1	EST_HUMAN	UI-H-B11-ael-12-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6382	18886	31708	1.62	3.4E-01	AL120544.1	EST_HUMAN	DKFZp761A249_r1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZp761A249 5'
6841	19431		1.32	3.4E-01	N95225.1	EST_HUMAN	zb53e12.s1 Soares_fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:307342 3'
7027	19561	32388	1.09	3.4E-01	AI468082.1	EST_HUMAN	tm83g05.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
7847	20389		0.51	3.4E-01	AE000493.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
8179	20720	33635	0.51	3.4E-01	Y14930.1	NT	Homo sapiens TCRAV28 gene, allele A4, partial
8424	20864		1.92	3.4E-01	AA337063.1	EST_HUMAN	EST41765 Endometrial tumor Homo sapiens cDNA 5' end
8498	21037	33958	0.88	3.4E-01	L04690.1	NT	Crcetulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
8788	21325	34249	1.63	3.4E-01	9633624	NT	Bovine enterovirus strain K2577, complete genome
9139	21674	34616	3.89	3.4E-01	P28013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9139	21674	34617	3.89	3.4E-01	P28013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9342	21856		0.59	3.4E-01	AB017510.1	NT	Ephydratia fluviatilis mRNA for PLC-gammaS, complete cds
9367	20306	33208	4.77	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9367	20306	33209	4.77	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9812	22112	35075	0.88	3.4E-01	U68763.1	NT	Glycine max putative transcription factor SCOF-1 (scf-1) mRNA, complete cds
9804	22302	35288	1.99	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10373	22887		0.54	3.4E-01	AE004096.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
10895	23416		4.42	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
10932	23450	36471	2.61	3.4E-01	P06925	SWISSPROT	PROBABLE E4 PROTEIN.
10969	23484	36512	2.72	3.4E-01	AF045981.1	NT	Rutillus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11164	23671	36716	1.89	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11164	23671	36717	1.89	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11372	23824	36887	2.27	3.4E-01	AB036507.1	NT	Rattus norvegicus mRNA for s-glycerin/MUC18, complete cds
11401	23852	36917	4.36	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
11614	24056	37121	1.75	3.4E-01	BF061848.1	EST_HUMAN	7k89d12.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3480646 3'
11655	24882		2.12	3.4E-01	U93604.1	NT	Citrus variegation virus putative replicase gene, partial cds
11771	24160		1.44	3.4E-01	Z21621.1	NT	S. cerevisiae RIB5 gene encoding Riboflavin synthase
11873	24836		1.8	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Owp8p (owp8) gene, complete cds
11998	24303		14.59	3.4E-01	L26336.1	NT	Human autoantigen mRNA, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12023	24865		3.18	3.4E-01	BE218652.1	EST_HUMAN	h42h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13
12075	24974		2.44	3.4E-01	9838361	NT	PTR5 repetitive element;
12198	24424	30850	2.68	3.4E-01	AJ287131.1	NT	Beta vulgaris mitochondrion, complete genome
12427	25068		1.25	3.4E-01	AJ288948.1	NT	Mus musculus SIL_MAP_17, CYP_a, SCL & CYP_b genes
							Clostridium cellulyticum partial spoVB gene and spo0A gene, strain ATCC 35319
12523	24639		2.55	3.4E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-
12851	24723		2.71	3.4E-01	11486174	NT	hydroxylase (CYP21B), complement component C4 (C4B) G11, helixase (SK12W), RD, complement factor B
16	12695	25151	13.68	3.3E-01	X07990.1	NT	(Bf) and complement component C2 (C2) genes,>
110	12695	25151	3.75	3.3E-01	X07990.1	NT	Neogleria gruberi mitochondrion, complete genome
473	13106	25599	1.08	3.3E-01	AL161545.2	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
681	13285	25768	1.87	3.3E-01	7662485	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
1242	13840	26358	2.96	3.3E-01	Q12446	SWISSPROT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
1350	13945	26469	3.58	3.3E-01	BF568880.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
1648	14241	26775	1.43	3.3E-01	6753685	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1773	14363		1.44	3.3E-01	AA332734.1	EST_HUMAN	PROLINE-RICH PROTEIN LAS17
2075	14665		1.22	3.3E-01	AF031148.1	NT	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
2450	15017		5.41	3.3E-01	4507834	NT	Mus musculus disintegrin 5 (Dign5), mRNA
2976	15592	28074	2.14	3.3E-01	AJ251805.1	NT	EST36722 Embryo, 8 week [Homo sapiens cDNA 5' end
3049	15685		0.68	3.3E-01	O02743	SWISSPROT	Methylobacterium capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds
3091	15706	28178	0.82	3.3E-01	AJ007932.2	NT	Homo sapiens uridine monophosphate synthetase (urate phosphoribosyl transferase and orotidine-5'-
3542	16147	28629	0.99	3.3E-01	AB012922.1	NT	decarboxylase) (UMPS) mRNA
3882	16480	28942	2.14	3.3E-01	O84845	SWISSPROT	Bacteriophage phi-Ye03-12 complete genome
3890	16489	28949	0.95	3.3E-01	P22602	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION
4037	16635	29104	1.49	3.3E-01	AL161498.2	NT	FACTOR 35 KD SUBUNIT (CLMF P35)
4073	16669	29130	1.95	3.3E-01	AF200446.1	NT	Streptomyces argillaceus mihramycin biosynthetic genes
4457	17043		1.44	3.3E-01	D31682.1	NT	Homo sapiens MTA1-L1 gene, complete cds
4769	17377		1.57	3.3E-01	AI539114.1	EST_HUMAN	EXODEOXYRIBONUCLEASE V BETA CHAIN
4984	17538	29980	1.44	3.3E-01	D64003.1	NT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT
							PROTEINASE (HC-PRO); PROTEIN P3]
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
							Hypoxylon fragiforme chitin synthase gene, partial cds
							Rattus norvegicus DNA for regucalcin, partial cds
							tp78b12.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN
							PEPTIDE TRANSPORTER 1 (HUMAN);
							Synochocystis sp. PCC6803 complete genome, 22/27, 2755703-2868768

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriplor
5527	18159	30573	2.75	3.3E-01	X89819.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5527	18159	30574	2.75	3.3E-01	X89819.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
6101	18717	31468	1.72	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3875753 3'
6101	18717	31469	1.72	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3875753 3'
6188	18798	31567	12.71	3.3E-01	P05691	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
6969	19546	32369	4.8	3.3E-01	A1628131.1	EST_HUMAN	ty64h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
6969	19546	32370	4.8	3.3E-01	A1628131.1	EST_HUMAN	repetitive element; contains element L1 repetitive element ;
7758	20266	33162	1.81	3.3E-01	N85148.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
8497	21036	33957	17.55	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
8693	21202	34120	0.48	3.3E-01	BF210322.1	EST_HUMAN	60187328F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'
8696	21235	34157	0.49	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
8696	21235	34158	0.49	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
9042	21579	34508	0.83	3.3E-01	Q62925	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9300	21900	34848	0.98	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9300	21900	34849	0.98	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9430	21939	34887	3.24	3.3E-01	N69866.1	EST_HUMAN	za67h01.s1 Soares fetal lung N6HL19W Homo sapiens cDNA clone IMAGE:287649 3'
9471	21870	34819	2.93	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
9902	22398		2.16	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
10600	23134	36147	2.93	3.3E-01	X63953.1	NT	D. mauritiana Adh gene
10600	23134	36148	2.93	3.3E-01	X63953.1	NT	D. mauritiana Adh gene
10905	23424		1.8	3.3E-01	BF528499.1	EST_HUMAN	602070802F1 NCI_CGAP_Bme4 Homo sapiens cDNA clone IMAGE:4213585 5'
11110	23620	36661	17.52	3.3E-01	BE219351.1	EST_HUMAN	nv51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
							GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
11223	23754	36812	4.97	3.3E-01	P47953	SWISSPROT	L-29 (CBP30)
11565	24012		4.68	3.3E-01	AA806821.1	EST_HUMAN	cb71g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
11584	12695	25151	2.48	3.3E-01	X07890.1	NT	Rhizobium leguminosarum syn plasmid pRL 5J1 nodX gene
11759	24153	36771	1.96	3.3E-01	6598319	NT	Homo sapiens aldehyde oxidase 1 (AOX1). mRNA
12510	24631		36.28	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (2/7)
482	13115		1.78	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
747	13367		0.76	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1204	13804	28317	27.96	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1325	13919	26441	1.39	3.2E-01	Z50202.1	NT	P. vulgaris arcs-1 gene
1434	14027	26555	7.37	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1811	14401	26946	0.92	3.2E-01	Z36041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172c
1819	14409	26954	6.36	3.2E-01	AW957194.1	EST_HUMAN	EST369284 MAGE resequences, MAGD Homo sapiens cDNA
1819	14409	26955	6.36	3.2E-01	AW957194.1	EST_HUMAN	EST369284 MAGE resequences, MAGD Homo sapiens cDNA
1883	14469	27026	1.22	3.2E-01	AL111655.1	NT	Bobyts cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2205	14781	27354	2.89	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2578	15140		2.24	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pbxox1), mRNA
2734	16289	27857	1.09	3.2E-01	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3668	16269		0.76	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4023	16621		0.61	3.2E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4483	17088	28518	1.64	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4597	17181	29628	1.56	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4844	17422		6.52	3.2E-01	BF693617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
5009	17582	30025	0.63	3.2E-01	Q57081	SWISSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P69)
5174	17741	30170	0.98	3.2E-01	BE782748.1	EST_HUMAN	601465591F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868789 5'
5392	17950	30363	0.93	3.2E-01	AY008847.1	NT	Homo sapiens interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds
5476	18110	30519	2.5	3.2E-01	BE173994.1	EST_HUMAN	CM0-HT0569-060300-269-f10 HT0569 Homo sapiens cDNA
6112	18728	31481	1.18	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
6831	19421		1.03	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
8113	20654	33563	1.33	3.2E-01	M60266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
8210	20751	33665	0.51	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat; map NOS-D12W ox1
8308	20849	33772	11.34	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8311	20852	33777	16.78	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
8398	20938		1.43	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8437	20977	33981	1.22	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8437	20977	33982	1.22	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8508	21047	33968	2.72	3.2E-01	AE002015.1	NT	Dainococcus radiodurans R1 section 152 of 228 of the complete chromosome 1
8605	21144	34058	0.69	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8605	21144	34059	0.69	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
8997	21535	34465	0.58	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9007	21544		2.08	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9077	21613	34547	0.48	3.2E-01	AF041828.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9077	21613	34548	0.48	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9905	22402	35378	3.22	3.2E-01	U44814.1	NT	Borrelia burgdorferi glapmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
10100	22595	35588	0.51	3.2E-01	BE326230.1	EST_HUMAN	h99f05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181569 3'
10213	22708		3.03	3.2E-01	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
10548	23084	36098	3.28	3.2E-01	T08813.1	EST_HUMAN	EST04702 Fetal brain, Stragene (cat#938206) Homo sapiens cDNA clone HFBDDZ21
11796	24989		4.31	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12344	24525		4.65	3.2E-01	O89217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12441	24819		3.37	3.2E-01	AF157625.1	NT	Bos taurus inositol 1,4,5-bisphosphate receptor type I mRNA, complete cds
12489	24618		1.94	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
12550	25041	30504	1.98	3.2E-01	BE385778.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618748 5'
2895	15252	27823	2.39	3.1E-01	R18051.1	EST_HUMAN	ye90H06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN);
2722	15403	27843	3.67	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2722	15403	27844	3.67	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2883	15501		1.35	3.1E-01	AW629036.1	EST_HUMAN	h46h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3'
3208	15820		3.53	3.1E-01	AB029069.1	NT	Mus musculus gene for Ser/Thr Kinase KKIAMRE, exon 6
3978	16576	28046	0.91	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5055	17628	30072	0.79	3.1E-01	S68245.1	NT	carbonic anhydrase IV [rats, Sprague-Dawley, lung, mRNA, 1205 nt]
5097	17670	30109	0.82	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
5206	17771	30194	0.98	3.1E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
5669	18296	30776	10.8	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5786	18411	31127	0.75	3.1E-01	Z74883.1	NT	S. cerevisiae chromosome XV reading frame ORF YOL141w
5796	18421		0.99	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5945	18565	31285	2.16	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6592	19189	31992	2.63	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-3 T0300-011-b04 HN0001 Homo sapiens cDNA
6654	19250	32052	0.87	3.1E-01	AJ284458.1	EST_HUMAN	q138d01.x1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1874889 3'
6784	19375	32191	0.81	3.1E-01	X71887.1	NT	H. sapiens gene for immunoglobulin kappa light chain variable region AB and A9
6863	19597		0.9	3.1E-01	AW377354.1	EST_HUMAN	MR2-CT0222-281099-005-h05 CT0222 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7048	24741	30458	2.4	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7671	20183	33071	1.18	3.1E-01	4885390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8582	21121	34041	1.22	3.1E-01	R45318.1	EST_HUMAN	yg46f01.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35639 3'
9816	22314	36295	0.45	3.1E-01	6670322	NT	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
9978	22474	35456	0.81	3.1E-01	BF696039.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
9979	22474	35457	0.81	3.1E-01	BF696039.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10035	22530	35525	1.7	3.1E-01	A1244001.1	EST_HUMAN	qj61e11.x1 NCI CGAP_K143 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S55700 HYDROXYMETHYLGUTARYL-COA LYASE PRECURSOR (HUMAN);
10204	22699		0.54	3.1E-01	T55325.1	EST_HUMAN	yc47h08.s1 Stragene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:74367 3' similar to similar to gb:M91036.maz2 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
10717	23245	36281	1.95	3.1E-01	BF216117.1	EST_HUMAN	601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'
11411	23892	36923	2.03	3.1E-01	7662281	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
11921	24257		2.13	3.1E-01	AF294308.1	NT	Andis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
11960	24292		1.95	3.1E-01	AF304162.1	NT	Sitostation vitreum 40S ribosomal protein S11 mRNA, partial cds
12108	24370		3.31	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
							Homo sapiens transcription factor IGIM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel α
12496	24624		3.89	3.1E-01	AF196779.1	NT	Mus musculus peptidoglycan recognition protein-like (Pglytp1-pending), mRNA
12535	25035		1.62	3.1E-01	10946623	NT	Mus musculus protein kinase C, epsilon (Pkc ϵ), mRNA
76	15382	25234	1.37	3.0E-01	6755083	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
275	12932	25419	11.51	3.0E-01	AJ271735.1	NT	xs63f08.x1 NCI CGAP_K141 Homo sapiens cDNA clone IMAGE:2774343 3'
1266	13863	26380	2.05	3.0E-01	AW300400.1	EST_HUMAN	Balaenoptera physalus gene encoding atrial natriuretic peptide
1555	14147	26680	6.64	3.0E-01	AJ006755.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polyglutamate lyase, complete cds
3248	15860		1.4	3.0E-01	AB030481.1	NT	PM1-ST0282-261199-001-g01 ST0262 Homo sapiens cDNA
3932	16530	28997	2.1	3.0E-01	AW817785.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 2/2
4046	16643	29109	1.01	3.0E-01	AJ271736.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
4611	17194	29640	1.78	3.0E-01	AJ006755.1	NT	601594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5554	18186	30601	5.34	3.0E-01	BE741629.1	EST_HUMAN	Canlagalo orthopoxvirus hemagglutinin gene, complete cds
5627	18256	30726	0.88	3.0E-01	AF229247.1	NT	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5695	18321	30820	4.03	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5695	18321	30821	4.03	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5731	18357	31062	4.57	3.0E-01	U01247.1	NT	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
6919	19576	32407	3.14	3.0E-01	D18313.1	NT	Mouse cyokeratin 15 gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6944	18062	30475	0.7	3.0E-01	U02369.1	NT	Strongylocentrotus purpuratus 34/67 kDa laminin-binding protein mRNA, partial cds
7005	19503	32322	0.86	3.0E-01	AF229247.1	NT	Canlagalo orthopoxvirus hemagglutinin gene, complete cds
7175	19707	32555	0.78	3.0E-01	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
7387	19893	32756	6	3.0E-01	10947007	NT	Mus musculus midnolin (Midn-pending), mRNA
7512	20033	32899	1.88	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
7867	20409	33316	1.07	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
8314	20855		3.82	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent), carbohydrate recognition domain) lectin, superfamily member 9 (Clec5f9), mRNA
8411	20951	33870	1.27	3.0E-01	BE566083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
8783	21302	34223	0.82	3.0E-01	AF141678.1	NT	Streptomyces sulfonolactams isopenicillin N synthase (pcbc) gene, partial cds
8805	21344		0.95	3.0E-01	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
9145	21680	34624	0.98	3.0E-01	AF220507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds; putative anthranilate phosphoribosyltransferase gene, partial cds; and unknown gene
9493	21893	34949	0.55	3.0E-01	P76389	SWISSPROT	HYPOTHEICAL 59.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION
9878	22375	35352	0.84	3.0E-01	BF574812.1	EST_HUMAN	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288336 5'
10294	22788	35778	0.56	3.0E-01	AW118111.1	EST_HUMAN	x603d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2606035 3'
10286	22790	35780	1.95	3.0E-01	AB030231.1	NT	Aspergillus oryzae bpaA gene for ER chaperone BiP, complete cds
10315	22809	35801	0.73	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301097 5'
10315	22809	35802	0.73	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301097 5'
11604	24047	37112	2.87	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
11604	24047	37113	2.87	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
11975	24287		1.37	3.0E-01	P54660	SWISSPROT	PONTICULIN PRECURSOR
12227	24984		2.93	3.0E-01	AJ287631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
12529	25033		2.51	3.0E-01	6877768	NT	Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA
1924	14509	27064	2.27	2.8E-01	5174502	NT	Homo sapiens membrane component, chromosome 11, surface marker 1 (M11S1) mRNA
2070	14650	27221	1.38	2.9E-01	AE000738.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2524	15088		1.22	2.9E-01	M32360.1	NT	Mouse apolipoprotein A-II (AIIp-2) gene, complete cds
3289	15900	28379	2.07	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171299-001-r12 CT0328 Homo sapiens cDNA
3289	15900	28380	2.07	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171299-001-r12 CT0328 Homo sapiens cDNA
3965	19563	29032	0.71	2.9E-01	AI610836.1	EST_HUMAN	tp21a11.x1 NCL_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A
4159	18751		0.87	2.9E-01	AW002802.1	EST_HUMAN	ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element
							wt02f10.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2480395 3'
							zs57d12.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;
4583	17166	29609	1.21	2.9E-01	AA284468.1	EST_HUMAN	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4793	17372		0.63	2.9E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
5148	17718		1.02	2.9E-01	U90756.1	NT	Lymantria dispar vitellogenin gene, complete cds
5154	17724	30155	1.43	2.9E-01	7682169	NT	Homo sapiens KIA00537 gene product (KIA00537), mRNA
5285	17847		1.7	2.9E-01	AI070899.1	EST_HUMAN	we06f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297309 3' similar to contains L1.12 L1 repetitive element;
5463	18098		1.25	2.9E-01	R37485.1	EST_HUMAN	y776t12.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
5592	19522	32344	0.79	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
5937	18558	31286	5.1	2.9E-01	X56098.1	NT	B. subtilis levansucrase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, 18, 28, 30 and levansucrase
5937	18558	31287	5.1	2.9E-01	X56098.1	NT	B. subtilis levansucrase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, 18, 28, 30 and levansucrase
5949	18570	31302	6.06	2.9E-01	6679862	NT	Mus musculus Eph receptor A8 (Epha8), mRNA
6208	18816	31587	1.26	2.9E-01	AA418145.1	EST_HUMAN	z097b12.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:767711 5'
6427	19030	31813	0.93	2.9E-01	AI797128.1	EST_HUMAN	we27c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.11 L1 repetitive element;
6467	19088	31854	2.3	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
6585	19183	31883	0.72	2.9E-01	R69184.1	EST_HUMAN	y39d08.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:141615 5'
6585	19183	31984	0.72	2.9E-01	R69184.1	EST_HUMAN	y39d08.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:141615 5'
7062	18081	30437	1.35	2.9E-01	AF142329.1	NT	Mus musculus Filh protein (Filh) gene, complete cds; and Lghn protein (Lghn) gene, partial cds
7153	19685	32527	2.87	2.9E-01	Q04399	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR508C
7213	19744	32598	1.61	2.9E-01	AF100958.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bng1 (BNG1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta 1, 3-galactosyl transferase (beta 1,3-galactosyl tr- galactosyl transferase (beta 1,3-galactosyl tr-
7860	20402	33308	1.92	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
7860	20402	33309	1.92	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8103	20844		0.89	2.9E-01	BF217743.1	EST_HUMAN	601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5'
8531	21070	33590	0.66	2.9E-01	AU150910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
8856	21395	34318	1.07	2.9E-01	AF225908.1	NT	Arabidopsis thaliana sulfonylurea receptor-like protein mRNA, complete cds
8963	21501	34423	0.71	2.9E-01	M22452.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9170	21747	34689	0.77	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9170	21747	34690	0.77	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
10773	23297	36302	2.24	2.9E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11041	23555	36589	2.88	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11041	23555	36590	2.88	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11453	23903	36970	2.07	2.9E-01	AA955373.1	EST_HUMAN	ny35h02.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR&12 LTR8 repetitive element;
11456	23906	36973	5.52	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 5/6
12172	24411	30944	1.54	2.9E-01	AW005671.1	EST_HUMAN	wz88f05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element
12262	24472	30932	1.47	2.9E-01	AF092453.1	NT	MER29 repetitive element;
12313	24505		1.4	2.9E-01	BE788199.1	EST_HUMAN	Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds
12586	24679	30877	1.57	2.9E-01	Y08937.1	NT	601482059F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884559 5'
12586	24679	30878	1.57	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
594	13224		2.06	2.8E-01	U67136.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
590	13228		0.75	2.8E-01	L28145.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
1122	13725	26238	3.14	2.8E-01	AF168050.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1320	13914	26435	3.51	2.8E-01	BE313442.1	EST_HUMAN	Guinea oocyte maturation factor Mos (c-mos) gene, partial cds
1320	13914	26436	3.51	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1334	13928	26448	1.03	2.8E-01	D86550.1	NT	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1765	14355	26902	2.01	2.8E-01	AW860020.1	EST_HUMAN	Human mRNA for serine/threonine protein kinase, complete cds
2057	14638	27210	2.12	2.8E-01	AL047620.1	EST_HUMAN	QV1-CT0364-120200-065-b05 CT0364 Homo sapiens cDNA
2175	14752	27322	3.53	2.8E-01	AW511195.1	EST_HUMAN	DKFZp586i2321_r1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp586i2321
2511	15075	27648	2.41	2.8E-01	AE000494.1	NT	hd44b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2511	15075	27649	2.41	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2584	15147		2.75	2.8E-01	AL161565.2	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2686	15246	27813	1.21	2.8E-01	AB020975.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2698	15614		1.7	2.8E-01	AF178480.1	NT	Arabidopsis thaliana mRNA for lipolytic lipase, complete cds
2699	15615	28094	2.36	2.8E-01	Z14037.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2699	15615	28095	2.36	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
3425	16033	28513	1.26	2.8E-01	AP000004.1	NT	B.taurus microsatellite (ETH121)
4068	16664	28125	2.06	2.8E-01	AE001180.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt position (417)
4202	16791		0.62	2.8E-01	AE004450.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4276	16862		2.75	2.8E-01	A080868.1	EST_HUMAN	Pseudomonas aeruginosa PAO1, section 11 of 529 of the complete genome
4553	17136	29584	1.32	2.8E-01	AL021127.2	NT	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
4559	17142	29590	2.47	2.8E-01	P13615	SWISSPROT	Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) ⁺ steroid dehydrogenase and Zinc finger protein 185
4897	17472	29828	1.07	2.8E-01	D15050.1	NT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
							Human mRNA for transcription factor AREB6, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4897	17472	29929	1.07	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4937	17512	29958	1.02	2.8E-01	AW594539.1	EST_HUMAN	hg86d05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2950569 3'
4949	17524	29965	1.17	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4955	17530	29972	3.5	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4986	17560	30003	1.67	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180129 5'
5013	17587	30030	2.82	2.8E-01	A1272699.1	EST_HUMAN	q159c11.x1 Soares_NHMFu_S1 Homo sapiens cDNA clone IMAGE:1876828 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element ;
5514	24744	30558	21.59	2.8E-01	AA349997.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5791	18416	31132	2.76	2.8E-01	AB018625.1	NT	Homo sapiens OCTN2 gene, complete cds
5983	18603		0.97	2.8E-01	AW992583.1	EST_HUMAN	CM1-BN0024-150200-118-g12 BN0024 Homo sapiens cDNA
6078	18695	31442	0.69	2.8E-01	AA765296.1	EST_HUMAN	ca01d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gb:M34539 FK506-BINDING PROTEIN (HUMAN);
6323	25114		0.75	2.8E-01	M36668.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6366	18970	31748	1.55	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6366	18970	31749	1.55	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6829	19419	32235	8.4	2.8E-01	BF511215.1	EST_HUMAN	UJ-HB14-ect-f-04-0-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
7467	19989		1.19	2.8E-01	U05633.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) gene, chloroplast gene encoding chloroplast protein, partial cds
7768	20276	33174	0.69	2.8E-01	BE537151.1	EST_HUMAN	601063105F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449569 5'
8036	20578	33482	1.12	2.8E-01	A1348126.1	EST_HUMAN	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
8036	20578	33483	1.12	2.8E-01	A1348126.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8150	20691	33605	2.16	2.8E-01	U51688.1	NT	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
8451	20991	33909	0.47	2.8E-01	AA911629.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8525	21064		6.69	2.8E-01	BF347847.1	EST_HUMAN	Homo sapiens lantosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
9387	21810	34761	1.22	2.8E-01	U17251.1	NT	g02h05.s1 NCI_CGAP_Cot12 Homo sapiens cDNA clone IMAGE:1419983 3' similar to gb:M87789 IG
9627	22127		1.03	2.8E-01	L13654.1	NT	GAMMA-1 CHAIN C REGION (HUMAN);
9803	22301	35288	1.04	2.8E-01	AF132728.1	NT	602022987F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158525 5'
9803	22301	35287	1.04	2.8E-01	AF132728.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scon-2) gene, complete cds
9861	22358	35338	0.64	2.8E-01	AF204393.1	NT	Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
9972	22467	35451	1.91	2.8E-01	7706163	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
							Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
							Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b;
							nuclear gene for mitochondrial product
							Homo sapiens hypothetical protein (LOC51319), mRNA

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10215	22710		0.81	2.8E-01	9826154	NT	Fujinami sarcoma virus, complete genome
10255	22750	35738	0.47	2.8E-01	BE959727.2	EST_HUMAN	601854922R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839785 3'
10622	23154	36166	2.26	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
10622	23154	36167	2.26	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
10651	23183	38197	2.83	2.8E-01	BF695970.1	EST_HUMAN	601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
10760	23284	36287	3.31	2.8E-01	AF051662.1	NT	Drosophila heteronema fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11158	23665		4.56	2.8E-01	BF874023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
12213	24436		15.74	2.8E-01	DB3329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12328	24514	30920	8.89	2.8E-01	BE178699.1	EST_HUMAN	PM4-HT0606-030400-001-a07 HT0606 Homo sapiens cDNA
12356	24533	30927	1.25	2.8E-01	BE900116.1	EST_HUMAN	601873020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955996 5'
12519	24988		2.21	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
502	13134	25622	3.21	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
641	13264	25740	2.53	2.7E-01	AA450081.1	EST_HUMAN	z339b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element;
1304	13898	26418	1.68	2.7E-01	AB004906.1	NT	Iponomea purpurea transposable element Tip100 gene for transposase, complete cds
1662	14255		2.17	2.7E-01	X79815.1	NT	G.lambila SR2 gene
1767	14357	26903	3.34	2.7E-01	W56087.1	EST_HUMAN	z022h10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1813	14403	26948	4.14	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2181	15459		2.77	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monocanine transporter type 2, promoter region and exon 1
2405	14973	27545	7.35	2.7E-01	Y13668.1	NT	Feline immunodeficiency virus env gene, isolate ITT0088PIU (M88), partial
2496	15060	27634	3.82	2.7E-01	AB310958.1	EST_HUMAN	ta43c11.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element;
3013	15629		0.73	2.7E-01	BF088284.1	EST_HUMAN	GM1-HT0875-060900-385-a05 HT0875 Homo sapiens cDNA
4082	16678	28138	1.98	2.7E-01	AB28015.1	EST_HUMAN	w092611.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
4096	16691	29147	0.79	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds
4096	16691	29148	0.79	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds
4101	16695	29151	2.31	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
5020	17594	30037	0.98	2.7E-01	L27516.1	NT	Triticum aestivum (Wcs66) gene, complete cds
5183	17758		3.82	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-a03 CT0286 Homo sapiens cDNA
5471	18105	30424	2.07	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOXA-4 (CHOX-1.4)
5681	18308		0.96	2.7E-01	AB033171.1	NT	Astrocypa myriophthalma mitochondrial cytb gene for cytochrome b, partial cds
6724	19318	32122	1.07	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6724	19318	32123	1.07	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6875	19609	32443	2.03	2.7E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
7085	19656	32495	0.76	2.7E-01	U15967.1	NT	Drosophila melanogaster rfc40 protein, Rop protein (Rop), and small GTP binding protein (DRas2) genes, complete cds
7393	19918	32782	0.87	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X
7562	20078	32954	0.95	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7562	20079	32955	0.95	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7677	20188	33076	2.21	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7677	20188	33077	2.21	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7720	20228	33116	0.92	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7720	20228	33117	0.92	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7805	20348	33256	0.95	2.7E-01	AA013147.1	EST_HUMAN	ze35b11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element
7989	20511		0.51	2.7E-01	AF048920.1	NT	Carassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8079	20621	33534	0.59	2.7E-01	AW888503.1	EST_HUMAN	MR1-SN0062-100500-002-009 SN0062 Homo sapiens cDNA
8127	20668	33577	0.48	2.7E-01	R39257.1	EST_HUMAN	yc91h08.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:23511 3'
8232	20773	33684	0.94	2.7E-01	AL181552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8694	21233	34154	0.83	2.7E-01	Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
8957	21495	34418	0.53	2.7E-01	X03216.1	NT	Staphylococcus aureus transposon Tn554
9256	21782	34734	9.93	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE--TRNA LIGASE) (THRRS)
9256	21782	34735	9.93	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE--TRNA LIGASE) (THRRS)
9259	21785		2.02	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
9716	22214	35188	0.67	2.7E-01	D89660.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
9993	22488	35476	0.91	2.7E-01	AF091848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
10026	22521	35517	2.5	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds
10148	22843	35634	0.69	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10148	22843	35635	0.69	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10691	23221	36233	2.31	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
10691	23221	36234	2.31	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10702	23231	30244	3.65	2.7E-01	AJ133269.1	NT	Homo sapiens cavedin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12296	24863		1.72	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12501	24627		3.98	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exon 6
495	15418	25615	2.08	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
506	13139		1.24	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1437	14030	26558	2.19	2.6E-01	BE895087.1	EST_HUMAN	601510838F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3912345 5'
1485	14078	26616	1.36	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1941	14525	27080	6.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1941	14525	27081	6.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04d10.x1 NIH_MGC 14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gbM36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gbM14689_cds1 Mouse surfact locus surfact 3 protein gene (MOUSE);
2140	14718		13.12	2.6E-01	AW733152.1	EST_HUMAN	
2197	14773	27347	1.41	2.6E-01	M11844.1	NT	Human prealbumin gene, complete cds
2512	15076		2.09	2.6E-01	Y12996.1	NT	B.martinius fbcl gene
2583	15148		10.77	2.6E-01	BE272440.1	EST_HUMAN	601126018F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:2990043 5'
3640	16243	28719	0.86	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3705	16306	28775	2.13	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLO) gene, exons 1A, 2, 3, 4, and 5
4175	16766	29214	0.7	2.6E-01	AW959510.1	EST_HUMAN	EST371580 IMAGE resequences, MAGF Homo sapiens cDNA
4234	16822	29273	19.88	2.6E-01	BE080588.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
							Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4448	17034	29477	1.57	2.6E-01	AF175293.1	NT	
4593	17176	29622	0.78	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4593	17176	29623	0.78	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4648	17228	29684	1.35	2.6E-01	AA457617.1	EST_HUMAN	aa89d07.r1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4752	17333	29776	1.63	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds
4825	17403	29858	1.47	2.6E-01	AF142703.1	NT	Ophrestia reticulosa maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
5107	17579	30118	3.56	2.6E-01	H04858.1	EST_HUMAN	y51e05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5195	17760		0.98	2.6E-01	AA894625.1	EST_HUMAN	am33b11.st Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1488605 3'
5544	18176		1.29	2.6E-01	AB035972.1	NT	Paramecium caudatum gene for PAP, complete cds
5640	18269	30742	0.68	2.6E-01	M96060.1	NT	Acetobacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCAx and CcpAx genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5760	18388		0.81	2.6E-01	AI862388.1	EST_HUMAN	td16a03.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element ;
5847	18568	31299	0.69	2.6E-01	AF207550.1	NT	Homo sapiens protein translocase, JM26 protein, UDP-galactose translocator, plm-2 protooncogene homolog plm-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM enhancer 3 genes, partial cds, and unknown g>
6221	25113		2.36	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
6348	18953	31732	1.89	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64298 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element L TR1 repetitive element ;
6348	18953	31733	1.89	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64298 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element L TR1 repetitive element ;
6554	19152	31848	1.05	2.6E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 617
7103	19873	32512	0.97	2.6E-01	AI014380.1	EST_HUMAN	w448c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331366 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7457	24783		0.96	2.6E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 416
7721	20229	33118	1.6	2.6E-01	R10365.1	EST_HUMAN	Y37a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
7781	20334	33240	1.14	2.6E-01	R02411.1	EST_HUMAN	ye82a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212 5'
7845	20387	33280	1.18	2.6E-01	BE144331.1	EST_HUMAN	MRO-H10166-181199-003-d12 HT0166 Homo sapiens cDNA
8083	20625	33538	0.87	2.6E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8083	20625	33539	0.87	2.6E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8276	20817	33738	2.99	2.6E-01	BF343588.1	EST_HUMAN	602014422F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4150398 5'
8349	20890	33810	1.89	2.6E-01	Q10199	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
8627	21166	34080	4.49	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
8627	21166	34081	4.49	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9388	21811	34762	0.96	2.6E-01	X17804.1	NT	S. occidentalis INV gene for invertase (EC 3.2.1.26)
9654	22153		0.5	2.6E-01	AF057121.1	NT	Lentia ceradensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9782	22280	35265	0.93	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
9782	22280	35266	0.93	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
10083	22588		0.5	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10403	22897		0.91	2.6E-01	Y10198.1	NT	Homo sapiens PHEX gene
10500	22994		0.51	2.6E-01	AI078681.1	EST_HUMAN	wf58b09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491865 3'

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11300	23752	36809	2.18	2.6E-01	P48280	SWISSPROT	CELL DIVISION PROTEIN FTSW HOMOLOG
11400	23851		30.98	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11777	24165		1.72	2.6E-01	10190855	NT	Mus musculus jerky (Jrk), mRNA
11973	24991		4.06	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12042	24329	30898	4.8	2.6E-01	AF316898.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXD2) gene, complete cds, alternatively spliced
12398	24558		1.34	2.6E-01	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
12478	24612		1.96	2.6E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
12526	24641		1.37	2.6E-01	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
12567	24666		3.74	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
262	12921	25407	1.48	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
263	12921	25407	1.77	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
276	12933		4.28	2.5E-01	M2650.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
865	13480	25994	1.02	2.5E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1098	13703		1.03	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1180	13763	26274	11.59	2.5E-01	T89837.1	EST_HUMAN	ye11g07.1 Stralegene lung (#937210) Homo sapiens cDNA clone IMAGE:117488 5'
1566	14153	26689	0.87	2.5E-01	AL115624.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1766	14356		6.09	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1927	15454	27067	1.29	2.5E-01	BE69604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
1927	15454	27068	1.29	2.5E-01	BE69604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
2452	15019		12.93	2.5E-01	AE000675.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2536	15100	27673	0.93	2.5E-01	6679216	NT	Mus musculus protein-L-isoelectrophoretic (D-aspartate) O-methyltransferase 1 (Pcm1), mRNA
2540	15104		1.49	2.5E-01	AA251987.1	EST_HUMAN	zs11a12.1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
3459	16068		3.41	2.5E-01	AW973471.1	EST_HUMAN	EST385464 MAGE sequences, MAGM Homo sapiens cDNA
3587	16191	28675	0.84	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3603	16207	28685	7.97	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
4143	16735		1.36	2.5E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4409	16894		0.9	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4722	17303	28747	0.59	2.5E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-16
4860	17438		1.47	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4863	17445	28898	4.88	2.5E-01	AF007788.1	NT	Chlorostaura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4896	17471	28927	2.82	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4924	17499		3.21	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and 98g portion of MuERV-L (murine endogenous retrovirus) element
4959	17534	28878	0.61	2.5E-01	BE886785.1	EST_HUMAN	601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922600 5'
5282	12933		0.65	2.5E-01	M26501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
5529	18161	30576	12.86	2.5E-01	S83390.1	NT	T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]
6114	18730		0.84	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6738	18332	32138	0.83	2.5E-01	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
7389	18914	32778	0.82	2.5E-01	U13992.1	NT	Feline calicivirus CFI/68 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds; and unknown gene
7413	19938		1.35	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7632	20144	33025	4.48	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
7786	20329	33236	2.31	2.5E-01	BF105040.1	EST_HUMAN	7157a03.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
7797	20340	33248	0.7	2.5E-01	BE960712.1	EST_HUMAN	601653391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828198 3'
8168	20709	33625	2.2	2.5E-01	BF038595.1	EST_HUMAN	601459238F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862809 5'
8336	20877	33788	0.72	2.5E-01	P04492	SWISSPROT	E1B PROTEIN, SMALL T-ANTIGEN (E1B 19K)
8571	21110	34029	3.03	2.5E-01	H53238.1	EST_HUMAN	yB4f07.r1 Soares fetal liver spleen TNF- α mRNA, exon 10
8808	21347	34271	0.88	2.5E-01	M88628.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9435	21961	34909	15.98	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9435	21961	34910	15.98	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9492	21948	34897	2.09	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9492	21948	34898	2.09	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10010	22505	35496	1.66	2.5E-01	AW581997.1	EST_HUMAN	RC3-ST0188-130100-015-a07 ST0188 Homo sapiens cDNA
10436	22930	35937	1.53	2.5E-01	AW152248.1	EST_HUMAN	xq40c10.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
10439	22933	35941	1.31	2.5E-01	X58491.1	NT	Mouse L1Md LINE DNA
10459	22953	35962	2.03	2.5E-01	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
10459	22953	35963	2.03	2.5E-01	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
10955	23470	36495	4.3	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
11712	24122	37153	5.29	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (CesA-4) mRNA, complete cds
11740	25075		10.13	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
578	13209	25987	1.87	2.4E-01	AA836316.1	EST_HUMAN	on70d04.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
881	13485	26014	2.4	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1347	13942	26464	21.36	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1347	13942	26465	21.36	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1427	14020	26348	0.93	2.4E-01	Y17293.1	NT	Homo sapiens FLI1 gene, partial
1891	14478		27.27	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1944	14528	27084	1.17	2.4E-01	AF251708.1	NT	Zaocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds
2079	14659	27230	1.49	2.4E-01	AJ742958.1	EST_HUMAN	wg76d05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371017 3' similar to TR:O60287 O60287 KIAA0512 PROTEIN. ;
2183	14759	27329	1.04	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2213	14788		1.04	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2302	14875	27451	1.78	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2425	14993	27568	1.26	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENILA
2575	15138	27708	3.05	2.4E-01	Z36634.1	NT	O42586 26S PROTEASE REGULATORY SUBUNIT 6A. ;
2760	15343	27913	1.79	2.4E-01	X71783.1	NT	D discoideum (Ax3-K) ponA gene
2812	15364	27933	3.88	2.4E-01	AF030154.1	NT	S pombe swi6 gene
3166	15780		3.27	2.4E-01	U72726.1	NT	Bovine adenovirus 3 complete genome
3182	15795	28287	1.38	2.4E-01	X74209.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3724	16325	28792	1.26	2.4E-01	AF169793.1	NT	H. sapiens AGT gene, Pal fragment of intron 4
3824	16424	28886	0.83	2.4E-01	AE000312.1	NT	Podosporea anserina HET-C protein (Het-c) gene, complete cds
4103	16897		0.6	2.4E-01	D29860.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
5008	17581	30024	1.08	2.4E-01	AE000305.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
5220	17785	30203	0.93	2.4E-01	BE737592.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 195 of 400 of the complete genome
5302	17864		1.55	2.4E-01	K02402.1	NT	601572862F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839775 5'
5653	18280	30758	0.83	2.4E-01	A1925707.1	EST_HUMAN	Human coagulation factor IX gene, complete cds
5653	18280	30759	0.83	2.4E-01	A1925707.1	EST_HUMAN	w033405.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5676	18303	30785	0.85	2.4E-01	D50871.1	NT	w033405.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5836	18460	31182	7.92	2.4E-01	AF091216.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5836	18460	31183	7.92	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
8050	24754		1.02	2.4E-01	AJ133836.2	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
						NT	Branchiostoma floridae mRNA for calmodulin 2 (caM2 gene)
6054	18672	31411	2.36	2.4E-01	BF592336.1	EST_HUMAN	7154d04.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFRA4_HUMAN
6138	18752	31510	2.5	2.4E-01	AF035546.1	NT	Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ;contains element TAR1 TAR1 repetitive element
						NT	Drosophila melanogaster p38a MAP kinase gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6240	18949	31819	2.26	2.4E-01	7661801	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6280	18998	31869	0.8	2.4E-01	AV733787.1	EST_HUMAN	AV733787 cDNA Homo sapiens cDNA clone cDAAD11 5'
6656	19252	32055	2.43	2.4E-01	AI698989.1	EST_HUMAN	wc62c11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2329220 3' similar to gb-J03484
7381	19907	32772	8.84	2.4E-01	L43001.1	NT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7708	20218	33108	1.06	2.4E-01	AF229644.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
8139	20680	33591	0.71	2.4E-01	AJ006397.1	NT	Mus musculus DXImx48a protein (DXImx48a) mRNA, complete cds
8139	20680	33592	0.71	2.4E-01	AJ006397.1	NT	Streptococcus pneumoniae r08 and h08 genes; two component system 08
8280	20831	33752	1.06	2.4E-01	AJ012585.1	NT	Streptococcus pneumoniae r08 and h08 genes; two component system 08
8535	21074	33964	0.97	2.4E-01	BF242794.1	EST_HUMAN	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
8588	21127	BF678275.1	0.58	2.4E-01	BF678275.1	EST_HUMAN	601877679F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106298 5'
9059	21596	34526	0.58	2.4E-01	AL139077.2	NT	602086188F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250372 5'
9059	21596	34527	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11108 complete genome; segment 4/8
9482	21881	34828	6.84	2.4E-01	AI693515.1	EST_HUMAN	Campylobacter jejuni NCTC11108 complete genome; segment 4/8
9620	22120	35083	0.6	2.4E-01	AF220087.1	NT	w43402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains
9620	22120	35084	0.6	2.4E-01	AF220087.1	NT	MER22.b1 TAR1 repetitive element;
10335	22829	35823	1.95	2.4E-01	Q03692	SWISSPROT	Drosophila melanogaster SKPB gene, complete cds
10847	23179	36192	3.25	2.4E-01	AL161494.2	NT	Drosophila melanogaster SKPB gene, complete cds
10715	23243	36260	2.9	2.4E-01	AF030196.1	NT	Drosophila melanogaster SKPB gene, complete cds
11081	23593		2.28	2.4E-01	Z21847.1	NT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11665	24089	37145	1.91	2.4E-01	AF217491.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11807	24853		2.65	2.4E-01	AF004213.1	NT	Mus musculus type 1 elgma receptor gene, complete cds
11866	24220		2.02	2.4E-01	AJ278191.1	NT	P. asiatica mosaic virus genomic RNA
12086	24838		2.18	2.4E-01	V01507.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exon 6
12320	25081		1.5	2.4E-01	BF229975.1	EST_HUMAN	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
12562	24682		2.31	2.4E-01	AL163281.2	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)
412	13047	25538	0.91	2.3E-01	S75898.1	NT	Gallus gallus gene coding for a-actin
665	13289		4.4	2.3E-01	U9713.1	NT	RC3-C70413-100800-023-b06 C70413 Homo sapiens cDNA
695	13318	25903	17.02	2.3E-01	U67596.1	NT	Homo sapiens chromosome 21 segment HS21C081
969	13580	26092	3.44	2.3E-01	BE311893.1	EST_HUMAN	aromatase [Poephila guttata=zebra finches, ovary, mRNA, 3188 nt]
1847	14239	26774	1.19	2.3E-01	AJ245480.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
1974	14266	26800	2.75	2.3E-01	Y10887.2	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
2089	14668		1.29	2.3E-01	AJ293533.1	NT	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
							Brassica napus sig gene for S-locus glycoprotein, cultivar T2
							Mus musculus cdh5 gene, exon 1, partial
							Homo sapiens partial intron 3 of the wild type AF-4/FEL gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2489	15054	27626	2.03	2.3E-01	BE287718.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2878	15236	27803	1.16	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2851	14024	28552	1.42	2.3E-01	AB015033.1	NT	Mariniliablia agarovorans gyB gene for DNA gyrase subunit B, partial cds, strain:FO 14957
2990	15608	28086	0.93	2.3E-01	AA601378.1	EST_HUMAN	no16d06.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element THR repetitive element;
3120	15734		6.96	2.3E-01	R21732.1	EST_HUMAN	yt21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3417	16025	28507	0.78	2.3E-01	H69836.1	EST_HUMAN	yt97h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3908	16507	28669	1.02	2.3E-01	S82821.1	NT	GSTA5=glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
4009	16607		5.14	2.3E-01	7682133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4442	17028	28468	0.83	2.3E-01	R82252.1	EST_HUMAN	yt17f01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4489	17074		2.4	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4548	17131	29378	0.87	2.3E-01	D90899.1	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
4586	17169	29613	2.16	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4652	17234	29690	6.13	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
5180	17585	30028	0.62	2.3E-01	J03280.1	NT	Human phenylethanolamine N-methyltransferase gene, complete cds
5202	17787	30191	0.82	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5403	17981	30372	0.9	2.3E-01	AE000240.1	NT	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome
5507	18140	30552	2.39	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5821	18250	30718	2.05	2.3E-01	BF058381.1	EST_HUMAN	7k30b06.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15: INNER COAT PROTEIN P12: CORE SHELL PROTEIN P30: NUCLEOPROTEIN P10];
5721	18347	31050	4.56	2.3E-01	X66587.1	NT	C.familiaris rom1 gene
5831	18455		1.19	2.3E-01	L39112.1	NT	Vittiforma corneum small subunit ribosomal RNA gene
5928	18548	31274	0.78	2.3E-01	S60371.1	NT	23S rRNA [Leuconostoc carnosum, Genomic, 2866 nt]
6096	18712	31461	2.34	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barslead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6096	18712	31462	2.34	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barslead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6762	19355	32164	0.76	2.3E-01	AF198039.1	NT	Oryctolagus cuniculus cytochrome oxidase subunit Via (coxVia2) mRNA, complete cds; nuclear gene for mitochondrial product
6959	19536	32360	4.1	2.3E-01	A1718148.1	EST_HUMAN	as42f12.x1 Barslead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element
7165	19697	32544	0.7	2.3E-01	8923323	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA

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7331	19858	32721	0.69	2.3E-01	AF000227.1	NT	Sacale cereale omega secalin gene, complete cds
7445	19969	32837	2.42	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
7603	20116		3.63	2.3E-01	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
7608	20121	32998	1.63	2.3E-01	BE898071.1	EST_HUMAN	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
7732	20240		2.98	2.3E-01	N80993.1	EST_HUMAN	zai2e08.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:292358 5'
7793	20336	33243	0.58	2.3E-01	AL161558.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
7835	20477	33387	1.93	2.3E-01	N68931.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8430	20970	33882	0.6	2.3E-01	U57999.1	NT	Mus musculus prosaposin (psap)SGP-1) gene, complete cds
9087	21604	34534	0.87	2.3E-01	AA372184.1	EST_HUMAN	EST84081 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63388)
9087	21604	34535	0.87	2.3E-01	AA372184.1	EST_HUMAN	EST84081 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63388)
9501	22001	34958	0.65	2.3E-01	6678318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (PIK3cd), mRNA
9644	22144	35112	0.51	2.3E-01	BE277880.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2966739 5'
9697	22166	35169	0.76	2.3E-01	AW964460.1	EST_HUMAN	EST376533 MAGE resequences, MAGH Homo sapiens cDNA
9746	22244	35225	1.22	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
9781	22279	35284	0.55	2.3E-01	AW364633.1	EST_HUMAN	PM2-DT0036-281298-001-f04 DT0036 Homo sapiens cDNA
9847	22345	35326	2.6	2.3E-01	BE173080.1	EST_HUMAN	MRO-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
9903	22400	35373	1.93	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10339	22833	35828	0.94	2.3E-01	AF201928.1	NT	Murine hepatitis virus strain 2, complete genome
10351	22845		5.88	2.3E-01	BF133577.1	EST_HUMAN	601846155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
10893	23414	36432	1.85	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
10893	23414	36433	1.85	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11088	23580	36819	1.85	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11088	23580	36820	1.85	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11230	23761	36817	2.49	2.3E-01	AE002187.2	NT	Chlamydomonas reinhardtii AR39, section 4 of 94 of the complete genome
11624	24066		1.6	2.3E-01	AV709736.1	EST_HUMAN	AV709736 ADC Homo sapiens cDNA clone ADCAGH01 5'
11788	24172		2.82	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
11876	24226		57.94	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT29M6 Homo sapiens cDNA clone HCOE44 5'
11899	24904		1.31	2.3E-01	AA089819.1	EST_HUMAN	chm1424 seq F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
11908	24246		1.81	2.3E-01	AW863940.1	EST_HUMAN	PM4-SN0012-030400-001-506 SN0012 Homo sapiens cDNA
11989	25002	30810	3.1	2.3E-01	AW303623.1	EST_HUMAN	xv21d07.x1 Soares NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175 Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2, contains PTRS.b2 TAR1 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12007	25053	30511	10.96	2.3E-01	BE82484.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
12057	24340		1.94	2.3E-01	BF663319.1	EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
12107	24369		3.11	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12205	24429		1.36	2.3E-01	U48645.1	NT	Pleurodeles walli distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
12211	24369		1.67	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12480	24614		2.67	2.3E-01	BF475811.1	EST_HUMAN	nac39h12.x1 Lupsid_sclafic_nerve Homo sapiens cDNA clone IMAGE:3959550 3' similar to contains element
12688	24888	30710	1.26	2.3E-01	AA094108.1	EST_HUMAN	MER38 repetitive element ;
93	12769	25252	0.81	2.2E-01	AI052180.1	EST_HUMAN	cl1864.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
1611	14204	28738	2.85	2.2E-01	AF187850.1	NT	oz14a10.x1 Soares_fetal_liver_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675280 3' similar to
2063	14643		3.89	2.2E-01	AF171901.1	NT	TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN ;
2138	14714	27287	3.16	2.2E-01	M34640.1	NT	Homo sapiens PPAR delta gene, promoter region
2447	15014	27586	5.61	2.2E-01	BF677538.1	EST_HUMAN	Trimeresurus malabaricus cyb gene, partial cds; mitochondrial gene for mitochondrial product
2623	15185	27751	1.27	2.2E-01	BE618238.1	EST_HUMAN	Fresh-water sponge Emfr1 alpha collagen (COLF1) gene
2623	15185	27752	1.27	2.2E-01	BE618238.1	EST_HUMAN	602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249689 5'
2703	15260		1.17	2.2E-01	AL163218.2	NT	601462828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2806	15523	27993	4.28	2.2E-01	BE155625.1	EST_HUMAN	601462828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2806	15523	27994	4.28	2.2E-01	BE155625.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C018
2947	15563		1.64	2.2E-01	AF020503.1	NT	PM2-HT0353-281:299-003-a12 HT0353 Homo sapiens cDNA
3439	16047		2.67	2.2E-01	AL161562.2	NT	PM2-HT0353-281:299-003-a12 HT0353 Homo sapiens cDNA
3886	16484		1.18	2.2E-01	AF155728.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
4281	16877		1.26	2.2E-01	AF119102.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
4300	16886	28330	7.03	2.2E-01	AF155142.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4350	16937	29378	2.59	2.2E-01	AF117340.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4350	16937	29378	2.59	2.2E-01	AF117340.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4447	17033	28475	1.36	2.2E-01	U01307.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4447	17033	28476	1.35	2.2E-01	U01307.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4952	17527		1.35	2.2E-01	D50804.1	NT	Human scRNA (BC200 beta) pseudogene
4957	17532	29874	2.88	2.2E-01	AA211216.1	EST_HUMAN	Human beta-cytoplasmic actin (ACTBP9) pseudogene
5188	17761		1.33	2.2E-01	L13289.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
5203	17768		1.79	2.2E-01	AE001137.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
							zz87c05.11 Stratagene hNT neuron (#897233) Homo sapiens cDNA clone IMAGE:648968 5'
							Mus musculus Vinculin gene, exon 3
							Borrelia burgdorferi (section 23 of 70) of the complete genome

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5281	17853	30277	1.2	2.2E-01	BE141035.1	EST_HUMAN	MR0-HT0067-201099-002-c10 HT0067 Homo sapiens cDNA
5318	17878		0.9	2.2E-01	S57565.1	NT	histamine H2-receptor [rats, Genomic, 1928 nt]
5919	18541	31267	2.48	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5930	18552		3.53	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
6150	18763	31525	0.73	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6150	18763	31528	0.73	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6807	19398	32212	0.85	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
7093	19664	32503	9.14	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC08 5'
7183	19715	32562	1.46	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphodiglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7183	19715	32563	1.46	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphodiglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7333	19860	32723	2.01	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7333	19860	32724	2.01	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7688	20197	33085	0.68	2.2E-01	AF287987.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
7863	20505		3.08	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
8032	20574	33479	0.84	2.2E-01	Z49933.1	NT	E. coli sepA and sepB genes
8815	21354	34277	0.57	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
8815	21354	34278	0.57	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
8827	21365	34290	3.48	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
8847	21386	34310	1.02	2.2E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
8952	21490		3.12	2.2E-01	AW855039.1	EST_HUMAN	PM3-CT0263-241299-009-b07 CT0263 Homo sapiens cDNA
9043	21580	34509	1.82	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Droscophila) (Dera1), mRNA
9128	21661	34604	1.85	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110900-008-c02 TN0045 Homo sapiens cDNA
9213	21730	34673	1.24	2.2E-01	W02888.1	EST_HUMAN	z60408.1 Soares melanocyte 2N8M Homo sapiens cDNA clone IMAGE:291591 5'
9231	21953	34603	14.03	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9274	21900	34750	0.74	2.2E-01	A1009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xklp3)
9285	21885	34830	0.71	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9288	21898	34845	3.69	2.2E-01	M89643.1	NT	Brachydanio rerio ependymin beta and gamma chains (Epd) gene, complete cds
9339	22039	35000	0.59	2.2E-01	Q90980	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9729	22227	35204	3.1	2.2E-01	AF197841.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds;
9864	22361	35341	2.23	2.2E-01	BF206507.1	EST_HUMAN	nuclear gene for chloroplast product
10078	22674	35669	0.87	2.2E-01	9625871	NT	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10340	22834		0.81	2.2E-01	AF071001.1	NT	Human herpesvirus 5, complete genome
10384	22878	35870	0.72	2.2E-01	AE001582.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds
10384	22878	35871	0.72	2.2E-01	AE001582.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11005	23519	36554	1.6	2.2E-01	AF257772.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11299	23751	36808	5.58	2.2E-01	X01918.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11335	23033	36042	3.18	2.2E-01	7706215	NT	Drosophila 68C glue gene cluster
11715	24125		1.8	2.2E-01	BE870959.1	EST_HUMAN	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
11827	25065		6.34	2.2E-01	U82671.2	NT	601446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5'
11910	24248		5.37	2.2E-01	AF188843.1	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (GALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
12024	18029	30491	1.7	2.2E-01	AW361098.1	EST_HUMAN	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12025	24317		1.85	2.2E-01	AW681822.1	EST_HUMAN	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
12575	25058		4.05	2.2E-01	AV694801.1	EST_HUMAN	h17b02.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972523 3'
12659	24730	30855	2.44	2.2E-01	BF243095.1	EST_HUMAN	AV694801 GKO Homo sapiens cDNA clone GKCAHB02 5'
1006	13617	26132	1.36	2.1E-01	AA566289.1	EST_HUMAN	601876452F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104996 5'
1009	13619	26134	1.27	2.1E-01	AL161504.2	NT	nm31e11.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
1163	13765		2.41	2.1E-01	AE002314.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1240	13838	26354	0.85	2.1E-01	6754299	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1240	13838	26355	0.85	2.1E-01	6754299	NT	Mus musculus Interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1557	14149	26881	3.45	2.1E-01	AJ249895.1	NT	Mus musculus Interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1957	14541	27097	1.84	2.1E-01	AA908824.1	EST_HUMAN	Mus musculus mas proto-oncogene and lgt2r gene for Insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
2201	14777	27350	3.39	2.1E-01	BF695073.1	EST_HUMAN	ok73602.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1518610 3' similar to gb:K02765
2385	14964	27526	2.01	2.1E-01	6753235	NT	COMPLEMENT C3 PRECURSOR (HUMAN);
2951	15567	28041	2.53	2.1E-01	6912445	NT	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
3879	16477		6.58	2.1E-01	9838361	NT	Mus musculus calcium channel, voltage dependent, alpha2/delta subunit 3 (Ca α 2d3), mRNA
4129	16721	29176	1.22	2.1E-01	P11675	SWISSPROT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
							Beta vulgaris mitochondrion, complete genome
							IMMEDIATE-EARLY PROTEIN IE180

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4129	16721	29177	1.22	2.1E-01	P11875	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4338	16923		1.38	2.1E-01	AF124526.1	NT	Orchestria cavitana calcium-binding protein BP23 precursor (BP23) gene, complete cds
4465	17051		1.51	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4676	17258	28709	1.83	2.1E-01	AB010273.1	NT	Homo sapiens pshp47 gene, complete cds
5083	17658	30097	1.83	2.1E-01	U76409.1	NT	Lycopodium esculentum homeobox 1 protein (THox1) mRNA, partial cds
5434	17990	30396	0.98	2.1E-01	J05082.1	NT	Vampire bat (D. rotundus) plasminogen activator mRNA, complete cds
5504	18138	30548	6.55	2.1E-01	BF672695.1	EST_HUMAN	602152001FT NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5'
6967	19544	32388	1.16	2.1E-01	AJ223392.1	NT	Doto fragilis mitochondrial 16S rRNA gene, partial
6979	19477	32269	2.04	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7438	19960	32825	1.24	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7438	19960	32828	1.24	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7447	19971		2.17	2.1E-01	AE000872.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7692	20201	33088	2.02	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
7731	20239	33130	1.14	2.1E-01	AF066897.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7731	20239	33131	1.14	2.1E-01	AF066897.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7785	20273		0.88	2.1E-01	T87354.1	EST_HUMAN	yd83b01.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:114793 5'
8017	20559		1.19	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1i3), mRNA
8439	20979	33894	4.93	2.1E-01	U86399.1	NT	Haemophilus influenzae hmcD, putative haemocin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcI) genes, complete cds
8732	21271	34190	0.82	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0614 5'
8732	21271	34191	0.82	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0614 5'
8898	21426		0.47	2.1E-01	AB022524.1	NT	Homo sapiens APC gene, exon 9
8967	21505	34428	5.93	2.1E-01	Z35788.1	NT	S.cerevisiae chromosome II reading frame ORF YBL025w
9423	21932	34880	0.6	2.1E-01	N42536.1	EST_HUMAN	wy1e10.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:270954 5'
9423	21932	34881	0.6	2.1E-01	N42536.1	EST_HUMAN	wy1e10.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:270954 5'
9432	21958	34908	2.95	2.1E-01	X97378.1	NT	A.thaliana mRNA for ARArBP1b protein
8536	22036	34956	1.57	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
10232	22727	35719	1.04	2.1E-01	Z87067.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10263	22758	35745	1.98	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10269	22784	35751	0.87	2.1E-01	BF574254.1	EST_HUMAN	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831 5'

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10505	22999	36007	0.5	2.1E-01	AF294286.1	NT	Anolis lineatopus isolate NG NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
11438	23888		2.24	2.1E-01	11036847	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11451	23901	36969	2.34	2.1E-01	BE180422.1	EST_HUMAN	RC3-HT0622-040500-013-b11 HT0622 Homo sapiens cDNA
11841	24802		1.39	2.1E-01	X57624.1	NT	Drosophila melanogaster ALA-E6 DNA, repeat region
12183	24418		1.46	2.1E-01	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
12465	24593		1.72	2.1E-01	BE622149.1	EST_HUMAN	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915675 5'
12807	24891	30858	2.08	2.1E-01	BE872330.1	EST_HUMAN	7a59402.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3223034 3'
12812	24895	30861	1.26	2.1E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
214	12875	25362	1.86	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avena, complete cds
559	13190		2.2	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
728	13348	25840	1.24	2.0E-01	M77085.1	NT	O.cuniculus germline IgH heavy chain V-H pseudogene, allotype VH2
843	13459	25968	1.76	2.0E-01	AF027885.1	NT	Mus musculus Major Histocompatibility Locus class II region
1049	13556	26167	0.72	2.0E-01	D90905.1	NT	Synechocystis sp. PCC6803 complete genome, 7/27, 761449-920915
1164	13766	26276	3.24	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1297	13891	28414	1.37	2.0E-01	AJ132895.5	NT	Homo sapiens rac1 gene
1351	13946	28470	1.22	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-291298-002-c06 HT0422 Homo sapiens cDNA
1507	14099		1.22	2.0E-01	AJ243957.1	NT	Plum pox virus strain M, complete genome, isolate PS
1534	14126	26663	23.08	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1599	14191	26722	3.03	2.0E-01	AB007874.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1604	14196	26728	1.23	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1735	14326	26868	1.17	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1755	14345		1.83	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1795	14385		1.99	2.0E-01	U87525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1834	14518	27073	1.14	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1834	14518	27074	1.14	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1937	14521	27077	1	2.0E-01	8922238	NT	Homo sapiens hypothetical protein FLJ10120 (FLJ10120), mRNA
2386	14955		1.84	2.0E-01	X82877.1	NT	H. sapiens Nat-D-glucose cotransport regulator gene
2915	15532		0.86	2.0E-01	AF074990.1	NT	Homo sapiens full length insert cDNA YH85A11
3534	18139	28621	0.7	2.0E-01	P46907	SW/ISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3628	16229		0.82	2.0E-01	AW238005.1	EST_HUMAN	xp15b002.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element MER21 repetitive element ;
3768	16369	28835	0.8	2.0E-01	P34841	SW/ISSPROT	CED-11 PROTEIN

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4028	16626	29098	0.78	2.0E-01	Z46906.1	NT	Sus scrofa
4102	16698	29152	0.88	2.0E-01	X83997.1	NT	C.parasitica espC gene
4522	17106	28552	0.76	2.0E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-18
4665	17247		8.43	2.0E-01	BE626185.1	EST_HUMAN	QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA
5192	17757	30188	7.09	2.0E-01	8922080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5228	18139	28821	0.82	2.0E-01	P46907	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
5638	18265	30737	2.38	2.0E-01	X56600.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5918	18538	31263	2	2.0E-01	11432640	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
6008	18626	31361	0.88	2.0E-01	X91856.1	NT	F.rubripes DNA encoding for valyl-tRNA synthetase
6210	18820	31591	6.48	2.0E-01	U15300.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
6321	18928		0.71	2.0E-01	M75987.1	NT	Human hepatocyte growth factor gene, exon 1
6560	19158	31855	3.94	2.0E-01	X61033.1	NT	M.aurealis mu class glutathione transferase gene
6950	19246	32049	3.63	2.0E-01	AW360865.1	EST_HUMAN	PM1-CT0247-141099-001-g06 CT0247 Homo sapiens cDNA
7251	19780	32636	0.88	2.0E-01	U39724.1	NT	Mycoplasma genitalium section 46 of 51 of the complete genome
7338	19863	32727	1.18	2.0E-01	AF250371.1	NT	Mus musculus phosphofructokinase-1 C isozyme (Pfkfb) gene, exons 3 through 7
7775	20284	33181	1.53	2.0E-01	AK024427.1	NT	Homo sapiens mRNA for FLJ00016 protein, partial cds
7895	20437		6.45	2.0E-01	AF028026.1	NT	Andes virus strain O123133 glycoprotein G1 and G2 precursor, gene, partial cds
8142	20883	33595	2.91	2.0E-01	X91151.1	NT	M.musculus scp2 gene exon 14
8958	21197		0.53	2.0E-01	BE562247.1	EST_HUMAN	601344848F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677794 5'
9273	21799	34749	1.03	2.0E-01	U82511.1	NT	Dicystostelium discoidium random slug cDNA19 protein (rsc19) mRNA, partial cds
9312	21826	34775	0.65	2.0E-01	U71122.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9475	21874		4.35	2.0E-01	AE001278.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
9661	22160	35132	0.51	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9661	22160	35133	0.51	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9808	22304		1.98	2.0E-01	AF146882.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
9954	22449	35431	1.79	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
9954	22449	35432	1.79	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10072	22567	35562	0.53	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10072	22567	35563	0.53	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10115	22810		0.72	2.0E-01	X78388.1	NT	D.melanogaster DNA mobile element (hoppe)
10304	22798	35789	0.88	2.0E-01	X97121.1	NT	R.norvegicus mRNA for NTR2 receptor
10720	23248	36283	2.77	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferin, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10720	23248	36284	2.77	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
12162	24402		1.34	2.0E-01	AF206637.2	NT	Pimephales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12374	24887		1.95	2.0E-01	AF302773.1	NT	Homo sapiens ninein-Lm isoform (ninein) mRNA, complete cds
12386	24807	30788	2.81	2.0E-01	AW975297.1	EST_HUMAN	EST387405 MAGE resequences, MAGN Homo sapiens cDNA
12425	24610	30888	3.97	2.0E-01	AI023592.1	EST_HUMAN	ov80a10.s1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3'
12448	24584		17.08	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
115	12788		6.22	1.8E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Arl1), mRNA
374	13023	25509	5.4	1.9E-01	AF004353.1	NT	Mus musculus pelle ear (ep) gene, wild type allele, 3' region, partial cds
684	13308	25792	1.47	1.9E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
684	13308	25793	1.47	1.9E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
691	13315	25800	6.6	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-401 BT0502 Homo sapiens cDNA
692	13315	25800	6.82	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-401 BT0502 Homo sapiens cDNA
1023	13633		1.92	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (Il2rg), mRNA
1143	13748	26258	10.04	1.9E-01	AA358813.1	EST_HUMAN	EST167784 Fetal lung II Homo sapiens cDNA 5' end
1413	14006	26534	2.41	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1482	14075		4.02	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2185	14761	27331	1.29	1.9E-01	AA918492.1	EST_HUMAN	GLIA DERIVED NEXIN PRECURSOR (HUMAN);
2422	14990	27563	3.27	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2949	15565	28038	4.1	1.9E-01	U66096.1	NT	Sigmoidon hispidus p53 gene, partial cds
2965	15580		6.58	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3033	15649	28128	1.05	1.9E-01	U25148.1	NT	Rattus norvegicus brush border myosin-I (BBMI) mRNA, partial cds
3442	16050	28528	4.19	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3528	16131	28611	5.24	1.9E-01	R16487.1	EST_HUMAN	y42f10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129547 5'
3877	16475	28939	0.76	1.9E-01	AF264017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
4064	16661	29123	3.85	1.9E-01	AB008784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4157	16749	29202	1.86	1.9E-01	AW754106.1	EST_HUMAN	GM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4315	16901	29345	1.17	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-290700-007-d04 FN0010 Homo sapiens cDNA
4568	17151	29597	0.69	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
5158	17728		1.11	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5789	18414		5.46	1.9E-01	AW130149.1	EST_HUMAN	x729807.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC
5828	18450	31173	7.81	1.9E-01	AF127937.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
6005	18625	31360	0.73	1.9E-01	AF091216.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
						NT	Mus musculus Wrm protein (Wrm) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6046	18665		2.52	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6469	19070	31855	1.07	1.9E-01	AF162391.1	EST_HUMAN	wf54h02.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:2394099 3'
6523	19123	31915	1.23	1.9E-01	AW148462.1	EST_HUMAN	xf14c08.x1 NCL CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7050	18069	30460	1.37	1.9E-01	R43212.1	EST_HUMAN	y909a12.s1 Soerres infant brain 1N1B Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element;
7072	18644	32481	0.91	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7072	18644	32482	0.91	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7503	20025	32889	1.3	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
7543	20063	32937	2.89	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme 1 (sbe1) gene, complete cds
7927	20469	33378	1.71	1.9E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8820	21159	34074	12.12	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1188 protein, partial cds
8875	21414	34337	1.38	1.9E-01	MT14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
8875	21414	34338	1.38	1.9E-01	MT14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
9789	22287	35271	0.72	1.9E-01	AA912488.1	EST_HUMAN	cl86g10.s1 NCL CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537506 3' similar to contains Alu repetitive element
10140	22635	35626	0.71	1.9E-01	BE830353.1	EST_HUMAN	RC5-E70082-060700-022-A02 E70082 Homo sapiens cDNA
10140	22635	35627	0.71	1.9E-01	BE830353.1	EST_HUMAN	RC5-E70082-060700-022-A02 E70082 Homo sapiens cDNA
10523	23081	36071	2.02	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10523	23081	36072	2.02	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10635	23167	36178	2.06	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11377	23829	36891	1.68	1.9E-01	M22253.1	NT	Rattus norvegicus sodium channel 1 mRNA, complete cds
11571	24018	37088	2.69	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12207	24431		1.33	1.9E-01	AF055900.1	NT	Drosophila melanogaster clathrin light chain mRNA, complete cds
12582	24874		3.69	1.9E-01	AF001168.1	NT	Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds
34	12713	25172	2.58	1.8E-01	U73200.1	NT	Mus musculus p18Rip mRNA, complete cds
281	15412	25423	1.67	1.8E-01	AB022090.1	NT	Mus musculus Ccrg gene for chaperonin containing TCP-1 gamma subunit, partial cds
383	13039	25530	1.76	1.8E-01		4502532 NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
776	13395	25896	0.77	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
1018	13628	26141	0.78	1.8E-01	AI912212.1	EST_HUMAN	wd1102.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1130	13732	26242	1.26	1.8E-01	AF000580.1	NT	Dictyostelium discoideum plasmid Ddp5, complete genome
1332	13928	26447	6.97	1.8E-01	AL1117188.1	NT	Yersinia pestis plasmid pCD1

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1551	14143	26676	1.31	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1551	14143	26677	1.31	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1887	14472		2.79	1.8E-01	4505038	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1907	14492		2.22	1.8E-01	AI733708.1	EST_HUMAN	qg22a10.x5 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE;
1958	14542	27088	1.52	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2718	15273		2.28	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081299-036-g04 DT0018 Homo sapiens cDNA
2923	15540		2.36	1.8E-01	AF184589.1	NT	Jonopsidium acaule LEAFY protein (LEAFY2) gene, partial cds
2828	15544	28020	1.18	1.8E-01	AW182300.1	EST_HUMAN	xi41a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3158	15772	28239	1.31	1.8E-01	AW985178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3413	16021	28501	0.71	1.8E-01	BF183582.1	EST_HUMAN	601809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040621 3'
3683	16284	28752	0.79	1.8E-01	H03369.1	EST_HUMAN	ij45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3683	16284	28753	0.79	1.8E-01	H03369.1	EST_HUMAN	ij45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4333	16920	28362	0.78	1.8E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4426	17012		4.07	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BdLA-DQB), complete cds
4654	17238	28691	6.59	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4886	17461	29914	2.51	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
4928	17503	29950	1.03	1.8E-01	X92179.1	NT	S.tuberosum mRNA for alcohol dehydrogenase
5188	17763	30188	2.18	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151298-112-g06 ST0203 Homo sapiens cDNA
5216	17781	30200	1.59	1.8E-01	A1792382.1	EST_HUMAN	an28q07.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5257	17820	30245	1.5	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-tauracholate cotransporting polypeptide mRNA, partial cds
5281	17843	30270	1.07	1.8E-01	AI439981.1	EST_HUMAN	is57e04.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5288	17850	30278	0.59	1.8E-01	AF132115.1	NT	Arabidopsis thaliana cytochrome b-561 (CYTB561) gene, partial cds
5338	17899	30314	0.78	1.8E-01	AJ132844.1	NT	Broad bean wilt virus 2 genes encoding 119kDa protein, 104kDa protein, large coat protein, small coat protein
5338	17899	30315	0.78	1.8E-01	AJ132844.1	NT	Broad bean wilt virus 2 genes encoding 119kDa protein, 104kDa protein, large coat protein, small coat protein
5398	17956	30387	2.04	1.8E-01	AW809402.1	EST_HUMAN	MR4-ST0121-041199-019-b01 ST0121 Homo sapiens cDNA

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5978	18598	31331	1	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6082	18699	31446	1.01	1.8E-01	N28629.1	EST_HUMAN	yc38h08.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:284063 5'
6277	18885	31653	1.1	1.8E-01	6678428	NT	Mus musculus Trif receptor-associated factor 6 (Trif6), mRNA
6277	18885	31654	1.1	1.8E-01	6678428	NT	Mus musculus Trif receptor-associated factor 6 (Trif6), mRNA
6635	19231	32035	2.03	1.8E-01	Q8QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
6675	19271		2.24	1.8E-01	N94853.1	EST_HUMAN	y62h02.r1 Soares multiple sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:278163 5'
7077	19649	32487	1.22	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
7077	19649	32488	1.22	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
7117	19457	32272	0.71	1.8E-01	BE961353.1	EST_HUMAN	601848361R2 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3932247 3'
8547	21086	34009	0.47	1.8E-01	AW966118.1	EST_HUMAN	EST378191 MAGE resequences, MAGI Homo sapiens cDNA
9286	21792	34741	1.13	1.8E-01	M73258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9296	21896	34843	1.39	1.8E-01	9626232	NT	Bacteriophage like, complete genome
9412	21921		0.55	1.8E-01	AA493751.1	EST_HUMAN	nh02a05.s1 NCJ CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943088 similar to contains L1.3 L1
9494	21994	34950	1.13	1.8E-01	P15272	SWISSPROT	repetitive element ;
9494	21994	34950	1.13	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9532	22032	34990	0.95	1.8E-01	M26019.1	NT	S. commune cratidine-5-phosphate decarboxylase (URA1) gene, complete cds
9532	22032	34991	0.95	1.8E-01	M26019.1	NT	S. commune cratidine-5-phosphate decarboxylase (URA1) gene, complete cds
9694	22193	35166	0.62	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9698	22197	35170	0.69	1.8E-01	U07548.1	NT	Methanococcus jannaschii section 90 of 150 of the complete genome
10039	22534		0.64	1.8E-01	AF200252.1	NT	Aquarius amplus cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10271	22768	35753	1.22	1.8E-01	X63440.1	NT	M.musculus mRNA for P19-protein tyrosine phosphatase
10516	23054	36068	2.37	1.8E-01	X77336.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
10558	23094	36108	7.47	1.8E-01	U38906.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, holin and lysin genes, complete cds
10615	19649	32487	3.07	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
10615	19649	32488	3.07	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
10616	23148	36160	4.49	1.8E-01	AF019107.1	NT	Dictyostelium discoideum unknown (DG1041) gene, complete cds
10897	23417	36434	1.84	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11337	23035	36045	4.3	1.8E-01	X57033.1	NT	B.taurus mRNA for potassium channel
11599	24042	37111	2.74	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA
11626	24068	37132	1.6	1.8E-01	U40487.1	NT	Mycobacterium smegmatis proton antiporter efflux pump (Ifra), complete cds
11748	24148		2.04	1.8E-01	10086561	NT	Bovine ephemeral fever virus, complete genome

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11814	24186	31032	1.41	1.8E-01	BF348623.1	EST_HUMAN	602019928F1 NC1_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155318 5'
12218	13926	26447	1.3	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
12291	24491		5.61	1.8E-01	Q96682	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN)(PTP PROTEIN)
12416	24569		23.47	1.8E-01	R24494.1	EST_HUMAN	YH48H10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
12459	24590		2.75	1.8E-01	Y11114.1	NT	E. dispar mRNA for hexokinase (hdx1)
12502	25045	30507	1.58	1.8E-01	9508952	NT	Rattus norvegicus procollagen C-proteinase enhancer protein (Pcolce), mRNA
603	13232	25705	5.53	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
898	13454	25984	2.99	1.7E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
898	13608		8.63	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1096	13701	26210	0.67	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolydnavirus, complete genome
1096	13701	26211	0.67	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolydnavirus, complete genome
1853	14441	26998	0.95	1.7E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
2025	14607		2.84	1.7E-01	AF255051.1	NT	Homo sapiens BNIIP3H (BNIIP3H) gene, complete cds; nuclear gene for mitochondrial product
2885	15503	27973	1.98	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2885	15503	27974	1.98	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2853	15569	28044	1.53	1.7E-01	AA336909.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
3027	15843	28121	1.9	1.7E-01	AJ238736.1	NT	Naja naja atra ctb-1 gene, exons 1-3
3027	15643	28122	1.9	1.7E-01	AJ238736.1	NT	Naja naja atra ctb-1 gene, exons 1-3
3139	15753	28220	1.91	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3412	16020	28500	1.11	1.7E-01	N55763.1	EST_HUMAN	J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3494	16099	28574	1.26	1.7E-01	AJ289505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
4012	16610	29083	4.99	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4658	17240		1.63	1.7E-01	X52936.1	NT	Schistosoma gregaria alpha repetitive DNA
4877	17452	28904	0.84	1.7E-01	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
4985	17539	28981	1.07	1.7E-01	AJ247635.1	EST_HUMAN	qh57e09.x1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF b1 ORF repetitive element;
5210	17775		0.88	1.7E-01	U28376.1	NT	Zea mays calcium-dependent protein kinase (MZECDPK2) mRNA, complete cds
5242	17806	30227	1.02	1.7E-01	BF689719.1	EST_HUMAN	602186630F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298648 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5297	17859		1.08	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme IIb (ae) gene, complete cds
5342	17903	30319	0.6	1.7E-01	BF030010.1	EST_HUMAN	601557256F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827197 5'
5421	17978	30386	7.82	1.7E-01	J04479.1	NT	S.pneumoniae DNA polymerase I (polA) gene, complete cds
5604	18233	30683	1.92	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5604	18233	30684	1.92	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5779	18404	31120	0.7	1.7E-01	U43599.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6471	19072	31856	20.9	1.7E-01	H72118.1	EST_HUMAN	ysd2q06.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:213658 3'
6522	19122	31813	1.33	1.7E-01	A1370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6522	19122	31814	1.33	1.7E-01	A1370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6937	18045	30467	0.71	1.7E-01	BE300286.1	EST_HUMAN	600944067T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960248 3'
6960	19537		2.26	1.7E-01	AF026552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
7074	19646		0.67	1.7E-01	Z82910.1	NT	Homo sapiens HFE gene
7272	19800	32657	2.83	1.7E-01	AF000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7339	19868	32730	8.92	1.7E-01	BE734179.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843984 5'
7494	20017	32882	1.16	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HLF0 PROTEIN)
7508	24784	32893	0.73	1.7E-01	Q01955	SWISSPROT	COLLAGEN ALPHA 3(IV) CHAIN PRECURSOR
7802	20345	33253	1.28	1.7E-01	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
7904	20446	33352	0.54	1.7E-01	AF150669.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8219	20760	33874	6.62	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8219	20760	33875	6.62	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8631	21170	34087	0.58	1.7E-01	AW982873.1	EST_HUMAN	RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA
8662	21201	34119	3.28	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
8778	21317	34239	0.68	1.7E-01	AF217413.1	NT	Homo sapiens neurologin 3 isoform gene, complete cds, alternatively spliced
8778	21317	34240	0.68	1.7E-01	AF217413.1	NT	Homo sapiens neurologin 3 isoform gene, complete cds, alternatively spliced
9095	21631	34568	0.46	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9095	21631	34570	0.46	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9509	22009	34987	7.72	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
9814	22114	35077	0.56	1.7E-01	AW977455.1	EST_HUMAN	EST388564 MAGE sequences, MAGO Homo sapiens cDNA
9814	22114	35078	0.56	1.7E-01	AW977455.1	EST_HUMAN	EST388564 MAGE sequences, MAGO Homo sapiens cDNA
9831	22131	35096	2.47	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
9704	22203	35174	1.27	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
9704	22203	35175	1.27	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9722	22220	35195	0.81	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
10132	22627		2.24	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10293	22787	35777	0.99	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA
10295	22789	35779	1.72	1.7E-01	AA627872.1	EST_HUMAN	ng60e07.s1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb.L25081
10560	23096	36109	9.23	1.7E-01	BE390835.1	EST_HUMAN	TRANSFORMING PROTEIN RHOC (HUMAN);
10885	23215	36227	2.63	1.7E-01	AA814617.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813258 5'
10991	23505	36536	8.7	1.7E-01	7108300	NT	d43a03.s1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1426924 3'
10991	23505	36537	8.7	1.7E-01	7108300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11558	24008		2.18	1.7E-01	P15272	SWISSPROT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11643	24604		1.45	1.7E-01	AJ272584.1	NT	AMP NUCLEOSIDASE
11647	24078	37143	4.09	1.7E-01	11418157	NT	Bilobella aurantiaca mitochondrial partial COI gene for cytochrome c oxidase subunit II
11782	25004		1.94	1.7E-01	AL163278.2	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
12333	24517		1.38	1.7E-01	N40825.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
12381	24548	30905	12.95	1.7E-01	U01317.1	NT	yw82c12.1 Soares_placenta_8to9weeks_2NbHP8a6w Homo sapiens cDNA clone IMAGE:258742 5'
12608	24693		1.33	1.7E-01	AJ132510.1	NT	Human beta globin region on chromosome 11
131	12798	25285	1.57	1.6E-01	AF217532.1	NT	Sus scrofa c-fos gene, exons 1-4
708	15388	25816	1.58	1.6E-01	R31497.1	EST_HUMAN	Homo sapiens mevalonate kinase gene, exon 6 and 7
1589	14161	26682	4.35	1.6E-01	AF298117.1	NT	yw75f12.1 Soares_placenta_Nb2HP Homo sapiens cDNA clone IMAGE:135599 5'
1668	14552	27108	2.8	1.6E-01	P22063	SWISSPROT	Homo sapiens homeobox protein OTX2 gene, complete cds
2028	14610		1.08	1.6E-01	U10334.1	NT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2427	15466	27569	0.96	1.6E-01	X84232.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2535	15099	27672	1.12	1.6E-01	AB037729.1	NT	H. sapiens mRNA for novel T-cell activation protein
2917	15534	28008	11.95	1.6E-01	AF185589.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2917	15534	28007	11.95	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3041	15857	28137	1.17	1.6E-01	AE001862.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3695	16296	28765	1.35	1.6E-01	AJ003165.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
3695	16296	28768	1.35	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
3840	16439	28901	0.71	1.6E-01	AE000982.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
4072	16668		2.65	1.6E-01	AE004413.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4422	17007	28450	11.02	1.6E-01	AF179680.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4554	17137		3.42	1.6E-01	AW868601.1	EST_HUMAN	Homo sapiens epilin gene, complete cds
							EST380677 IMAGE resequences, MAGJ Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4563	17146		4.68	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
5057	17630	30074	0.84	1.6E-01	P40631	SWISSPROT	MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA]
5080	17653	30083	1.45	1.6E-01	AA088343.1	EST_HUMAN	z184h09.s.1 Stralagena colon (#937204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955
5101	17673	30112	1.26	1.6E-01	AJ006356.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV. ;
5101	17673	30113	1.28	1.6E-01	AJ006356.1	NT	Lycopersicon esculentum Rsa1 fragment 2, satellite region
5358	17918		1.81	1.6E-01	BF20302.1	EST_HUMAN	Lycopersicon esculentum Rsa1 fragment 2, satellite region
5358	17919	30333	1.23	1.6E-01	AI874074.1	EST_HUMAN	601872523F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4096885 5'
5597	18218	30688	0.76	1.6E-01	L40608.1	NT	wm48c08.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2439182 3'
5713	18339	30844	2.76	1.6E-01	AW197496.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5713	18339	30845	2.76	1.6E-01	AW197496.1	EST_HUMAN	hm43101.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984
5725	18351	31054	2.12	1.6E-01	AF034716.1	NT	HYPOTHETICAL 127.6 KD PROTEIN ;
6179	18789	31558	0.84	1.6E-01	BE925803.1	EST_HUMAN	hm43101.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984
6559	19157	31953	2	1.6E-01	AL161588.2	NT	HYPOTHETICAL 127.6 KD PROTEIN ;
6559	19157	31954	2	1.6E-01	AL161588.2	NT	Rattus norvegicus COAAT/enhancer binding protein epsilon (cebpe) gene, complete cds
7043	18063	30453	3.49	1.6E-01	AW291215.1	EST_HUMAN	RC3-BN0034+310800-113-h01 BN0034 Homo sapiens cDNA
7753	20261	33157	1.44	1.6E-01	AW246359.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7770	20278		0.75	1.6E-01	AU136525.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7810	20353	33282	1.43	1.6E-01	L49349.1	NT	UI-H-B12-egl-b-08-Q-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7968	20510		0.55	1.6E-01	BE244087.1	EST_HUMAN	2822248.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
8062	20604	33515	0.76	1.6E-01	U38243.1	NT	AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004468 5'
8567	21106	34025	0.77	1.6E-01	Z99119.1	NT	Gorilla gorilla androgen receptor gene, partial exon
8760	21299	34220	0.65	1.6E-01	R13673.1	EST_HUMAN	TCBP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAPO607
8863	21402		0.64	1.6E-01	L36861.1	NT	Bacteroides vulgatus beta-lactamase (ctxA) gene, complete cds and mobilization protein (mobA) gene, complete cds
8901	21439	34362	1.91	1.6E-01	Z49501.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410
9039	21576		0.8	1.6E-01	AF111167.2	NT	y60h08.r1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:26873 5'
9559	22089		1.93	1.6E-01	BF375171.1	EST_HUMAN	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
9572	22072	35033	1.86	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9807	22107		1.06	1.6E-01	BE156684.1	EST_HUMAN	PM2-HT0353-270100-004-f11 HT0353 Homo sapiens cDNA
10536	23073	36087	2.7	1.6E-01	AW850853.1	EST_HUMAN	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
10880	23401	36418	1.55	1.6E-01	BE259849.1	EST_HUMAN	601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
10994	23508		8.03	1.6E-01	AF106084.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11289	23741	36768	10.86	1.6E-01	6671552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
11660	25019		1.72	1.6E-01	8879486	NT	Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA
11784	24169	36776	5.34	1.6E-01	AV719585.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
12095	24382	30968	1.55	1.6E-01	L14933.1	NT	Rat convertase PCS mRNA, 5' end
12128	24382		1.75	1.6E-01	AW839711.1	EST_HUMAN	RC1-LT0074-120200-014-h01_1 LT0074 Homo sapiens cDNA
12229	24821		11.74	1.6E-01	AB045310.1	NT	Cucumis sativus KS mRNA for ent-kaurene synthase, complete cds
12407	24564		5.11	1.6E-01	AK024495.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
12497	24625		3.96	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
12521	24637	30886	1.88	1.6E-01	9508522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
269	12928	25412	1.76	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
269	12928	25413	1.76	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
613	15387		2.16	1.5E-01	AV711698.1	EST_HUMAN	AV711698 DCA Homo sapiens cDNA clone DCAADH06 5'
815	13433	25938	1.04	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1131	13734	26244	0.84	1.5E-01	AJ008735.1	NT	Cyprinus carpio mRNA for EGG522 myosin heavy chain, 3' UTR
1136	13739	26248	2.28	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1152	13755		1.61	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1258	13855	26371	0.79	1.5E-01	AW195516.1	EST_HUMAN	xn39d11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2696085 3'
1318	13912	26432	3.12	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1318	13912	26433	3.12	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1529	14121	26600	1.84	1.5E-01	AF117340.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1951	14535	27091	1.62	1.5E-01	AW444451.1	EST_HUMAN	Mus musculus MAP kinase kinase 1 (Meck1) mRNA, complete cds
2736	15291	27859	1.17	1.5E-01	BF695381.1	EST_HUMAN	UI-H-B13-atb-b-09-0-J1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733841 3'
2938	15554		1.01	1.5E-01	AW572516.1	EST_HUMAN	602083299F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
3070	15685	28157	0.62	1.5E-01	M81441.1	NT	xw56e02.x2 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:4247537 5'
3395	16003	28484	0.87	1.5E-01	AA835049.1	EST_HUMAN	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3415	16023	28504	0.65	1.5E-01	Z23104.1	NT	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3415	16023	28505	0.65	1.5E-01	Z23104.1	NT	cc68d05.s1 NCL_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
							RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);
							L. stagnalis mRNA for G protein-coupled receptor
							L. stagnalis mRNA for G protein-coupled receptor

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3474	16080	28553	0.99	1.5E-01	AW612237.1	EST_HUMAN	h22902.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2956539 3' similar to contains element MER16 repetitive element ;
3819	18419	28881	2.13	1.5E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3835	18434	28996	0.94	1.5E-01	7108358	NT	XYNA; Thermotoga bacterium; xyna; 4182 base-pairs
3849	18447	28908	0.58	1.5E-01	M97882.1	NT	N10106.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
3934	18532	28999	2.74	1.5E-01	AW665983.1	EST_HUMAN	Populus trichocarpa cv. Trichobol ABI3 gene
3951	18549	28017	0.9	1.5E-01	AJ003185.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
3951	18549	28018	0.9	1.5E-01	AJ003185.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
4124	18717	28173	0.82	1.5E-01	AW366659.1	EST_HUMAN	RC2-HT0149-19-1099-012-c09 HT0149 Homo sapiens cDNA
4282	18848	29298	0.82	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4833	17411	29864	1.29	1.5E-01	BF687685.1	EST_HUMAN	602037192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5'
4863	15291	27859	2.03	1.5E-01	BF695381.1	EST_HUMAN	602033299F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4906	17481	28938	0.92	1.5E-01	BE173798.1	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4906	17481	28939	0.92	1.5E-01	BE173798.1	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
5139	17711	30141	1.59	1.5E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5461	18096	30414	1.96	1.5E-01	P07998	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5489	18123	30530	0.8	1.5E-01	AF256652.1	NT	Caiman crocodilus MHC class II beta chain (hclibeta) gene, complete cds
5531	18163		5.6	1.5E-01	P15198	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN)
5729	18355	31059	4.88	1.5E-01	AW850754.1	EST_HUMAN	IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA
5787	18393	31106	6.87	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5787	18393	31107	6.97	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
6156	18769	31532	1.4	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6156	18769	31533	1.4	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6194	18804	31573	1.98	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6342	18948	31725	3.23	1.5E-01	BE172768.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6394	18967		1.86	1.5E-01	4508396	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6484	19085	31887	1.75	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6628	24765	32027	1.94	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6652	19248	32050	4.63	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6663	19259	32063	1.5	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6702	19297	32101	2.16	1.5E-01	Q28482	SWISSPROT	AMELOGENIN
6766	19377	32192	0.95	1.5E-01	AA714760.1	EST_HUMAN	nm30d10.s1 NCJ CGAP CG80 Homo sapiens cDNA clone IMAGE:1241971 3'
6813	19404	32220	1.59	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7055	18074	30464	6.39	1.5E-01	AW970295.1	EST_HUMAN	EST382376 MAGE sequences, MAGK Homo sapiens cDNA
7268	19796		1.9	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7423	19947	32813	1.5	1.5E-01	AF973157.1	EST_HUMAN	wr52c08.x1 NCJ CGAP_U1 Homo sapiens cDNA clone IMAGE:2491310 3'
7589	20104	32979	1.02	1.5E-01	AF298073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7589	20104	32980	1.02	1.5E-01	AF298073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7596	20110	32984	1.71	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BN0-akk-d-05-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7596	20110	32985	1.71	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BN0-akk-d-05-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7722	20230	33119	0.71	1.5E-01	U46560.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of lost-1 (SOL3) gene, complete cds
8002	20544	33446	1.1	1.5E-01	P21303	SWISSPROT	MEROZOITE RECEPTOR PK66 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN)
8161	20702	33617	0.95	1.5E-01	AA970317.1	EST_HUMAN	oo85g12.s1 NCJ CGAP_Kids Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062
8254	20795		1.11	1.5E-01	BE884799.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8339	20880		11.5	1.5E-01	C16800.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8372	20912	33832	1.82	1.5E-01	L27835.1	NT	C16800 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-529H09 5'
8529	21058	33987	2.04	1.5E-01	D84476.1	NT	Pangasinanodon gigas growth hormone (GH) mRNA, complete cds
8550	21059		0.86	1.5E-01	P43446	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
8772	21311	34234	1.23	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
9033	21570	34499	2.46	1.5E-01	N74226.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
9121	21657	34598	1.06	1.5E-01	BF585465.1	EST_HUMAN	ze59g06.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:296866 3' similar to PIR:S44443 S44443 RAD23 protein homolog 2 - human ;
9128	21663		2.63	1.5E-01	AV764819.1	EST_HUMAN	GVO000404 Human Psoriasis Differential Display Homo sapiens cDNA
9326	21840		0.94	1.5E-01	AU130007.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
9374	20313	33215	7.21	1.5E-01	U00455.1	NT	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5'
9731	22229	35206	0.48	1.5E-01	M77144.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
9835	22333	35314	8.51	1.5E-01	AF007570.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
9835	22333	35315	8.51	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10104	22598	35591	2.54	1.5E-01	X98852.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10198	22683		3.34	1.5E-01	AB027759.1	NT	P. lentusculcus mRNA for integrin beta subunit
							Mesocricetus auratus mRNA for collagen type XVII, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10210	22705	35698	2.82	1.5E-01	AB14046.1	EST_HUMAN	wk53h12.x1 NCL CGAP_P22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10210	22705	35699	2.82	1.5E-01	AB14046.1	EST_HUMAN	wk53h12.x1 NCL CGAP_P22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10288	22783	35775	1.75	1.5E-01	U40932.1	NT	Danio rerio transcription factor Pax9b (Pax9) mRNA, complete cds
10433	22927	35933	1.97	1.5E-01	AJ011984.1	NT	Claviceps purpurea ps1 gene
10433	22927	35934	1.97	1.5E-01	AJ011984.1	NT	Claviceps purpurea ps1 gene
10704	23233	36245	5.45	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10704	23233	36246	5.45	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10954	23469	38494	1.71	1.5E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
11045	19947	32813	2.44	1.5E-01	A1973157.1	EST_HUMAN	wf52c08.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
11739	24875		79.5	1.5E-01	BF700582.1	EST_HUMAN	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
12125	24381		1.43	1.5E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12190	24898		7.05	1.5E-01	R83077.1	EST_HUMAN	yp87604.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:194430 5'
12288	24920		3.12	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDA6004 5'
12406	24924	30794	16.12	1.5E-01	AL193074.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 1/6
12821	24699	30882	3	1.5E-01	Q92078	SWISSPROT	VOLTAGE-DEPENDENT T-TYPE CALCIUM CHANNEL ALPHA-1I SUBUNIT (CAVT.3)
12832	24709	30865	11.33	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
321	12975		1.48	1.4E-01	AF008683.1	NT	Homo sapiens T cell receptor beta locus, TCRBV85P to TCRBV21S2A2 region
943	13556		2.71	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5-)methyltransferase, complete cds
1302	13696		1.59	1.4E-01	T91894.1	EST_HUMAN	yd54c01.st Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:112032 3'
1784	14374		1.35	1.4E-01	6679880	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1787	14377	26921	1.39	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
2029	14811		10.08	1.4E-01	AA720615.1	EST_HUMAN	ny72d07.st NCL CGAP_GCBT Homo sapiens cDNA clone IMAGE:1283821 3'
2514	15078	27650	1.4	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2818	15370	27840	4.1	1.4E-01	A1933496.1	EST_HUMAN	wm74d01.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2441685 3'
4253	16841	28290	10.32	1.4E-01	A1599094.1	EST_HUMAN	b56c02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4253	16841	28291	10.32	1.4E-01	A1599094.1	EST_HUMAN	b56c02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4321	16907	28349	3.71	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
							z150b01.st Soares fetal liver spleen 1NfLS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to gb:X01057.ma1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);contains Alu repetitive element;
4501	17085		0.61	1.4E-01	AA768287.1	EST_HUMAN	Homo sapiens phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2) (PDE4A), mRNA
4784	17364	29815	0.59	1.4E-01	5453861	NT	

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5329	17890		1.74	1.4E-01	BE910013.1	EST_HUMAN	601498056F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900157 5'
5509	18142	30554	4.49	1.4E-01	T90877.1	EST_HUMAN	y913c11.s1 Stragelene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5532	18164	30577	4.24	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5532	18164	30578	4.24	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6440	19042	31830	2.7	1.4E-01	BE326891.1	EST_HUMAN	h87c02.x1 NCL_CGAP_Kid111 Homo sapiens cDNA clone IMAGE:3133538 3'
6608	19205	32012	6.4	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6608	19205	32013	6.4	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6888	19282	32085	3.78	1.4E-01	AW082796.1	EST_HUMAN	x871d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
6899	19285		1.93	1.4E-01	BE286536.1	EST_HUMAN	601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
6718	19312	32115	2.07	1.4E-01	BF378533.1	EST_HUMAN	QV1-UM0036-080300-103-409 UM0036 Homo sapiens cDNA
7180	19712		0.81	1.4E-01	AL118588.1	EST_HUMAN	DKFZp781A0910_r1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781A0910 5'
7419	19843		1.83	1.4E-01	AW015373.1	EST_HUMAN	UI-H-BIO-sar-c-09-0-UJ.st NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7617	20130	33005	1.94	1.4E-01	U85645.1	NT	Oryctolagus cuniculus fructose 1,6-bisphosphate aldolase (AldB) gene, complete cds
7733	20241	33132	1.77	1.4E-01	A305192.1	EST_HUMAN	q180b12.x1 Soares_NitHMPu_S1 Homo sapiens cDNA clone IMAGE:1679583 3'
8410	20950		1.26	1.4E-01	AV658047.1	EST_HUMAN	AV658047 GLC Homo sapiens cDNA clone GLCF5H06 3'
8719	21258		0.62	1.4E-01	AI436093.1	EST_HUMAN	h92b12.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to TR:O02710 O02710 GAG POLYPROTEIN ;
8844	21383	34308	4.58	1.4E-01	AA307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' and
8924	21462	34379	0.62	1.4E-01	AW023636.1	EST_HUMAN	df58b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9050	21587	34518	1.21	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9050	21587	34519	1.21	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9114	21650	34591	8.48	1.4E-01	BF310959.1	EST_HUMAN	601805465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9199	21716	34680	1.09	1.4E-01	W93411.1	EST_HUMAN	z994s04.r1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element ;
9280	21808	34757	1.47	1.4E-01	Y10198.1	NT	Homo sapiens PHEX gene
9280	21808	34758	1.47	1.4E-01	Y10198.1	NT	Homo sapiens PHEX gene
9371	20310	33213	1.95	1.4E-01	AF121381.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Ial (IAL), and zinc finger protein (DNZ1) genes, complete cds
9898	22395	35371	1.18	1.4E-01	AF023813.1	NT	Macromitrium levatum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein, partial cds
10000	22495	35484	0.51	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10000	22495	35485	0.51	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10157	22652	35645	0.72	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-g08 ST0218 Homo sapiens cDNA
10157	22652	35646	0.72	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-g08 ST0218 Homo sapiens cDNA

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10360	22854		0.73	1.4E-01	T84293.1	EST_HUMAN	yc47d03.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:111365 5'
10489	22983	35991	0.7	1.4E-01	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21); from 2589451 to 2812870
10587	23122		1.89	1.4E-01	AA811480.1	EST_HUMAN	ca99a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320364 3'
10722	23250	36265	3.2	1.4E-01	R53400.1	EST_HUMAN	y70c05.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154088 5'
							INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD49E)
10974	23489	36519	1.56	1.4E-01	P08648	SWISSPROT	
11172	23678	36724	1.82	1.4E-01	X66092.1	NT	C.perfringens ORF for putative membrane transport protein
11210	19943		1.98	1.4E-01	AW015373.1	EST_HUMAN	U-H-BID-aal-c-09-0-UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
							Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11344	23042	36052	2.4	1.4E-01	U28760.1	NT	P.salina plastid gene secY
12061	24344	30963	4.44	1.4E-01	X74773.1	NT	Rattus norvegicus desmin (Des), mRNA
12074	24352		3.85	1.4E-01	11868117	NT	
12123	25082		1.52	1.4E-01	BE513802.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
							Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycylamide ribonucleotide transformylase (GART) genes, complete cds
12223	24444		9.33	1.4E-01	AF083221.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
12235	24451		1.96	1.4E-01	D84004.1	NT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12315	25098		1.77	1.4E-01	P10447	SWISSPROT	zx30a12.r1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788014 5' similar to contains
							Alu repetitive element;
12340	24522		2.01	1.4E-01	AA452305.1	EST_HUMAN	
12545	24900		3.55	1.4E-01	D82983.1	NT	Mus musculus mRNA for prolidase, complete cds
12627	24705		1.33	1.4E-01	AW377998.1	EST_HUMAN	MRO-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA
344	12998	25481	2.28	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
344	12998	25482	2.28	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
555	13188	25684	3.25	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
664	13288	25769	3.03	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
664	13288	25770	3.03	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
877	13491	26009	0.78	1.3E-01	X63330.1	NT	P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
927	13540	26058	1.44	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1064	13669	26179	1.36	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1168	13768		2.03	1.3E-01	AL115265.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1257	13854	26370	1.36	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAF05 5'
1493	14095		0.97	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2002	14584	27143	2.32	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2215	14780		1.21	1.3E-01	AJ243578.1	NT	Rhodopsin pseudomonas acidophila pucB5, pucA6, pucB7, pucA8, pucB8, pucA8 and pucC genes and ORF151
2329	14800		1.56	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191089-032-412 ST0173 Homo sapiens cDNA
2421	14889		3.74	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 81 of 172 of the complete genome
2622	15184	27750	1.55	1.3E-01	M86918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3402	16011	28490	0.61	1.3E-01	AF196779.1	NT	Homo sapiens transcription factor 1GHI enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
3498	16103	28578	0.99	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolylacyl transacylase mRNA, complete cds
3785	16385	28850	1.19	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/7)
3785	16385	28851	1.19	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/7)
3781	16391	28856	0.6	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrodialdehyde dehydrogenase 4 [AKR1C4], exon 2
3848	16385	28850	0.62	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/7)
3848	16385	28851	0.62	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/7)
3875	16473	28937	0.74	1.3E-01	6978840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
4060	16657		1.3	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4125	13288	25768	1.65	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
4125	13288	25770	1.65	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
4218	16808		0.95	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4238	16828		4.04	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081299-036-a03 DT0018 Homo sapiens cDNA
4248	16834	28285	2.25	1.3E-01	AF028805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4285	16851	28299	21.7	1.3E-01	AW273741.1	EST_HUMAN	x2310.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995.3
4404	16989		1.55	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4577	17160	29603	0.62	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolylacyl transacylase mRNA, complete cds
4631	17214	29685	2.35	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063.5
4998	18009		0.94	1.3E-01	BE884017.1	EST_HUMAN	601510347F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911987.5
5056	17629	30073	1.05	1.3E-01	D78842.1	EST_HUMAN	HUM520C02B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-520C02.5
5279	17841	30288	4.06	1.3E-01	A1432531.1	EST_HUMAN	th38c10.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120562.3
5398	17954	30365	0.65	1.3E-01	AP000005.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 994001-1166000 nt, position (5/7)

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5444	17969	30402	13.68	1.3E-01	AA991841.1	EST_HUMAN	α45e07.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1619748 3' similar to SW:YEY6_YEAST P40093 HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION. [1];
5444	17969	30403	13.68	1.3E-01	AA991841.1	EST_HUMAN	α45e07.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1619748 3' similar to SW:YEY6_YEAST P40093 HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION. [1];
5528	18160	30575	0.69	1.3E-01	AW465988.1	EST_HUMAN	hα7b06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872879 3' similar to contains L1.b1 L1 L1 repetitive element;
5565	18198	30842	2.76	1.3E-01	AW804417.1	EST_HUMAN	QVO-JM0093-100400-189-e06 UM0093 Homo sapiens cDNA
5992	18318		0.78	1.3E-01	AF107783.1	NT	Emicella nidulans DNA-dependent RNA polymerase II (RPB140 (RPB2) gene, partial cds
5772	18397		0.76	1.3E-01	AF050880.1	NT	Hepatitis C virus 68_CL10 genome polyprotein gene, partial cds
5899	18521	31246	0.89	1.3E-01	BF210920.1	EST_HUMAN	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6609	19206	32014	15.81	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6884	19280	32083	2.07	1.3E-01	X88891.1	NT	C.jacchus intron 4 of visual pigment gene (red allele)
6983	19618		0.82	1.3E-01	W26367.1	EST_HUMAN	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7305	19833		1.94	1.3E-01	H48684.1	EST_HUMAN	Y33402.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:207075 5'
7900	20442		0.67	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890063 5'
7914	20456	33392	1.62	1.3E-01	11423294	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
7945	20487	33397	0.99	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
8180	20721		0.47	1.3E-01	BE562528.1	EST_HUMAN	601335829F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689934 5'
8286	20827		4.61	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL054c
8325	20866		3.78	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8465	21005	33923	1.05	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
8878	21416	34339	0.52	1.3E-01	R11172.1	EST_HUMAN	Y39g11.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
8878	21416	34340	0.52	1.3E-01	R11172.1	EST_HUMAN	Y39g11.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9146	21681	34625	1.84	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9146	21681	34626	1.64	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9393	21816	34766	5.08	1.3E-01	AF023129.1	NT	Oryctolagus cuniculus H+K+ATPase alpha 2c subunit mRNA, complete cds
9896	22185		0.8	1.3E-01	N89348.1	EST_HUMAN	J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL RECEPTOR ASSOCIATED PROTEIN (BAP) 29
9904	22459		0.8	1.3E-01	8393940	NT	Rattus norvegicus peptidyl arginine deiminase, type IV (Pd14), mRNA
10036	22531	35526	0.83	1.3E-01	AW851596.1	EST_HUMAN	MR2-CT0222-201098-001-e01 CT0222 Homo sapiens cDNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10292	24797	35778	0.8	1.3E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
10417	22911	35911	0.82	1.3E-01	AU121237.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10511	23049		3.33	1.3E-01	BF30999.1	EST_HUMAN	MR4-BT0358-130700-010-008 BT0358 Homo sapiens cDNA
10975	23490	36520	1.58	1.3E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11130	23638		5.15	1.3E-01	6671745	NT	Mus musculus cofilin 2, muscle (Cif2), mRNA
11468	23918	36984	3.61	1.3E-01	BE278449.1	EST_HUMAN	601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
11902	24241	31007	1.64	1.3E-01	BE618346.1	EST_HUMAN	601462741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5'
12048	24332		3.27	1.3E-01	AJ242790.1	NT	Gallus gallus scyl1 gene for lympholactin, exons 1-3
12466	24594		1.53	1.3E-01	AW001114.1	EST_HUMAN	wu24d09.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to
12847	24721		1.84	1.3E-01	BE958903.1	EST_HUMAN	TR-O60287 O60287 KIAA0539 PROTEIN. ;
406	13081	25573	10.81	1.2E-01	A1421744.1	EST_HUMAN	601644622R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929980 3'
449	12678		1.43	1.2E-01	U66912.1	NT	tf3b02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_rnat
573	13203		2.58	1.2E-01	AF039442.1	NT	ANNEXIN V (HUMAN);
1419	14012	26541	2.31	1.2E-01	AU149146.1	EST_HUMAN	Dichystellium discoidium ORF DG1016 gene, partial cds
1419	14012	26542	2.31	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1426	14019		3.26	1.2E-01	AV735249.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1431	14023		6.69	1.2E-01	AL445066.1	NT	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1554	14146		1.19	1.2E-01	AA897474.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdaAJB11 5'
1673	14265	26796	1.48	1.2E-01	Q14934	SWISSPROT	Thermoplasma acidophilum complete genome; segment 4/5
1691	14283	26819	2.77	1.2E-01	A1285402.1	EST_HUMAN	el48b09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671
1805	14395		21.02	1.2E-01	X89211.1	NT	Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1864	14648		2.23	1.2E-01	AW449388.1	EST_HUMAN	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
2228	14801	27373	1.31	1.2E-01	BF248490.1	EST_HUMAN	q16909.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960553 3'
2325	14896	27470	1.08	1.2E-01	AL163213.2	NT	q16909.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960553 3'
2416	14984		1.05	1.2E-01	Z21405.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
2625	15187	27754	1.38	1.2E-01	AW996556.1	EST_HUMAN	UI-H-B13-aki-e-10-Q-Ui.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2754	15309	27875	1.11	1.2E-01	A1823388.1	EST_HUMAN	601821667F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4046224 5'
2868	15486	27859	1.22	1.2E-01	U18018.1	NT	Homo sapiens chromosome 21 segment HS21C013
							HSAAEBZT TEST1, Human adult Testis tissue Homo sapiens cDNA
							QV3-BN0046-220300-129-f10 BN0048 Homo sapiens cDNA
							ts18q07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048
							COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] ;contains element PTR5 repetitive element ;
							Human E1A enhancer binding protein (E1A-F) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2827	15543	28019	2.37	1.2E-01	A1720470.1	EST_HUMAN	as80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb.L05095
2861	15577	28056	3.28	1.2E-01	M16364.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN);
3037	15653	28132	0.83	1.2E-01	X56882.1	NT	Human creatine kinase-B mRNA, complete cds
3267	15878	28362	2.08	1.2E-01	AW370688.1	EST_HUMAN	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3286	15907		1.19	1.2E-01	U67800.1	NT	QV1-8T0259-281099-021-005 BT0259 Homo sapiens cDNA
3525	16130		0.82	1.2E-01	Z99118.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3573	16177	28659	0.82	1.2E-01	X56882.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3573	16177	28660	0.82	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3668	16130		0.08	1.2E-01	Z99118.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3833	16432		0.84	1.2E-01	BF128551.1	EST_HUMAN	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
4261	16847	28294	1.98	1.2E-01	Z54255.1	NT	601810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053688 3'
4261	16847	28295	1.98	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MR17)
4402	16987	28431	0.6	1.2E-01	M15861.1	NT	P.clarkii mRNA; repeat region (ID 2MR17)
4930	17408	29862	0.08	1.2E-01	Z48183.1	NT	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19
							L.esculentum mRNA for glycylase-1
							Rana ridibunda pituitary adenylate cyclase-activating polypeptide variant 2 precursor, mRNA, complete cds, alternatively spliced
4909	17484		2.93	1.2E-01	AF221633.1	NT	
5163	17732	30159	1.06	1.2E-01	BF577357.1	EST_HUMAN	602135185F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4280185 5'
5275	17836	30262	10.23	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5275	17836	30263	10.23	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5423	17980		1.99	1.2E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 6/7
5457	18092	30408	0.71	1.2E-01	AA744369.1	EST_HUMAN	ny63c04.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3'
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5503	18137	30547	1.13	1.2E-01	AF223391.1	NT	
5513	18146	30557	2.28	1.2E-01	W33035.1	EST_HUMAN	zc08d02.r1 Soares_parethyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321699 5'
5571	18202	30852	2.3	1.2E-01	Z98266.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5698	18322	30822	0.89	1.2E-01	Z48234.1	NT	M.domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6347	18652	31731	1.81	1.2E-01	BE620945.1	EST_HUMAN	601483518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6395	18698	31777	0.81	1.2E-01	P10942	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE PI
6441	19043	31831	2.38	1.2E-01	AW84527.5.1	EST_HUMAN	IL0-CT0031-221089-113-e04 CT0031 Homo sapiens cDNA
6502	19102	31887	1.59	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6755	19348	32157	0.98	1.2E-01	BF347885.1	EST_HUMAN	602023112F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158386 5'
7833	20375		1.31	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-290300-002-009 BN0137 Homo sapiens cDNA

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7803	20445	33351	3.58	1.2E-01	A1913753.1	EST_HUMAN	wc98g03.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW_GST2_HUMAN
7950	20492	33401	0.72	1.2E-01	Q02369	SWISSPROT	Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II:
8251	20782	33709	0.9	1.2E-01	A1832881.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (CI-B22)
8335	20878		9.03	1.2E-01	AW083652.1	EST_HUMAN	at71b10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'
							xc49d07.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
8355	20895		4.17	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8392	20932	33852	0.92	1.2E-01	J03956.1	NT	N crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8392	20932	33853	0.92	1.2E-01	J03956.1	NT	N crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8537	21076		0.83	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
8623	21162		2.14	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
8957	21198		0.85	1.2E-01	X15191.1	NT	M. musculus DNA fragment of Apolipoprotein B gene
9491	21947	34898	2.66	1.2E-01	X77961.1	NT	S. cerevisiae HXT5 gene
9918	22414	35389	2.65	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CuAAKE08 5'
10155	22850	35844	0.48	1.2E-01	A1718395.1	EST_HUMAN	es59g09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2333056 3'
10766	23290		3.58	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
10944	23460		3.87	1.2E-01	BE962324.2	EST_HUMAN	601655578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848283 3'
11026	23540		1.62	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11134	23642	36882	2.87	1.2E-01	AF190483.1	NT	Homo sapiens dynein intermediate chain DNAL1 (DNAL1) gene, exon 17
11193	23698	36748	1.57	1.2E-01	R40249.1	EST_HUMAN	y80c02.s1 Soares infant brain T1NB Homo sapiens cDNA clone IMAGE:28880 3'
11362	23834		1.8	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
11687	24090		4.22	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCF12 3'
12029	24319		4.43	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
12109	25038	30503	3.9	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
12228	24447		1.95	1.2E-01	AF188892.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntaxin gene, partial cds
12230	13203		17.84	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12345	24526		1.81	1.2E-01	X53981.1	NT	R. norvegicus NF68 gene for 68kDa neurofilament
12440	24577	30915	6.5	1.2E-01	A1299903.1	EST_HUMAN	qn20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12463	24591		2.19	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12468	24972		8.71	1.2E-01	O98433	SWISSPROT	CYCLIN T

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12848	18130		1.65	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
590	13220	25696	0.8	1.1E-01	AI661003.1	EST_HUMAN	h18d08.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167983 3'
643	13266	25743	2.98	1.1E-01	AA569006.1	EST_HUMAN	mm08g11.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06685_ma1 HEME OXYGENASE 1 (HUMAN);
1092	13697	26207	1.54	1.1E-01	BF697308.1	EST_HUMAN	602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1124	13727		1.48	1.1E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1201	15435	26314	3.68	1.1E-01	AW972158.1	EST_HUMAN	EST384142 MAGE resequences, MAGL Homo sapiens cDNA
1292	13887	28411	1.89	1.1E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
1568	14160	26691	2.94	1.1E-01	AU140363.1	EST_HUMAN	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2353	14924		3.72	1.1E-01		NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
2576	15401		1.24	1.1E-01	6978676	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2602	15164		1.06	1.1E-01	AW821909.1	EST_HUMAN	RCO-ST0378-210100-032-g04 ST0378 Homo sapiens cDNA
2880	15498	27968	1.17	1.1E-01	S82418.1	NT	interleukin-12 p35 subunit [mouse, Genomic, 700 nt, segment 4 of 5]
3068	15683	28155	0.78	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02.3'
3385	15994		1.87	1.1E-01	6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA
3468	16075	28548	2.27	1.1E-01	BE393188.1	EST_HUMAN	601308678F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3489	16104	28578	1.59	1.1E-01	X62135.1	NT	C.reinhardtii nuclear gene on linkage group XIX
3338	16143	28628	0.58	1.1E-01	R96946.1	EST_HUMAN	y462g08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains Alu repetitive element;
3642	16245	28720	0.8	1.1E-01	Y07695.1	NT	A.immersus gene for transposase
3763	16364		1.35	1.1E-01	P97384	SWISSPROT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3771	16372	28837	1.61	1.1E-01	X52708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4188	16778	29223	1.61	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-290100-025-g07 ST0280 Homo sapiens cDNA
4188	16778	29224	1.61	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-290100-025-g07 ST0280 Homo sapiens cDNA
4339	16926		12.27	1.1E-01	AF157098.1	NT	Drosophila melanogaster Kirsicht protein (klar) mRNA, complete cds
4374	16961	29407	0.63	1.1E-01	AW802056.1	EST_HUMAN	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
4745	17328	29768	1.11	1.1E-01	S44957.1	NT	Tape-1 integral membrane protein TAPA-1 [mouse, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4958	17533	29975	1.21	1.1E-01	Y07695.1	NT	A.immersus gene for transposase
5169	16784		0.78	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complex
5431	17988	30392	4.82	1.1E-01	AV730599.1	EST_HUMAN	AV730599 HTF Homo sapiens cDNA clone HTFAAC12 5'
5431	17988	30393	4.82	1.1E-01	AV730599.1	EST_HUMAN	AV730599 HTF Homo sapiens cDNA clone HTFAAC12 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5435	18245	28720	0.57	1.1E-01	Y07695.1	NT	A. immsus gene for transposase
5850	18474		4.49	1.1E-01	AA747216.1	EST_HUMAN	rx76a03.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element; contains element MER35 repetitive element;
5914	18536	31261	1.17	1.1E-01	AF020927.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5974	18594	31328	0.84	1.1E-01	BF339518.1	EST_HUMAN	602039176F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4186818 5'
5974	18594	31328	0.84	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4186818 5'
6001	18621	31356	2	1.1E-01	X68851.1	NT	S. pombe sie8 gene encoding protein kinase
6031	18650	31391	5.02	1.1E-01	M86533.1	NT	Providencia rettgeri penicillin G amidase gene
6177	18787	31555	1.75	1.1E-01	AJ007073.1	NT	Homo sapiens LGMD2B gene
6197	18807	31576	1.6	1.1E-01	BE769152.1	EST_HUMAN	PM3-FT0024-130600-004-412 FT0024 Homo sapiens cDNA
6216	18828	31598	7.81	1.1E-01	AW853699.1	EST_HUMAN	RC3-CT0254-280999-011-a01 CT0254 Homo sapiens cDNA
6562	19160	31958	1.38	1.1E-01	AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL 43
6599	19196	32001	0.84	1.1E-01	AI216307.1	EST_HUMAN	qg78406.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6721	19315	32118	3.92	1.1E-01	Q69835	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME)
6805	19396		3.07	1.1E-01	AF032922.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6898	19623	32458	2.36	1.1E-01	11492372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
7238	25119		0.97	1.1E-01	BF382758.1	EST_HUMAN	601816524F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050653 5'
7345	24780	32737	0.92	1.1E-01	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (877)
7542	20062	32935	7.24	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
7542	20062	32936	7.24	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7651	20163	33051	1.85	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
7682	20193		0.7	1.1E-01	Z14098.1	NT	B. subtilis gene encoding hypothetical polyketide synthase
7683	20194	33082	3.53	1.1E-01	AA788784.1	EST_HUMAN	ah31b06.s1 Soares_parathyroid_tumor_Nb1-PA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483
7609	20451	33358	1.41	1.1E-01	U07482.1	NT	CHROMOGGRANIN A PRECURSOR (HUMAN);
8149	20690	33603	1.6	1.1E-01	AA493574.1	EST_HUMAN	Methanococcus jannaschii section 34 of 150 of the complete genome
8149	20690	33604	1.6	1.1E-01	AA493574.1	EST_HUMAN	nh04g10.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8197	20738	33650	1.18	1.1E-01	X01233.1	NT	nh04g10.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8235	20776		1.15	1.1E-01	AW817918.1	EST_HUMAN	H. sapiens IL15 gene
8292	20833	33755	1.54	1.1E-01	AL134349.1	EST_HUMAN	PM1-ST0270-080200-001-409 ST0270 Homo sapiens cDNA
8752	21291	34211	8.48	1.1E-01	U02482.1	NT	DKFZp547P194.1 547 (synonym: Mbr1) Homo sapiens cDNA clone DKFZp547P194 5'
8843	21362	34307	0.87	1.1E-01	A1807474.1	EST_HUMAN	Pedicroccus acidilactici H. plasmid pSMB74, pediocin ACh production (pap) gene cluster papA, papB, papC and papD genes, complete cds
							wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8938	21476	34397	0.48	1.1E-01	AF050081.1	NT	Homo sapiens C16orf3 large protein mRNA, complete cds
8973	21511	34433	2.22	1.1E-01	AA192153.1	EST_HUMAN	z993512.r1 Stratigene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
8973	21511	34434	2.22	1.1E-01	AA192153.1	EST_HUMAN	z993512.r1 Stratigene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9062	21599	34529	0.82	1.1E-01	Y12727.1	NT	P.furiosus partial dph5 gene and ergF gene
							y419h03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to
9092	21628	34585	2.28	1.1E-01	T72875.1	EST_HUMAN	gb:M81181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9119	21655		0.67	1.1E-01	BF893260.1	EST_HUMAN	601436972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5'
9343	21857		1.13	1.1E-01	BE142305.1	EST_HUMAN	CM3-HT0142-271099-026-g11 HT0142 Homo sapiens cDNA
9417	21926		2.2	1.1E-01	BF085149.1	EST_HUMAN	MR2-GN0027-040800-005-a08 GN0027 Homo sapiens cDNA
9824	22322		0.5	1.1E-01	AL161543.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10107	22602		1.03	1.1E-01	R80590.1	EST_HUMAN	y96a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147064 3'
10240	22735	35727	0.86	1.1E-01	U60529.1	NT	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
10554	23060	36104	1.8	1.1E-01	AF245277.1	NT	Dichostelium discoideum kinesin Unc104/KIF1a homolog (Unc104) mRNA, complete cds
10884	15683	28155	2.12	1.1E-01	F03265.1	EST_HUMAN	HSC-IRF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
10802	23325		3.23	1.1E-01	AF169032.1	NT	Carassius auratus activin beta A precursor, mRNA, complete cds
							y435f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu
10923	23442	36483	3.76	1.1E-01	R23708.1	EST_HUMAN	repetitive element; contains TAR1 repetitive element;
10931	23449	36470	1.85	1.1E-01	6981351	NT	Rattus norvegicus Phosphofructokinase, liver, B-type (Pfkf), mRNA
10947	18967	31298	1.56	1.1E-01	AL110985.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
11060	23572	36809	1.74	1.1E-01	X70058.1	NT	M.musculus cytokine gene
11085	23597	36633	3.35	1.1E-01	Z11970.1	NT	Z.mobilis lgt and lgt genes encoding lgtRNA guanine transglycosylase and DNA ligase
11085	23597	36634	3.35	1.1E-01	Z11970.1	NT	Z.mobilis lgt and lgt genes encoding lgtRNA guanine transglycosylase and DNA ligase
11166	23691	36738	2.99	1.1E-01	P17497	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11884	24231		4.81	1.1E-01	BE787023.1	EST_HUMAN	RC2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA
12143	24835		3.29	1.1E-01	BE974556.1	EST_HUMAN	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3'
12597	24684	30880	1.99	1.1E-01	BF239753.1	EST_HUMAN	601806350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1243	13841		2.35	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
							ws08d01.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13
1315	13909	26429	1.92	1.0E-01	A195499.1	EST_HUMAN	MER7 repetitive element;
1436	14029	26557	2.23	1.0E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
2531	15095	27687	0.97	1.0E-01	AW451365.1	EST_HUMAN	UI-H-B13-alc-d-07-Q-Ui.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3583	16167	28649	1.04	1.0E-01	BF033991.1	EST_HUMAN	601456301F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3959849 5'
3782	16382	28847	0.82	1.0E-01	BF239818.1	EST_HUMAN	601906489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
3904	16503	28954	1.41	1.0E-01	AF297061.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds, and unknown genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3804	18503	28865	1.41	1.0E-01	AF297061.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
4027	16625	29097	2.82	1.0E-01	BF365703.1	EST_HUMAN	QV2-NT0048-160800-310-905 NT0048 Homo sapiens cDNA
4498	17080	29529	1.82	1.0E-01	AE00285.2	NT	Chlamydomonas reinhardtii AR39, section 91 of 94 of the complete genome
4853	17235		0.97	1.0E-01	AI792349.1	EST_HUMAN	an32c04.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4822	17400	29853	1.8	1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (ter) mRNA, complete cds
4920	17495	29946	0.98	1.0E-01	AA765434.1	EST_HUMAN	oa05h03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304117 3'
5050	17623	30068	2.12	1.0E-01	AW952344.1	EST_HUMAN	EST364414 IMAGE resequences, MAGB Homo sapiens cDNA
5408	17665	30375	1.06	1.0E-01	AV721471.1	EST_HUMAN	AV721471 HTB Homo sapiens cDNA clone HTBQ10 5'
5415	17972		0.88	1.0E-01	AV763960.1	EST_HUMAN	AV763960 MDS Homo sapiens cDNA clone MDSBQB11 5'
5624	18156		8.57	1.0E-01	W88490.1	EST_HUMAN	zh62h04.s1 Soares fetal liver spleen INFLS_S1 Homo sapiens cDNA clone IMAGE:416895 3'
6040	18659		0.95	1.0E-01	AK024472.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
6175	18786	31554	11.01	1.0E-01	AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6477	19078	31861	0.98	1.0E-01	AA481879.1	EST_HUMAN	z441g10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:758258 3' similar to contains
6489	19090	31873	0.82	1.0E-01	AA406039.1	EST_HUMAN	L1.13 L1 repetitive element;
							z467c12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743062 3'
7091	19682		1.71	1.0E-01	R23821.1	EST_HUMAN	yh34h06.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element;
7717	20225		2.33	1.0E-01	Y12488.1	NT	M.musculus wtn gene
							ak32g01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407696 3' similar to gb:M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
7874	20416	33324	0.53	1.0E-01	AA861091.1	EST_HUMAN	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
8107	20648		0.6	1.0E-01	4758365	NT	x108b01.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2675689 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.13 TAR1 repetitive element;
8429	20969		0.83	1.0E-01	AW189797.1	EST_HUMAN	Rattus norvegicus synaptic SAPAP-interacting protein Synapton mRNA, complete cds
9113	21649	34590	1.08	1.0E-01	AF102855.2	NT	yj33h04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34549 3'
9416	21925	34873	0.49	1.0E-01	R44093.1	EST_HUMAN	Human pro-alpha-1 (V) collagen mRNA, complete cds
9426	21935		2.05	1.0E-01	M76729.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
9459	21988		2.67	1.0E-01	AE001501.1	NT	z466c10.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:327282 3'
9483	21940	34888	0.71	1.0E-01	W01955.1	EST_HUMAN	601805661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
9735	22233	35211	1.67	1.0E-01	BF240154.1	EST_HUMAN	Homo sapiens mRNA for KIAA1579 protein, partial cds
9848	22346	35327	8.17	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
9848	22346	35328	8.17	1.0E-01	AB046799.1	NT	EST369815 IMAGE resequences, MAGB Homo sapiens cDNA
10048	22543		2.05	1.0E-01	AW957425.1	EST_HUMAN	y629a06.s1 Stragelene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element
10053	22548	35542	0.61	1.0E-01	T51952.1	EST_HUMAN	

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10234	22729	35720	1.08	1.0E-01	BE792750.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939096 5'
10537	23074		2.11	1.0E-01	AU159127.1	EST_HUMAN	AU159127 THYR01 Homo sapiens cDNA clone THYR01000895 3'
10910	23429	36448	3.33	1.0E-01	BF242846.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
10910	23429	36449	3.33	1.0E-01	BF242846.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11278	23731	36786	5.03	1.0E-01	BE790543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5'
11870	24581		3.49	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12104	24368		1.74	1.0E-01	7662165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12122	24380		1.36	1.0E-01	X00854.1	NT	Drosophila melanogaster ftz gene
12336	24519		2.27	1.0E-01	AA737981.1	EST_HUMAN	rx11c08.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1255790 3'
12413	25031		4.74	1.0E-01	U52891.1	NT	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PPT1) mRNA, complete cds
12445	24581		2.17	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12495	24823		1.93	1.0E-01	BE158905.1	EST_HUMAN	QV4-H10401-211299-064-g03 HT0401 Homo sapiens cDNA
12511	25001		41.15	1.0E-01	U66834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
12578	24874		7.73	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
2808	15358	27925	0.93	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pke-R11) mRNA, complete cds
2813	15365	27934	1.95	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2813	15365	27935	1.95	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3305	15916	28383	1.98	9.9E-02	AF098810.1	NT	Homo sapiens neurexin II-alpha gene, partial cds
4025	16823	28095	0.64	9.9E-02	AB21837.1	EST_HUMAN	zu45c03.x5 Sceres ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740932 3'
7049	18068	30459	9.12	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blastidin S deaminase, complete cds
7856	20398	33304	0.65	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element
7858	20398	33305	0.65	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element
8181	21758	34704	1.1	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
589	13219		1.48	9.8E-02	X56338.1	NT	O. sativa RAmY9C gene for alpha-amylase
3179	15792	28263	4.23	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4308	16894	28337	8.69	9.8E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
4308	16894	28338	8.69	9.8E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
7495	20018		0.89	9.8E-02	X54133.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
9178	21755		1.05	9.8E-02	M61943.1	NT	Human laminin B1 chain gene, exon 28
11334	23032	36041	2.27	9.8E-02	BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'
11840	24203		1.46	9.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA

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1394	13988	28516	1.24	9.7E-02	AB005808.1	NT	Alce arborescens mRNA for NADP-malic enzyme, complete cds
1629	14221		1.75	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (echondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2301	14874	27450	2.11	9.7E-02	BE168650.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
4055	16652		4.76	9.7E-02	Q99795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5548	18180	30594	1.01	9.7E-02	AF098189.1	NT	Caulobacter crescentus thymidylate kinase (trk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5548	18180	30595	1.01	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (trk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
6165	18777	31541	1.29	9.7E-02	AW954476.1	EST_HUMAN	EST366548 MAGE resequences, MAGC Homo sapiens cDNA
7340	19867	32731	3.26	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 18 of 21): from 2997771 to 3213410
7924	20468	33374	1.29	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
7924	20468	33375	1.29	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8783	21322	34246	1.47	9.7E-02	AI953984.1	EST_HUMAN	wx78608.x1 NCI CGAP_Ox38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:X52851_mat
11076	23588		2.34	9.7E-02	U58337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
2050	14840	27213	1.33	9.6E-02	AI080721.1	EST_HUMAN	Mus musculus ligatin (Lgh) mRNA, partial cds
2080	14640	27214	1.33	9.6E-02	AI080721.1	EST_HUMAN	oz47d11.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4437	17023	29483	7.54	9.6E-02	Z32688.2	NT	oz47d11.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
5142	17713	30144	1.03	9.6E-02	AW966230.1	EST_HUMAN	Proteus mirabilis fimbrial operon, strain H4320
6254	18863		2.74	9.6E-02	BE910039.1	EST_HUMAN	EST378303 MAGE resequences, MAGI Homo sapiens cDNA
8317	20858		0.61	9.6E-02	AU137084.1	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
9463	21988	34944	1.34	9.6E-02	AV687898.1	EST_HUMAN	AU137084 PLACE1 Homo sapiens cDNA clone PLACE1005740 5'
9786	22284		1.35	9.6E-02	BE894895.1	EST_HUMAN	AV687898 GKC Homo sapiens cDNA clone GKCAAH02 5'
9952	22447	35429	1.21	9.6E-02	AJ243211.1	NT	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919063 5'
9952	22447	35430	1.21	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10055	22550	35544	1.28	9.6E-02	AB013985.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10055	22550	35545	1.26	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10159	22654	35649	3.43	9.6E-02	P06174	SWISSPROT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10621	23153	36165	7.28	9.6E-02	Z79702.1	NT	COMPLEMENT DECOY-ACCELERATING FACTOR PRECURSOR (CD55)
11566	24013	37082	1.81	9.6E-02	AA625755.1	EST_HUMAN	Mycobacterium tuberculosis H37Rv complete genome, segment 102/162
12486	24617		1.55	9.6E-02	H14599.1	EST_HUMAN	zu91g01.s1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:745392 3'
4177	16768	29217	2.24	9.5E-02	AW992395.1	EST_HUMAN	ym19h03.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3'
5286	17848	30274	1.12	9.5E-02	U63374.1	NT	GM2-BN0023-0200-087-412 BN0023 Homo sapiens cDNA
							Lycopodium obscurum polygalacturonase isoenzyme 1 beta subunit gene, complete cds

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5846	18470	31196	0.82	9.5E-02	F51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7344	10871	32736	4.47	9.5E-02	AB003473.1	NT	Timersurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
7569	20086	32963	6.95	9.5E-02	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7885	18470	31196	0.9	9.5E-02	F51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7821	20363	33271	2.04	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
7821	20363	33272	2.04	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10559	23095	36107	3.19	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10559	23095	36108	3.19	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
12557	24858		2.4	9.5E-02	AF272732.1	NT	Arabidopsis thaliana putative transcription factor (MYB110) mRNA, complete cds
1873	14459	27015	3.67	9.4E-02	BF671063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5'
1904	14489	27050	1.36	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
1904	14489	27051	1.36	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
3948	16547	29015	5.59	9.4E-02	Z33059.1	NT	M. capricolum DNA for CONTIG MC073
5383	17942		0.93	9.4E-02	X88106.1	NT	Lactobacillus bacteriophage phi17e complete genomic DNA
8459	19060	31846	0.73	9.4E-02	AF097363.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
8536	21075		2.32	9.4E-02	Z46863.1	NT	Acinetobacter sp. cysD, cobQ, cobQ, sodM, lysS, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes
10813	20107	32982	2.33	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vati genes, complete cds, and lpr35 gene, partial cds
11722	24934		6.48	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
12645	24719	30889	3.54	9.4E-02	U27689.1	NT	Human pepBGT-1 belaine-GABA transporter mRNA, complete cds
3018	16634		1.66	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3063	15678		7.31	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESP1), mRNA
3295	15906	28387	2.05	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289269 5'
4232	16920	28269	4.11	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4232	16920	29270	4.11	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4840	17418		1.28	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
5843	18467		0.73	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8190	20731	33643	0.52	9.3E-02	AW569007.1	EST_HUMAN	EST89 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
9052	21589		0.5	9.3E-02	AL113179.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9628	22126	35090	2.1	9.3E-02	BE982631.2	EST_HUMAN	601655988R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855981 3'
10094	22589	35581	3.16	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10094	22589	35582	3.16	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10222	22717		3.82	9.3E-02	AW206117.1	EST_HUMAN	UI-H-B11-afx-h-05-Q-U1 s1 NC1_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
11892	24854		2.27	9.3E-02	AJ249850.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit

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12379	24886		10.03	9.3E-02	AW488650.1	EST_HUMAN	h228h12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2810887 3'
12599	24933						Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), leucine (leucine), RAGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
249	12909	25380	3.18	9.3E-02	AF100956.1	NT	Molluscum contagiosum virus subtype 1, complete genome
249	12909	25391	5.24	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
249	12909	25392	5.24	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2269	14843		5.24	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
3213	15825	28302	1.58	9.2E-02	R54186.1	EST_HUMAN	y98807.r1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:41618 5'
3345	15955	28430	3.92	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3846	16249		0.86	9.2E-02	AA534354.1	EST_HUMAN	nt79601.31 NCI CGAP_Co3 Homo sapiens cDNA clone IMAGE:926136 3'
4322	16808		1.18	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
4398	16961		1.42	9.2E-02	U62048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4744	17325	29787	0.65	9.2E-02	BE299722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960176 5'
7951	20493	33402	1.44	9.2E-02	X98402.1	NT	G.gallus Mla-CK gene
8117	20658	33587	1.75	9.2E-02	T49920.1	EST_HUMAN	y98809.r1 Stratagene placenta (4937225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gb:X56008 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
12656	24930		2.11	9.2E-02	X95256.1	NT	H.vulgaris xylose isomerase gene
448	12677	25134	2.09	9.2E-02	Z22150.1	NT	S.dysgalactae fnbA gene
3733	16334		2.83	9.1E-02	X77685.1	NT	O. cuticulus k12 keratin gene
4592	17165	29608	0.95	9.1E-02	AW372569.1	EST_HUMAN	PM2-BT0349-161299-001-f02 BT0349 Homo sapiens cDNA
5905	18527	31253	1.55	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
7420	19944	32809					Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7698	20180	33067	11.98	9.1E-02	AW160658.1	EST_HUMAN	au74805.Y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781988 5'
7695	20204	33091	0.89	9.1E-02	AP000061.1	NT	Aeropyrum pernix genomic DNA, section 4/7
8855	21394	34317	0.68	9.1E-02	U93073.1	NT	Mus musculus thymopoietin zeta mRNA, complete cds
10325	22819		1.05	9.1E-02	Y14379.1	NT	Homo sapiens gamma adducin gene, exon 9
10354	22848	35842	1.39	9.1E-02	T02984.1	EST_HUMAN	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3' end
10380	22874	35867	1.52	9.1E-02	S74059.1	NT	Tg816-Cyt actin [Tritoneustes gratillae sea urchins, embryos, Genomic, 5275 nt]
11656	24093		0.73	9.1E-02	Y11187.1	NT	A.thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes
11898	25036		2.35	9.1E-02	9633494	NT	Bacteriophage Mu, complete genome
			1.62	9.1E-02	AA179901.1	EST_HUMAN	zp38h12.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;

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11978	24289		2.21	9.1E-02	AF052695.1	NT	Rattus norvegicus cell cycle protein p55ODC gene, complete cds
12467	24877		17.53	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
12672	24740		1.5	9.1E-02	AF226688.1	NT	Bombyx mori fibroin heavy chain Fib-H (fib-H) gene, complete cds
774	13393	25893	3.92	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1676	14268	26801	6.34	9.0E-02	BE220482.1	EST_HUMAN	h39g10.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;
2829	15381	27951	1.76	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2829	15381	27952	1.76	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
3380	15989	28488	0.83	9.0E-02	AF279135.1	NT	Dicotyledium discoidium spore coat structural protein SP65 (cotE) gene, complete cds
4387	16973	28422	0.59	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4387	16973	28423	0.59	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4775	17356	29808	1.68	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5401	17959	30370	1.12	9.0E-02	Q24597	SWISSPROT	REGULATORY PROTEIN ZESTE
6146	18780	31519	18.48	9.0E-02	W56037.1	EST_HUMAN	za68a12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297694 5' similar to PIR:S52171 S52171 small G protein - human ;
6820	19410		1.1	9.0E-02	BF062651.1	EST_HUMAN	7h63d03.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3320845 3' similar to contains Alu repetitive element;
6864	19598	32428	0.77	9.0E-02	R62805.1	EST_HUMAN	Y11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138803 3'
12300	24497						Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrfU (orfU), >
1486	14078	26617	2.42	9.0E-02	AF022236.1	NT	
1486	14078	26618	1.46	8.9E-02	BF701593.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2430	14997	27571	9.68	8.9E-02	BE153572.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
4277	16893		1.79	8.9E-02	AF286055.1	NT	PMO-HT0339-251169-003-d01 HT0339 Homo sapiens cDNA
4741	17322	29762	1.91	8.9E-02	AA424887.1	EST_HUMAN	Atrichum angustatum AtranFlo2 protein (AtranFlo2) gene, partial cds
6014	18634	31370	3.35	8.9E-02	AW452122.1	EST_HUMAN	zw03d04.s1 Soares NhrMPu_S1 Homo sapiens cDNA clone IMAGE:768199 3'
6014	18634	31371	3.35	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alo-f08-q-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
6026	18845	31387	3.24	8.9E-02	11433478	NT	UI-H-B13-alo-f08-q-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
7244	19773	32630	1.76	8.9E-02	P47259	SWISSPROT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
7559	20077		2.15	8.9E-02	Z79021.1	NT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE ; METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE]
							H. sapiens flow-sorted chromosome 9 HindIII fragment, SC6pA20F8

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7984	20536	33439	0.96	8.9E-02	P29475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8072	20614	33528	0.86	8.9E-02	BF701665.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8072	20614	33529	0.66	8.9E-02	BF701665.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8534	21073	33993	4.81	8.9E-02	AA309319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9538	22038	34998	0.83	8.9E-02	AI285627.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1 MER10 repetitive element ;
9538	22038	34999	0.83	8.9E-02	AI285627.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1 MER10 repetitive element ;
9648	22147	35118	0.55	8.9E-02	AA339356.1	EST_HUMAN	EST44454 Fetal brain 1 Homo sapiens cDNA 5' end
11721	24884		2.61	8.9E-02	P19524	SWISSPROT	MYOSIN-2 ISOFORM
11872	24224		4.62	8.9E-02	BF696918.1	EST_HUMAN	602129682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
12044	24330		3.07	8.9E-02	6680220	NT	Mus musculus hippocampus abundant gene transcript 1 (Hiat1), mRNA
12307	25104		1.57	8.9E-02	U40493.1	NT	Ceratitis capitata mariner transposase gene, complete cds
1416	14009	26538	1.36	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3971	16569	29038	1.08	8.8E-02	AA299128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end
4106	16700		4.3	8.8E-02	O00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIIID 135 KDA SUBUNIT (TAFII135) (TAFII-130) (TAFII130)
4390	16976		0.96	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), isoform b, mRNA
8918	21456	34376	1.16	8.8E-02	AA151872.1	EST_HUMAN	zn69a05.s1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
10997	23511	36543	3.11	8.8E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
10997	23511	36544	3.11	8.8E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11142	23650	36692	10.91	8.8E-02	AL040126.1	EST_HUMAN	DKFZp434D1313_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1313 5'
11848	24277	31019	1.73	8.8E-02	Z71591.1	NT	S.cerevisiae chromosome XIV reading frame ORF YNL285w
3756	16357	28828	3.9	8.7E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3756	16357	28827	3.9	8.7E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4816	17394	29847	1.42	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5264	17828		1.2	8.7E-02	AE000695.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome
5517	18149	30581	5.18	8.7E-02	AA288875.1	EST_HUMAN	zs55q08.st NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5517	18149	30562	5.18	8.7E-02	AA280875.1	EST_HUMAN	z55508.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
6931	19590	32421	0.75	8.7E-02	AJ271895.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6931	19590	32422	0.75	8.7E-02	AJ271895.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7803	20348		0.46	8.7E-02	AA284532.1	EST_HUMAN	z20e03.s1 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:713692 3'
8452	20992	33910	0.64	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
8452	20992	33911	0.64	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
10590	23125		2.71	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' and
11191	23698	36745	1.77	8.7E-02	AJ007763.1	NT	Glucobacter oxydans rRNA-1le and rRNA-Ala genes
11935	24269		2.35	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12142	24389		2.72	8.7E-02	6879057	NT	Mus musculus nidogen 2 (Nid2), mRNA
1295	13889	28412	6.51	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2286	14880	27435	2.47	8.6E-02	BE408667.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3222	15834	28312	2.42	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds
3708	16307		4.02	8.6E-02	AF153362.1	NT	Dictyostelium discoideum adenyl cyclase (acrA) gene, complete cds
4584	17167	29610	0.59	8.6E-02	U088179.1	NT	Oryctolagus cuniculus galeclin-3 gene, untranslated exon and 5' flanking region
6244	18953	31824	5.78	8.6E-02	Y10926.1	NT	Homo sapiens LCN1b gene
6512	19112	31899	1.58	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6512	19112	31900	1.56	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7591	20098	32974	1.14	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
7871	20413	33319	1.23	8.6E-02	5730068	NT	Homo sapiens Sni2-related CBP activator protein (SRCAP) mRNA
7871	20413	33320	1.23	8.6E-02	5730068	NT	Homo sapiens Sni2-related CBP activator protein (SRCAP) mRNA
8015	20557	33480	0.76	8.6E-02	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
8073	20615		0.65	8.6E-02	U60168.1	NT	Dictyostelium discoideum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds
9652	22151	35121	1.18	8.6E-02	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
9888	22187		1.27	8.6E-02	AW662153.1	EST_HUMAN	hi20c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972846 3'
10057	22552	35547	0.74	8.6E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1294 mRNA, complete cds
10824	23345	36360	1.68	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
10824	23345	36361	1.68	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11128	23636	36677	4.74	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11128	23636	36678	4.74	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11315	23013	36022	7.58	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
2440	15007	27579	2.52	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5885	18507		1.91	8.5E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
6162	18775	31537	5.84	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
8542	21081	34002	1.76	8.5E-02	6754779	NT	Mus musculus myosin XV (Myp15), mRNA
9750	22248	35230	3.08	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
9750	22248	35231	3.08	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10379	22873	35866	0.92	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11035	23549		12.56	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11050	23563	36598	4.42	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12554	24814		5.89	8.5E-02	AJ005586.1	NT	Antirrhinum majus mRNA for MYB-related transcription factor
12536	24847		2.27	8.5E-02	AA362834.1	EST_HUMAN	EST72738 Ovary II Homo sapiens cDNA 5' end
2690	15474	27816	3.71	8.4E-02	W69330.1	EST_HUMAN	z444e1.1 r1 Sceres_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343532 5'
5200	17765		1	8.4E-02	X01472.1	NT	Drosophila melanogaster copia-like element 17.6
5369	17928	30343	0.88	8.4E-02	5453817	NT	Homo sapiens nucleobindin 1 (NUCB1), mRNA
5315	18147	30559	9.48	8.4E-02	BE267153.1	EST_HUMAN	601160436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
6791	18382	32197	1.67	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
7972	20514	33421	7.35	8.4E-02	BE095074.1	EST_HUMAN	CM3-BT0760-260400-162-d05 BT0760 Homo sapiens cDNA
8776	21315	34237	1.13	8.4E-02	AF218890.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 2
							as88g10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
10285	22760	35747	1.61	8.4E-02	A1735184.1	EST_HUMAN	O88312 GOB-4.;
11858	24217	31042	1.92	8.4E-02	R79408.1	EST_HUMAN	y183h12.r1 Sceres placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
2056	14637	27208	2.06	8.3E-02	5835680	NT	lxodes hexagonus mitochondrion, complete genome
2058	14637	27209	2.06	8.3E-02	5835680	NT	lxodes hexagonus mitochondrion, complete genome
3652	16255	28728	8.98	8.3E-02	P75334	SWISSPROT	HYPOTHEICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3680	16281	28748	0.68	8.3E-02	A1436797.1	EST_HUMAN	th82g06.x1 Sceres_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
3680	16281	28749	0.68	8.3E-02	A1436797.1	EST_HUMAN	th82g06.x1 Sceres_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
5416	17973		1.71	8.3E-02	AW902857.1	EST_HUMAN	QV3-NN1025-030500-173-e04 NN1025 Homo sapiens cDNA
6408	18009	31791	0.89	8.3E-02	A1842338.1	EST_HUMAN	wo7911.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'
6504	18104	31889	3.05	8.3E-02	AF052683.1	NT	Homo sapiens protocadherin 43 gene, exon 1
7922	20464	33371	3.57	8.3E-02	AF195787.1	NT	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dp2) mRNA, complete cds
							og88g08.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1456422 3' similar to contains L1.11 L1 L1
7955	20497		1.31	8.3E-02	AA865285.1	EST_HUMAN	repetitive element;
8241	20762		4.14	8.3E-02	AA987873.1	EST_HUMAN	oq81f10.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3'
							ig05h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA
9457	21993	34935	1.55	8.3E-02	AW583503.1	EST_HUMAN	SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE.;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9470	21869		1.94	8.3E-02	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
10244	22739		0.56	8.3E-02	AF020409.1	NT	Dictyostellum discoideum DocA (docA) mRNA, complete cds
11550	23998	37070	1.7	8.3E-02	AA700756.1	EST_HUMAN	z62d04.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:435367 3' similar to contains element MER22 repetitive element:
11953	25040		1.38	8.3E-02	BE958458.1	EST_HUMAN	601644770F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3929993 5'
1421	14014		0.32	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for for OBCAM protein gamma isoform
1542	14134	26868	1.79	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3109	15724		2.23	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
3874	16472		1.66	8.2E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4078	16975	28136	1.29	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4371	16958	29400	7.76	8.2E-02	P48960	SW/SSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4371	16958	29401	7.76	8.2E-02	P48960	SW/SSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4371	16958	29402	7.76	8.2E-02	P48960	SW/SSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5240	17804	30225	3.53	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5400	17958	30369	0.9	8.2E-02	AU119830.1	EST_HUMAN	AU119830 HEMBA1 Homo sapiens cDNA clone HEMBA1008744 5'
5538	18170	30585	1.82	8.2E-02	BE897030.1	EST_HUMAN	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
7092	19663	32502	3.11	8.2E-02	AF309555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
8707	21246	34169	2.98	8.2E-02	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA
9517	22017	34974	4.86	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
9678	22177	35152	2.2	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355596 5'
11959	24281	31023	5.69	8.2E-02	AE002248.2	NT	Chlamydomonas reinhardtii growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
12383	24908		4.6	8.2E-02	AF275368.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5929	18551	31278	1.08	8.1E-02	AE004008.1	NT	Xylella fastidiosa, section 152 of 229 of the complete genome
6516	19116	31906	0.97	8.1E-02	T11532.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7248	19777		0.72	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7592	20087		1.03	8.1E-02	AI892881.1	EST_HUMAN	wd6608.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
8281	20822	33741	0.82	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8281	20822	33742	0.82	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
9826	23224		1.7	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactin precursor, gene, complete cds
11371	23823	36886	1.87	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
6	15405	25143	9.1	8.0E-02	AW954653.1	EST_HUMAN	EST366723 IMAGE resequences, MAGC Homo sapiens cDNA
971	13582	26095	1.13	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1738	15449	26869	10.86	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1738	15449	26870	10.86	8.0E-02	D28535.1	NT	Human gene for dihydriolpoamide succinyltransferase, complete cds (exon 1-15)
1947	14531	27087	3.32	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2413	14981	27558	1.14	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2413	14981	27557	1.14	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2509	15073		4.66	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2847	13733	26243	0.87	8.0E-02	M23449.1	NT	Dictyosellum discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2925	15541	28016	0.84	8.0E-02	AL445087.1	NT	Thermoplasma acidophilum complete genome; segment 5/5
3888	16487	28948	0.59	8.0E-02	AW966118.1	EST_HUMAN	EST378191 MAGE resequences, MAGI Homo sapiens cDNA
4146	16738		0.95	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4890	17465	29920	2.28	8.0E-02	AI434202.1	EST_HUMAN	tt31g02.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132114 3'
4939	17514		5.81	8.0E-02	X72794.1	NT	M.musculus gene for gelatinase B
6051	18669	31408	3.07	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7232	18669	31408	1.42	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8069	20671	33524	3.68	8.0E-02	AL114993.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9311	21825	34773	1.22	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
9311	21825	34774	1.22	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10053	22558		0.57	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10671	23203	36216	3.69	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
11993	24302	30988	3.6	8.0E-02	AJ003375.1	NT	Drosophila arena hunchback region
12595	16738		3.88	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2218	14793	27366	4.15	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5'
3007	15623	28101	11.7	7.9E-02	AI582029.1	EST_HUMAN	ar98c08.x1 Bartshead colon HPLR87 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:226876
3885	16483	28927	0.82	7.9E-02	AF030694.2	NT	Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), putative chloroquine resistance transporter (crt), CG9 (cg9), CG1 (cg1), CG6 (cg6), CG2 (cg2), and CG7 (cg7) genes, complete cds
3917	16515	28978	3	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3917	16515	28979	3	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4934	17509		1.36	7.9E-02	AB008019.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
6390	17948	30360	0.58	7.9E-02	AF035672.1	NT	Mus musculus MHC class I related protein 1 (MR1) gene, complete cds
5390	17948	30361	0.58	7.9E-02	AF035672.1	NT	Mus musculus MHC class I related protein 1 (MR1) gene, complete cds
6788	19388		1.08	7.9E-02	BF368016.1	EST_HUMAN	RC3-GN0042-310800-024-d11 GN0042 Homo sapiens cDNA
7975	20517	33424	3.32	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of Mif2 Smt4p (SMT4) gene, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9941	22436	35412	4.71	7.9E-02	A1081844.1	EST_HUMAN	ou63b05.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611:
9941	22436	35413	4.71	7.9E-02	A1081844.1	EST_HUMAN	ou63b05.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611:
12479	24613		1.42	7.9E-02	A1761639.1	EST_HUMAN	wg56h01.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370097 3' ou59d02.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element:
1252	13849	26365	1.36	7.8E-02	A1793275.1	EST_HUMAN	ou59d02.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element:
1252	13849	26366	1.36	7.8E-02	A1793275.1	EST_HUMAN	ou59d02.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element:
4912	17487	28943	0.67	7.8E-02	BE836331.1	EST_HUMAN	PM3-FN0058-140700-005-109 FN0058 Homo sapiens cDNA
5247	18412		2.77	7.8E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859693 5'
7136	19475	32297	1.34	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7136	19475	32298	1.34	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8720	21259	34179	1.46	7.8E-02	BE897947.1	EST_HUMAN	601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
8813	21352	34274	0.6	7.8E-02	X78344.1	NT	S.cerevisiae CA18 gene
8983	21521	34447	0.83	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
8983	21521	34448	0.83	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9283	21883	34828	1.08	7.8E-02	AA469354.1	EST_HUMAN	nc88b08.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:771731
9717	22215	35189	0.5	7.8E-02	Z99124.1	NT	Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814
10544	23081	36094	1.87	7.8E-02	U32323.1	NT	Human interleukin-11 receptor alpha chain gene, complete cds
12384	24550	30906	1.95	7.8E-02	U72847.1	NT	Homo sapiens enovoplatin (EVPL) gene, exons 15 through 18
1444	15442	26568	0.91	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3647	16250		2.62	7.7E-02	AJ238063.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5129	17701	30135	0.92	7.7E-02	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
7850	20392	33295	5.56	7.7E-02	AA402949.1	EST_HUMAN	zu53d11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN.:
9749	22247	35229	5.97	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10037	22532	35527	0.75	7.7E-02	A1318682.1	EST_HUMAN	ta80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
10037	22532	35528	0.75	7.7E-02	A1318682.1	EST_HUMAN	ta80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
10889	23410	36428	4.97	7.7E-02	11422757	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
12184	24894		1.91	7.7E-02	11438859	NT	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
3434	16042	28523	3.08	7.6E-02	BE514432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3455	16062	28537	0.67	7.6E-02	AA298447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to protocadherin 43
3615	16218	28637	0.67	7.6E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
4983	17567		2.04	7.6E-02	AW858844.1	EST_HUMAN	RC3-CT0347-110300-014-e05 CT0347 Homo sapiens cDNA
6247	18856	31627	0.7	7.6E-02	A061275.1	EST_HUMAN	an25g02.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'
6497	19088	31882	0.83	7.6E-02	BE376328.1	EST_HUMAN	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9292	21892	34839	1.24	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
9811	22309		1.7	7.6E-02	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
10120	22615	35606	0.52	7.6E-02	BE708002.1	EST_HUMAN	RC1-HT0545-020800-017-d06 HT0545 Homo sapiens cDNA
10251	22746		0.49	7.6E-02	BE959638.2	EST_HUMAN	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
10480	22874	35981	0.72	7.6E-02	X92656.1	NT	L. esculentum mRNA for triose phosphate translocator
10480	22874	35982	0.72	7.6E-02	X92656.1	NT	L. esculentum mRNA for triose phosphate translocator
11526	23974	37044	2.58	7.6E-02	AW898845.1	EST_HUMAN	QV3-BN0046-150400-151-e04 BN0046 Homo sapiens cDNA
817	13435	25940	1.18	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
817	13435	25941	1.18	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
4606	17189	20636	0.57	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for Interleukin-18, intron 1 and exon 2
8280	20821	33740	1.15	7.5E-02	A1864387.1	EST_HUMAN	w52602.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
8444	20894	33899	1.18	7.5E-02	AU116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000284 5'
9945	22440		0.5	7.5E-02	BF221730.1	EST_HUMAN	7d61c05.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element MER27 repetitive element;
10387	22891	35875	0.9	7.5E-02	BF206809.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
10481	22975	35983	0.71	7.5E-02	X79480.1	NT	C.fiml DSM 20113 16S rDNA
503	13135	25623	1.23	7.4E-02	AW838547.1	EST_HUMAN	RC6-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
1509	14101		0.97	7.4E-02	AF030027.1	NT	Equine herpesvirus 4 strain NS80567, complete genome

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2616	15178		1.04	7.4E-02	6755089	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
3654	16257	28728	0.84	7.4E-02	AI807885.1	EST_HUMAN	wf43h01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4814	17392	28844	1.33	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4911	17486	28942	2.82	7.4E-02	6978442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
5052	17625		1.65	7.4E-02	AE000886.1	NT	Methanobacterium thermoautotrophicum from bases 1076134 to 1086763 (section 92 of 148) of the complete genome
5076	17649	30090	1.67	7.4E-02	6678492	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrlp), mRNA
5393	17951	30364	0.93	7.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6821	19218		1.84	7.4E-02	R17477.1	EST_HUMAN	y914g06.r1 Soares_infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
7485	20008	32874	0.68	7.4E-02	AA605132.1	EST_HUMAN	no71d02.61 NC1 CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112259 3'
7842	20384	33288	1.23	7.4E-02	BE880112.1	EST_HUMAN	601493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895264 5'
8438	20878	33853	1.2	7.4E-02	U56089.1	NT	Human periodic tyrosine protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9093	21628	34566	0.92	7.4E-02	AW629605.1	EST_HUMAN	hh67d11.y1 NC1 CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867861 5' similar to SW:SCA2_HUMAN
9093	21628	34567	0.92	7.4E-02	AW629605.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
9360	20289	33197	0.72	7.4E-02	AI872939.1	EST_HUMAN	hh67d11.y1 NC1 CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867861 5' similar to SW:SCA2_HUMAN
9360	20289	33198	0.72	7.4E-02	AI872939.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
9728	22226	35203	0.85	7.4E-02	U62293.1	NT	wel74d02.x1 Soares_Dieckgraebe_colon_NHGD Homo sapiens cDNA clone IMAGE:2346819 3'
11600	24043		1.57	7.4E-02	U82282.1	NT	wel74d02.x1 Soares_Dieckgraebe_colon_NHGD Homo sapiens cDNA clone IMAGE:2346819 3'
11912	24250		1.29	7.4E-02	11525893	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
12187	25015		4.44	7.4E-02	AW379431.1	EST_HUMAN	Rattus norvegicus telomerase protein component 1 (TLP1) mRNA, complete cds
12351	24531	30926	2.8	7.4E-02	BF035099.1	EST_HUMAN	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
12361	24535	30901	1.37	7.4E-02	AJ223459.2	NT	CM4-HT0243-081199-037-411 HT0243 Homo sapiens cDNA
484	13127	25613	1.42	7.3E-02	BE964961.2	EST_HUMAN	601453813F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3867738 5'
494	13127	25614	1.42	7.3E-02	BE964961.2	EST_HUMAN	Aspergillus nidulans prnD, prnX, prnA genes
713	13334	25820	2.68	7.3E-02	AE001789.1	NT	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
1528	15444	26659	4.47	7.3E-02	AW900281.1	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
1885	15453		16.16	7.3E-02	AL163302.2	NT	Thermotoga maritima section 101 of 136 of the complete genome
							CM0-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C102
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S7
3838	16437		0.59	7.3E-02	U66059.1	NT	
5137	17709		1.11	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6580	19178	31978	1.56	7.3E-02	AA779977.1	EST_HUMAN	z24e02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb.L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
7484	20007	32872	4.36	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7484	20007	32873	4.36	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8109	20650		1.06	7.3E-02	7692107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
9137	21672		1.38	7.3E-02	AB011090.1	NT	Homo sapiens mRNA for KIAA0518 protein, partial cds
11095	19178	31978	3.07	7.3E-02	AA779977.1	EST_HUMAN	z24e02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb.L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
125	12794	25279	1.36	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
125	12794	25280	1.36	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1524	14116	26552	2.11	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1524	14116	26653	2.11	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2585	15148		2.76	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
3954	16552	28021	0.59	7.2E-02	AW298322.1	EST_HUMAN	UI-H-BW0-aj-e-05-0-JJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'
4438	17024	28484	3.65	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
5223	17788	30207	0.89	7.2E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
5491	18125	30533	2.8	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5492	18126	30534	8.6	7.2E-02	P11120	SWISSPROT	CALMODULIN
6255	18873		0.83	7.2E-02	BF217596.1	EST_HUMAN	601883905F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096224 5'
7220	19751	32607	1.27	7.2E-02	BF218086.1	EST_HUMAN	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
7261	19789		1.54	7.2E-02	5634897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8128	20689	33578	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8128	20689	33579	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8984	21532		0.5	7.2E-02	Y17217.1	NT	Lactococcus lactis cspE gene
9495	21995		0.57	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9529	22029	34986	2.28	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAAUG01 5'
9874	22173	35149	4.69	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
9828	22326	35307	1.01	7.2E-02	BF125399.1	EST_HUMAN	601765523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026436 5'
9914	22410	35396	2.73	7.2E-02	AW873187.1	EST_HUMAN	hq2411.x1 NCI_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN.1

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10254	22749	35737	2.11	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10370	22864	35857	5.88	7.2E-02	BE565003.1	EST_HUMAN	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
10392	22886		3.22	7.2E-02	BE539214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451859 5'
10702	23315	36324	6.18	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
11822	24192	31033	1.54	7.2E-02	AA773698.1	EST_HUMAN	af81a04.r1 Soares NIH-MP_u_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
11857	24216		4.88	7.2E-02	AJ230786.1	EST_HUMAN	AJ230796 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'
11914	24252		2.01	7.2E-02	AA584465.1	EST_HUMAN	nc05h08.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1099839 3'
11979	24290		3.59	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
11995	24858		7.52	7.2E-02	AW900982.1	EST_HUMAN	CM4-NN1009-200300-118-c11 NN1009 Homo sapiens cDNA
12514	24633		1.65	7.2E-02	AA401779.1	EST_HUMAN	z157c12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726454 5'
1948	14532	27088	1.42	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D8) proviral structural capsid protein (gag) gene, partial cds
2331	14902	27473	4.53	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5'
7848	20390	33292	0.84	7.1E-02	A1125284.1	EST_HUMAN	qd82a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922 3'
11700	24113		6.04	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
554	13185	25663	0.97	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1547	14139		1.43	7.0E-02	X68677.1	NT	M. artellia Mcut-1 gene
1798	14398	26933	0.94	7.0E-02	AA056343.1	EST_HUMAN	z165f02.s1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:509599 3'
3084	15890	28153	2.03	7.0E-02	AW138152.1	EST_HUMAN	UI-H-B11-acy-c-07-Q-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3966	16584	29033	1.71	7.0E-02	AA815438.1	EST_HUMAN	si65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375878 3' similar to gb:K03002 60S
4118	16712	29186	1.11	7.0E-02	BE070284.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4219	16807		1.11	7.0E-02	AW792862.1	EST_HUMAN	QV4-BT0407-280100-090-s10 BT0407 Homo sapiens cDNA
4294	16890	29327	1.28	7.0E-02	AF077821.1	NT	CM0-UM0001-090300-270-e12 UM0001 Homo sapiens cDNA
5063	17636	30079	9.56	7.0E-02	BF381987.1	EST_HUMAN	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
5580	18211		0.84	7.0E-02	Y09143.2	NT	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
7431	18955	32820	0.88	7.0E-02	AV689285.1	EST_HUMAN	Lumbricus rubellus mRNA for cyclophilin B
9027	21584	34483	1.41	7.0E-02	8628113	NT	AV689285 RBC Homo sapiens cDNA clone GKCGAE06 5'
9515	22015	34973	1.25	7.0E-02	K02901.1	NT	African swine fever virus, complete genome
9883	22360	35340	0.73	7.0E-02	U27286.1	NT	Rat Ig gamma epsilon H-chain gene C-region, 3' end
11251	23781	36837	2.68	7.0E-02	AA724285.1	EST_HUMAN	Human myosin binding protein H (MyBP-H) gene, complete cds ah99a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:U14837 TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
540	13171	25649	11.84	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
540	13171	25650	11.84	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1378	13971		1.34	6.9E-02	4507968	NT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP-1) mRNA, and translated products
3860	16458	28921	1.16	6.9E-02	Q08364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3860	16458	28922	1.16	6.9E-02	Q08364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
							Enterococcus faecium cysteine aminopeptidase (pepC) gene, partial cds; phospho-beta-glucosidase BglB (bglB), beta-glucoside specific transport protein (bglS), transcription antiterminator (bglR), enterocin B precursor (entB), enterocin B immunity protease
5381	17940	30354	3.58	6.9E-02	AF121254.1	NT	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
7096	20538		1.13	6.9E-02	U12022.1	NT	6013400681F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8488	21027	33944	1.1	6.9E-02	BE567435.1	EST_HUMAN	6013400681F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8488	21027	33945	1.1	6.9E-02	BE567435.1	EST_HUMAN	6013400681F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9048	21585	34518	0.61	6.9E-02	U22987.1	NT	Barbarie duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
11853	24213		17.91	6.9E-02	X74315.1	NT	Xlaevis XFD2 mRNA for fork head protein
12031	24321		1.98	6.8E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOF6 HOMOLOG
12258	24468		3.68	6.8E-02	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1928	14511	27065	1.83	6.8E-02	AA496759.1	EST_HUMAN	ae30702.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
							MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1928	14511	27066	1.83	6.8E-02	AA496759.1	EST_HUMAN	ae30702.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1950	14534	27090	3.99	6.8E-02	AF156673.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
2023	14805	27170	1.68	6.8E-02	BE263781.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBSCTR14) gene, complete cds
4651	17233		0.66	6.8E-02	BE141076.1	EST_HUMAN	601194141F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537706 5'
6980	19478		4.63	6.8E-02	BE081890.1	EST_HUMAN	MR0-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA
7324	19851	32713	8.08	6.8E-02	AL163268.2	NT	RC1-BT0254-090300-017-d09 BT0254 Homo sapiens cDNA
8230	20771	33690	5.36	6.8E-02	AJ248287.1	NT	Homo sapiens chromosome 21 segment HS21C068
8230	20771	33691	5.36	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
11046	25064		2.48	6.8E-02	T03214.1	EST_HUMAN	Pyrococcus abyssi complete genome, segment 5/6
11783	24168		2.42	6.8E-02	AA758014.1	EST_HUMAN	FB4A8 Fetal brain, Striatagene Homo sapiens cDNA clone FB4A8.3 and similar to LINE-1
12380	24547		1.37	6.8E-02	AW875839.1	EST_HUMAN	af87605.s1 Soares testis NHT Homo sapiens cDNA clone 1320705 3'
12444	24580		2.87	6.8E-02	9910585	NT	EST3878948 IMAGE:resquences, MAGN Homo sapiens cDNA
12650	25008	30814	1.54	6.8E-02	6978985	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1578	14169		1.51	6.7E-02	AF115536.1	NT	Rattus norvegicus Growth factor independent-1 (Gif), mRNA
4028	14522	27078	3.82	6.7E-02	AI270285.1	EST_HUMAN	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
4028	14522	27078	3.82	6.7E-02	AI270285.1	EST_HUMAN	9979e04.x1 Soares NFL T. GBC S1 Homo sapiens cDNA clone IMAGE:1841408 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3780	16380	28844	4.61	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOXD4 (CHOXA)
4842	17420	29873	3.51	6.7E-02	AF001514.1	NT	Bacillus halodurans genomic DNA, section 8/14
7782	20335	33241	0.63	6.7E-02	XG2695.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
7782	20335	33242	0.63	6.7E-02	XG2695.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
9518	22018	34975	0.75	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B11-act-g-01-Q-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
9518	22018	34976	0.75	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B11-act-g-01-Q-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
2225	14800	27372	3	6.6E-02	AJ289241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3510	16115	28594	9.7	6.6E-02	R64306.1	EST_HUMAN	yt18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3524	16129	28609	3.24	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3524	16129	28610	3.24	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4154	16746	28200	1.83	6.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5114	17686	30122	11.2	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5114	17686	30123	11.2	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5164	17733	30180	0.57	6.6E-02	AA393244.1	EST_HUMAN	z74407.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:104270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
5164	17733	30181	0.57	6.6E-02	AA393244.1	EST_HUMAN	z74407.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:104270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
6688	19294	32099	4.11	6.6E-02	X06411.1	NT	P. vulgaris mRNA for chalcone synthase
7888	20430	33339	1.58	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8409	20949	33869	0.72	6.6E-02	AF008055.1	NT	Dicotyledium discoidium darlin (darA) gene, complete cds
8714	21253	34312	0.49	6.6E-02	O60673	SWISSPROT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
8852	21391	34312	0.52	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
8852	21391	34313	0.52	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
8882	22359	35339	0.58	6.6E-02	A1458752.1	EST_HUMAN	197g05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2149498 3'
9699	22494	35483	1.54	6.6E-02	Y07848.1	NT	Homo sapiens EWS, gap22, rrp22 and bam22 genes
10029	22524	36379	0.53	6.6E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA
10842	23363	36379	7.09	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0064-010600-006-a12 SN0064 Homo sapiens cDNA
12251	24462		2.87	6.6E-02	9837991	NT	Mus musculus D1PB gene (D1pb), mRNA
12585	24678		1.36	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
608	13236	25710	1.65	6.5E-02	BF027639.1	EST_HUMAN	601671048F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
1024	13635	26151	2.61	6.5E-02	7706068	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1435	14028	26556	3.4	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1770	14360	26905	1.42	6.5E-02	AE000764.1	NT	Aquifex aeolicus section 96 of 109 of the complete genome
5349	17809	30324	0.88	6.5E-02	D45899.1	NT	Caenorhabditis elegans DNA for ryanodine receptor, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5747	18373	31081	1.79	8.5E-02	AA443991.1	EST_HUMAN	z46h12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038
6664	19260	32094	0.89	6.5E-02	BF665340.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
7051	18070	30481	0.96	6.5E-02	U22681.1	NT	602118837F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276029 5'
6854	22352	35332	0.65	6.5E-02	BE963200.2	EST_HUMAN	Azotobacter vinelandii ATCC 9046 negative regulator MucB (mucB) gene, partial cds
6854	22352	35333	0.65	6.5E-02	BE963200.2	EST_HUMAN	601656817R1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3865637 3'
10363	22857	35849	0.59	6.5E-02	BF106300.1	EST_HUMAN	601656817R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3865637 3'
10518	23056	36067	5.86	6.5E-02	AA195648.1	EST_HUMAN	601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
11689	24091		5.28	6.5E-02	M21486.1	NT	z32g05.s1 Soares_NhMMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3'
12040	24327		3.84	6.5E-02	AF102993.1	NT	Rabbit microsomal epoxide hydrolase
601	13230	25703	1.74	6.4E-02	X94549.1	NT	Nectria haematococca kinesis related protein 2 (KRP2) gene, complete cds
5841	18270	30743	1.21	6.4E-02	AI191856.1	EST_HUMAN	A. carterae precursor of peritrich-chlorophylla-protein (PCP) gene
6261	18869	31639	5.4	6.4E-02	AF052733.1	NT	q607b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3
6261	18869	31640	5.4	6.4E-02	AF052733.1	NT	LTR8 repetitive element;
6534	19134	31927	0.68	6.4E-02	AI672896.1	EST_HUMAN	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6907	19841	32477	4.7	6.4E-02	BE974448.1	EST_HUMAN	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
8278	20819		2.66	6.4E-02	6753323	NT	we73g12.x1 Soares_Dieckgraebe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2346790 3'
8599	21138	34052	3.59	6.4E-02	AA093305.1	EST_HUMAN	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3'
9055	21592	34522	0.85	6.4E-02	AF150195.1	EST_HUMAN	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA
9506	22006		0.61	6.4E-02	BE834083.1	EST_HUMAN	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9833	22133	35098	1.79	6.4E-02	AB011128.1	NT	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
10162	22657	35652	0.68	6.4E-02	AF087150.1	NT	RC1-OT0083-150800-014-g06 OT0083 Homo sapiens cDNA
10162	22657	35653	0.68	6.4E-02	AF087150.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
							Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
							Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
11554	24002	37074	2.05	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
11554	24002	37075	2.05	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
11831	24971		4.86	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
11896	24296	30883	2.86	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1791	14381	26926	3.03	6.3E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; smRNP, G7A, NG23, MufS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3664	16286		2.41	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6285	18853	31662	1.1	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
7291	19819		1.05	6.3E-02	X97869.1	NT	H. sapiens gene encoding La autoantigen
9215	21732	34675	0.96	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Domina gene, exons 1-3
9827	22423	35397	2.86	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
10172	22697		0.87	6.3E-02	AV698070.1	EST_HUMAN	AV698070 GKc Homo sapiens cDNA clone GKCAHE01 5'
10594	18883	31662	3.6	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
4337	16924	29365	3.3	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
4431	17017		1.04	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNP1) mRNA, complete cds
4682	17284		6.75	6.2E-02	Q82191	SWISSPROT	52 KD RO PROTEIN (SIOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
6889	19624	32459	0.75	6.2E-02	D49530.1	NT	Spurlina platensis DNA for adenylate cyclase, complete cds
7623	20136	33014	0.78	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8877	25123		0.61	6.2E-02	M81101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9267	21793	34742	0.5	6.2E-02	AA778450.1	EST_HUMAN	ef20a06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032178 3'
9401	21910	34859	1.05	6.2E-02	6677898	NT	Mus musculus stromal cell derived factor receptor 2 (Sdfr2), mRNA
11027	23541	36576	1.74	6.2E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
11226	23757	36814	1.89	6.2E-02	AJ242735.1	NT	Metarhizium anisopliae mRNA for Chymotrypsin (chy1 gene)
11770	25097		8.34	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12200	24426	30951	3.56	6.2E-02	BF112039.1	EST_HUMAN	7137h08.x1 Soares_NSF_F8_9w_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to TR:Q9Y4S6 Q9Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1];
277	12834	25420	4.8	6.1E-02	D18471.1	NT	Human mRNA, Xq terminal portion
4063	16660		2.78	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKC1) gene, complete cds
4759	17340	29786	1.09	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
4759	17340	29787	1.09	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
6262	18870		1.42	6.1E-02	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 3 (SMARCA3) mRNA
8207	20748	33661	3.31	6.1E-02	X99268.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8595	21134	34048	0.95	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
8595	21134	34049	0.95	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
10608	23142	36153	6.34	6.1E-02	BE179543.1	EST_HUMAN	IL3-HT0818-110500-136-C06 HT0818 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11726	25009		23.38	6.1E-02	X70969.1	NT	S japonicum mRNA for serine-enzyme
12317	24880		1.39	6.1E-02	A186681.1	EST_HUMAN	b59f07.x1 NCL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2282801 3'
12484	24592		7.98	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1305	13899	26419	1.01	6.0E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
2700	15257	27825	1.15	6.0E-02	AW668948.1	EST_HUMAN	EST380924 IMAGE resequences, MAGJ Homo sapiens cDNA
2801	15353		1.58	6.0E-02	AB031289.1	NT	Mesocricetus cordi mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2863	12777	25259	1.09	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
2963	12777	25280	1.09	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3266	15878	28360	1.24	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3266	15878	28361	1.24	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3697	16298		1.01	6.0E-02	BE864443.2	EST_HUMAN	601858150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
5104	17676	30116	0.95	6.0E-02	Z87739.2	NT	Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA
5595	18225		1.69	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-011199-013-b04 BT0253 Homo sapiens cDNA
6364	18988	31746	1.43	6.0E-02	AI807537.1	EST_HUMAN	wf48h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.11 L1 repetitive element;
7063	18082	30438	2.73	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7063	18082	30439	2.73	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7239	19788	32624	2.17	6.0E-02	BF382349.1	EST_HUMAN	601816274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049228 5'
7872	20184	33072	1.94	6.0E-02	AI204275.1	EST_HUMAN	qf58p08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754199 3'
8361	20901		0.57	6.0E-02	11466495	NT	Recitomonas americana mitochondrion, complete genome
9196	21713	34656	1.12	6.0E-02	AI823167.1	EST_HUMAN	ts78a06.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2237362 3'
9196	21713	34657	1.12	6.0E-02	AI823167.1	EST_HUMAN	ts78a06.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2237362 3'
9327	21841	34792	2	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9327	21841	34793	2	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9819	22317	35289	0.51	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like
9819	22317	35300	0.51	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like
11214	23717		2.13	6.0E-02	AA128386.1	EST_HUMAN	zn87c08.r1 Stragene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565166 5' similar to gb:X69181.60S RIBOSOMAL PROTEIN L31 (HUMAN);
11985	24295	30982	1.43	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
12394	24554		6.04	6.0E-02	AI809273.1	EST_HUMAN	wf69h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60288 O60288 KIAA0551 PROTEIN;

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
250	12810	25393	4.76	5.8E-02	AW934719.1	EST_HUMAN	RC1-DT0001-290100-012-e10 DT0001 Homo sapiens cDNA
3012	15628	28107	2.75	5.8E-02	AF190289.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4768	17349	28799	0.97	5.8E-02	AL181535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
4768	17349	28800	0.97	5.8E-02	AL181535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
4852	17430		0.6	5.8E-02	AF168111.1	NT	Duck parvovirus strain 90-2193 capsid protein (VP3) gene, partial cds
4998	17570	30014	0.96	5.8E-02	AF066304.1	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
6873	24774	32374	0.87	5.8E-02	AF145680.1	NT	Drosophila melanogaster LD23107 sting (sting) mRNA, complete cds
8552	21091	34011	1.99	5.8E-02	9055249	NT	Mus musculus Itroquils related homeobox 5 (Drosophila) (Irx5), mRNA
9372	20311		0.82	5.8E-02	BF242748.1	EST_HUMAN	601877609F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105994 5'
10864	23196		3.41	5.8E-02	6679870	NT	Mus musculus follistatin-like (Fst), mRNA
10999	23419	36436	2.35	5.8E-02	11433356	NT	Homo sapiens nirein (LOC51199), mRNA
11429	23880		1.83	5.8E-02	AJ240733.1	NT	Gallus gallus HKC9 telomere junction
968	13578		5.2	5.8E-02	D90110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
1700	14293	26828	1	5.8E-02	Q61768	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
2886	15504		0.98	5.8E-02	AJ223621.1	NT	Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5
3725	16326	28793	1.35	5.8E-02	AE001775.1	NT	Thermotoga maritima section 87 of 136 of the complete genome
4448	17032	29473	5.29	5.8E-02	AW051927.1	EST_HUMAN	w024c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4448	17032	29474	5.29	5.8E-02	AW051927.1	EST_HUMAN	w024c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4845	17227	29882	5.04	5.8E-02	AJ247505.1	EST_HUMAN	q156701.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4845	17227	29893	5.04	5.8E-02	AJ247505.1	EST_HUMAN	q156701.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4674	17256		1.98	5.8E-02	AF08264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
5294	17856	30282	0.57	5.8E-02	AF275368.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5294	17856	30283	0.57	5.8E-02	AF275368.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
6088	18895	31428	1.52	5.8E-02	AA190994.1	EST_HUMAN	zp86a11.s1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627088 3'
7670	20182	33069	2.73	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
7670	20182	33070	2.73	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
8601	21140	34054	0.76	5.8E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
11871	24223		2.86	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12177	25085		6.45	5.8E-02	AA604289.1	EST_HUMAN	no75e11.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3093	15708	28179	1.13	5.7E-02	A081644.1	EST_HUMAN	063b05.s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
3107	15722	28193	1.6	5.7E-02	AF119117.1	NT	CE08611 ; Homo sapiens dopamine transporter (SLC8A3) gene, complete cds
3769	16370		0.96	5.7E-02	AF001292.1	NT	Chironomus thummi thummi globin VIIA.1 (ctt-7A.1), globin 9.1 (ctt-9.1), globin II-beta (ctt-2beta), non-functional globin XIII (ctt-13RT), globin XII (ctt-12) and globin XI (ctt-11) genes, complete cds
3871	16469	28932	2.44	5.7E-02	AW969791.1	EST_HUMAN	EST378885 IMAGE resequences, MAGI Homo sapiens cDNA
4795	17373		1.06	5.7E-02	M95099.1	NT	Bos taurus lysozyme gene (cow 3), complete cds
5334	17895	30310	0.89	5.7E-02	AJ251873.1	NT	Homo sapiens partial steerin-1 gene
6039	18658		0.8	5.7E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8088	20637	33548	1.46	5.7E-02	AJ296090.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (kv9.2 gene)
8764	22262	35245	0.65	5.7E-02	6681260	NT	Mus musculus ec2 oncogene (Ec2), mRNA
11087	23579	36617	4.17	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11087	23579	36618	4.17	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11227	23758		1.56	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12085	24891		12.96	5.7E-02	D50320.1	NT	Pig DNA for SPAL-2, complete cds
12257	24467		1.71	5.7E-02	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12334	24965		3.31	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12483	25074		8.94	5.7E-02	AF261280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
12622	24700	30863	1.58	5.7E-02	R48513.1	EST_HUMAN	Y64410.s1 Scores breast 2NBHst Homo sapiens cDNA clone IMAGE:153523 3' similar to contains L1 repetitive element ;
1574	14167	26698	1.2	5.6E-02	AF094455.1	NT	Hydrocotyle reticulifolia ribosomal protein L16 (rp16) gene, intron; chloroplast gene for chloroplast product
4746	17327	29769	1.21	5.6E-02	AB013100.1	NT	Lycopodium esculentum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4806	17384	29834	1.2	5.6E-02	AA290599.1	EST_HUMAN	zs45c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
6766	19359	32168	5.98	5.6E-02	AW172708.1	EST_HUMAN	x02c10.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2858050 3' similar to TR:O94979 O94979 KIAA0905 PROTEIN ;
6971	19548	32372	0.9	5.6E-02	AA866182.1	EST_HUMAN	cd47f12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
7205	19736	32589	3.1	5.6E-02	BE008001.1	EST_HUMAN	QV0-BN0147-290400-214-q07 BN0147 Homo sapiens cDNA
8737	21276	34198	2.2	5.6E-02	BE542663.1	EST_HUMAN	601087159F1 NIH_MGC 10 Homo sapiens cDNA clone IMAGE:3453279 5'
8737	21276	34199	2.2	5.6E-02	BE542663.1	EST_HUMAN	601087159F1 NIH_MGC 10 Homo sapiens cDNA clone IMAGE:3453279 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9726	22224	35201	1.07	5.6E-02	AA482864.1	EST_HUMAN	n149d07.s1 NCL CGAP_A11 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859
11439	23989		2.33	5.6E-02	AF260225.1	NT	LAMINA ASSOCIATED POLYPEPTIDE 1C.
2679	15237	27804	6.14	5.5E-02	X97869.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
3251	15963	28345	3.83	5.5E-02		NT	H. sapiens gene encoding La autoantigen
4266	16862	28328	1.12	5.5E-02	L41561.1	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
5840	18464	31188	3.19	5.5E-02	Q01174	SWISSPROT	Gallid herpesvirus mRNA fragment
6176	18464	31188	3.86	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7412	19937	32802	1.77	5.5E-02	8755902	NT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
8063	20605	33516	0.77	5.5E-02	AF170911.1	NT	Mus musculus tuftelin 1 (Tuft1), mRNA
8063	20605	33517	0.77	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
9573	22073	35034	0.61	5.5E-02	10947034	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
9573	22073	35035	0.61	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9664	22163	35136	1.28	5.5E-02	U69492.1	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
10988	23418	36435	11.52	5.5E-02	U09771.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
3054	15670		0.85	5.4E-02	AJ277468.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), gene for putative Bowman Birk trypsin inhibitor
3469	18013		6.27	5.4E-02	BE073468.1	EST_HUMAN	Oryza sativa rbb13-1 gene for putative Bowman Birk trypsin inhibitor
3982	16580	29051	0.58	5.4E-02	U85808.1	NT	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
5119	17691	30129	2.48	5.4E-02	U53528.1	NT	Hirudo medicinalis SNAP-25 homodog mRNA, complete cds
8067	20609		1.11	5.4E-02	Z99116.1	NT	Xenopus laevis homeobox protein (Vox-1) mRNA, complete cds
9001	21538	34487	0.61	5.4E-02	AF260225.1	NT	Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2613730
10578	23113	36126	1.88	5.4E-02	U20790.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
11056	23570	36606	1.56	5.4E-02	BF371289.1	EST_HUMAN	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (OCR8) mRNA, complete cds
11056	23570	36607	1.56	5.4E-02	BF371289.1	EST_HUMAN	RC6-FN0112-190700-021-D06 FN0112 Homo sapiens cDNA
11968	24882	26205	2.9	5.4E-02	U44694.1	NT	RC6-FN0112-190700-021-D06 FN0112 Homo sapiens cDNA
1091	13696	26205	1.58	5.3E-02	AW391248.1	EST_HUMAN	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1091	13696	26206	1.58	5.3E-02	AW391248.1	EST_HUMAN	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1553	14145	26679	21.63	6.3E-02	T84759.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
2541	15105	27877	2.71	5.3E-02	AJ276408.1	NT	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
2869	15585	28066	0.88	5.3E-02	M58417.1	NT	ye37112.1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01508
						EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
						NT	Pseudomonas putida tfgS gene
						NT	Drosophila melanogaster laminin B2 gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2969	15585	28067	0.88	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3187	15789	28271	4.52	5.3E-02	AJ276408.1	NT	Pseudomonas putida tpgS gene
5248	17811	30234	0.75	5.3E-02	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
5250	17813	30236	8.25	5.3E-02	M80463.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5522	18154	30568	1.97	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
5522	18154	30569	1.97	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6251	18860	31832	0.71	5.3E-02	M85289.1	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
6964	19541	32363	4.23	5.3E-02	9695413	NT	Lymphocystis disease virus 1, complete genome
7149	19682	32523	1.55	5.3E-02	U32832.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7396	19921		2.05	5.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
7818	20290	33189	0.52	5.3E-02	P38742	SWISSPROT	HYPOTHETICAL 130.9 KD PROTEIN IN SNF6-SPO11 INTERGENIC REGION
8344	20885		0.54	5.3E-02	U10098.1	NT	Mus musculus 129/Sv cystatin C (cst3) gene, complete cds
8953	21590	34521	1.83	5.3E-02	X03127.1	NT	Podospora anserina mitochondrial epsilon-sen DNA
10038	22633	35528	0.54	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds
10038	22633	35530	0.54	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds
10156	22651		0.62	5.3E-02	Y07907.1	NT	D. rerio mRNA for zp-23 POU gene, splice variant (neurula, 9-18 hpf and postsomitogenesis, 20-28 hpf)
10235	22730	35721	0.85	5.3E-02	X68432.1	NT	B. rerio pou3 mRNA for transcription factor
2324	14895		116.52	5.2E-02	5031908	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3148	15762	28228	2.4	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3148	15762	28229	2.4	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4013	16611	29084	0.7	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds
4365	16952	28392	3.61	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nsr-1 mRNA, complete cds
4846	17424	29877	1.29	5.2E-02	L33246.1	NT	Drosophila melanogaster filament protein homolog (sep1) gene, complete cds
6076	18853	31439	0.89	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6255	18864		1.42	5.2E-02	AJ830965.1	EST_HUMAN	wj80604.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 MER15 repetitive element
7318	19845	32706	1.19	5.2E-02	P36322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAF) (DNA-BINDING GENE 18 PROTEIN)
8136	20677		1.98	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9845	22145	35113	1.97	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for capsid protein, complete cds
9845	22145	35114	1.97	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for capsid protein, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12224	24445		1.84	5.2E-02	Q03030	SWISSPROT	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
12327	24513		1.27	5.2E-02	D63362.1	NT	Mouse DNA for regligamma protein, complete cds
2402	14970		1.14	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D073 5'
4282	16868	26315	0.73	5.1E-02	AF081301.1	NT	Chlamydia trachomatis section 28 of 87 of the complete genome
4908	17483	29941	8.03	5.1E-02	AF085167.1	NT	Hordeum vulgare receptor-like kinase ARK1AS gene, partial cds
5205	17770	30193	1.14	5.1E-02	BE957423.2	EST_HUMAN	601693558R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838361 3'
6777	18369	32182	0.76	5.1E-02	AF280369.1	NT	HIV-1 patient 98 from Italy protease (pol) gene, complete cds
6942	18050	30472	1.6	5.1E-02	BF378625.1	EST_HUMAN	QV0-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA
8195	20736	33648	0.82	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8195	20736	33647	0.82	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8288	20829	33750	1.48	5.1E-02	AJ131966.1	NT	Spodoptera littoralis mRNA for 3-dehydrodysone 3beta-reductase
8818	21357	34282	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
8818	21357	34283	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9723	22221	35198	8.16	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10084	22579	35572	1.83	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
10709	23237	36250	2.86	5.1E-02	AF083330.1	NT	Homo sapiens ES18 mRNA, partial cds
10709	23237	36251	2.86	5.1E-02	AF083330.1	NT	Homo sapiens ES18 mRNA, partial cds
12232	24448		1.51	5.1E-02	AF062467.1	NT	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds
508	13141	25626	1.76	5.0E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1246	13843	26360	6.63	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21); from 1 to 213080
2034	14616	27182	3.63	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-F/PIF-S) (PROTEIN APROTEIN C) [CONTAINS: PEPTIDE P-C]
2845	13634	28150	1.78	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3381	15990		1.42	5.0E-02	7305810	NT	Mus musculus Uhc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3655	16258		1.08	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3747	16348	28818	5.6	5.0E-02	U12769.2	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
5102	17674	30114	1.11	5.0E-02	AF188530.1	NT	Homo sapiens ubiquitous tetrahydrobiopterin containing protein RoXan mRNA, partial cds
6279	18887	31658	0.74	5.0E-02	AF096264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6450	19051		1.23	5.0E-02	AJ242825.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7544	20064	32938	10.74	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
10101	22596	35589	1.13	5.0E-02	AF305238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fist3) mRNA, complete cds
11364	23816	36877	2.87	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
11736	24924		7.22	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
242	12901		23.23	4.8E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
392	13038	25528	3.62	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
392	13038	25528	3.62	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3328	15938	28414	1.58	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDULYSIAN ATROPHY PROTEIN)
3628	16231		0.83	4.9E-02	AA188940.1	EST_HUMAN	z448a12.s1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632926 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ;
3651	16254	28726	0.91	4.9E-02	AA400914.1	EST_HUMAN	z78e03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3651	16254	28727	0.91	4.9E-02	AA400914.1	EST_HUMAN	z78e03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4966	17640	29982	1.59	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
4966	17640	29983	1.59	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
5372	17931	30345	0.81	4.9E-02	7662616	NT	Homo sapiens PRO1848 protein (PRO1848), mRNA
5408	17964		0.91	4.9E-02	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
5425	17982		0.98	4.9E-02	AE001774.1	NT	Thermotoga maritima section 86 of 136 of the complete genome
5437	17992	30396	1.03	4.9E-02	M94063.1	NT	Brucella ovis heat shock protein hsp70 (dnaK) gene, complete cds; heat shock protein hsp40 (dnaJ) gene, complete cds
5573	18204	30654	1.95	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5573	18204	30655	1.95	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7199	19727	32578	0.99	4.9E-02	AE00080.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8551	21090		0.88	4.9E-02	AE002309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8689	21228	34149	0.7	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10193	22688	35681	0.54	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
11280	23733	36788	3.67	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12148	24391		1.44	4.9E-02	8923880	NT	Homo sapiens CS box-containing WD protein (LOC555884), mRNA
12431	24573		2.92	4.9E-02	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
352	13002	25487	1.15	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
353	13002	25487	1.87	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
514	13147	25631	9.43	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2312	14884	27459	1.96	4.8E-02	W51983.1	EST_HUMAN	zc49b02.s1 Soares senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3244	15956	28339	2.34	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
4778	17359		1.32	4.8E-02	Z54280.1	NT	S. scrofa gene for skeletal muscle ryanodine receptor
5309	17871	30293	0.67	4.8E-02	U91814.1	NT	Streptococcus constellatus D-alanine D-alanine ligase gene, partial cds
5380	17839	30352	4.1	4.8E-02	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
5380	17939	30353	4.1	4.8E-02	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8080	20622	33535	1.42	4.8E-02	AW388497.1	EST_HUMAN	MR2-ST0129-221098-012-002 ST0129 Homo sapiens cDNA
9057	21594	34524	1.3	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
9057	21594	34525	1.3	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
12018	24315		1.93	4.8E-02	9632893	NT	Streptococcus thermophilus bacteriophage Sf19, complete genome
6918	19577	32406	2.98	4.7E-02	W01153.1	EST_HUMAN	Y287F09.1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:281017 5' similar to contains Alu repetitive element
6955	19542	32384	0.78	4.7E-02	BF686625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
6955	19542	32385	0.78	4.7E-02	BF686625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
6998	19496	32317	1.57	4.7E-02	M62752.1	NT	Rat statin-related protein (s1) gene, complete CDS
8193	20734	33644	8.55	4.7E-02	X15543.1	NT	B taurinus mRNA for RF-38-DNA-binding protein
8883	21421	34346	1.12	4.7E-02	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
8906	21444		2.29	4.7E-02	AB026678.1	NT	Callus gallus Wpck-8 gene, complete cds
9154	21689	34633	6.91	4.7E-02	X15543.1	NT	B. taurinus mRNA for RF-38-DNA-binding protein
9595	22065	35024	0.55	4.7E-02	BF305237.1	EST_HUMAN	601892692F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5'
9850	22149		0.55	4.7E-02	A1873042.1	EST_HUMAN	we78c10.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
10634	23166	36177	1.55	4.7E-02	6754565	NT	Mus musculus ligand of numb-protein X (Lnx), mRNA
11430	23881	36945	1.69	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11430	23881	36946	1.69	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11851	25087		6.94	4.7E-02	AV648521.1	EST_HUMAN	AV648521 GLC Homo sapiens cDNA clone GLCBKD02 3'
12322	25089		1.47	4.7E-02	P52951	SWISSPROT	HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2)
282	12948	25435	0.81	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
769	13388	25887	2.44	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1335	13929		1.37	4.6E-02	AJ014255.1	EST_HUMAN	am50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P90533
1403	13996	26525	9	4.6E-02	AV727059.1	EST_HUMAN	Pe0533 LIMA ; contains element L TR1 repetitive element ;
2530	15094	27666	2.77	4.6E-02	AW236023.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTCBWC01 5'
2834	12948	25435	1.83	4.6E-02	BE153583.1	EST_HUMAN	xn24f03.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694853 3' similar to SW:GRF1_HUMAN
3042	15658	28138	0.7	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1 ;
3543	15658	28138	0.95	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4201	16780		0.97	4.6E-02	AF220365.1	NT	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
							Mus musculus nuclear RNA helixase II/Gu (ddx21) gene, complete cds
							Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (GnRH2) gene, complete cds
5909	18531	31256	1.44	4.6E-02	AF076962.1	NT	
6377	18981	31760	3.77	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atp8) mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6377	18981	31761	3.77	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
6891	18625	32481	1.39	4.6E-02	A1149574.1	EST_HUMAN	qc60b06.x1 Soares_placenta_8to9weeks_2NbHP8t08W Homo sapiens cDNA clone IMAGE:1713971 3'
8560	21129	34046	2.82	4.6E-02	BE154006.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element ;
11281	23734	36789	4.26	4.6E-02	AA913328.1	EST_HUMAN	PMO-HT0339-Q60400-009-G12 HT0339 Homo sapiens cDNA
12541	24651		2.54	4.6E-02	X37808.1	NT	oi27h09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
472	13105	25588	2.71	4.5E-02	P22448	SWISSPROT	Human germ-line immunoglobulin lambda light chain gene
1260	13857	26373	0.78	4.5E-02	AF005730.1	NT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1260	13857	26374	0.78	4.5E-02	AF005730.1	NT	Marburg virus strain WIS.Africa/Johannesburg/1975/Ozlin VP35 gene, complete cds
1840	14428	26880	3.54	4.5E-02	P32182	SWISSPROT	Marburg virus strain WIS.Africa/Johannesburg/1975/Ozlin VP35 gene, complete cds
2156	14733	27308	3.65	4.5E-02	AE003984.1	NT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
3786	16386	28852	3.84	4.5E-02	AL163276.2	NT	Xylella fastidiosa, section 110 of 229 of the complete genome
6378	18982	31762	1.88	4.5E-02	AJ400877.1	NT	Homo sapiens chromosome 21 segment HS21C078
6831	19227	32032	0.89	4.5E-02	AL163280.2	NT	Homo sapiens ASCL3 gene, CEGP 1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8332	20873	33795	1.8	4.5E-02	AF036684.1	NT	Homo sapiens chromosome 21 segment HS21C080
9860	22357	35337	5.91	4.5E-02	AA325216.1	EST_HUMAN	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
10117	22612	35602	0.77	4.5E-02	AB000470.1	NT	EST28167 Cerebellum II Homo sapiens cDNA 5' end similar to neuro-D4 protein
11947	24276	31018	2.92	4.5E-02	11418013	NT	Gallus gallus mRNA for alpha1 Integrin, complete cds
12387	24973	30636	6.27	4.5E-02	AA191087.1	EST_HUMAN	Homo sapiens ret finger protein-like 3 (RPL3), mRNA
237	12897		3.08	4.4E-02	BE972733.1	EST_HUMAN	zq43f1.1 r1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5'
2144	14722		6.8	4.4E-02	P31588	SWISSPROT	607652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
2532	15098	27688	2.62	4.4E-02	AW875475.1	EST_HUMAN	HYPOTHELICAL PROTEIN (ORF 2280)
3702	16303	28771	1.5	4.4E-02	AF159160.1	NT	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
4733	17314	29756	1.23	4.4E-02	AF109907.1	NT	Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4733	17314	29757	1.23	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7172	19704	32551	1.56	4.4E-02	AF095824.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7172	19704	32552	1.56	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8687	21226	34148	2.04	4.4E-02	AA736989.1	EST_HUMAN	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
10951	23486	36489	4.58	4.4E-02	AF060689.1	NT	nm13h03.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
11080	23592	36629	2.63	4.4E-02	AA496739.1	EST_HUMAN	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
							ae33104.r1 Gessler Wllms tumor Homo sapiens cDNA clone IMAGE:897631 5'

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11864	24088		3.26	4.4E-02	AB040928.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
813	13431	25936	8.91	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2603	15165	27732	1.16	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBA0H08 5'
3477	16083	28557	8.12	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3720	16321		1.12	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6822	18219	32023	5.71	4.3E-02	P30427	SWISSPROT	PLECTIN
6822	18219	32024	5.71	4.3E-02	P30427	SWISSPROT	PLECTIN
6830	19420	32236	0.68	4.3E-02	AA652266.1	EST_HUMAN	ns68c12.s1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188986
8450	20950	33908	0.74	4.3E-02	AF293359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
8736	21276	34196	0.98	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
8736	21275	34197	0.98	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
855	13471	25982	1.57	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
889	13513		2.24	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
929	13542	28060	0.69	4.2E-02	AW003645.1	EST_HUMAN	wx34g01.x1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291
1758	14348		1.32	4.2E-02	AL445066.1	NT	L1 RETROPOSON, ORF2 mRNA; contains L1 L3 L1 L1 repetitive element;
							Thermoplasma acidophilum complete genome; segment 4/5
3180	15802	28274	0.88	4.2E-02	A1493472.1	EST_HUMAN	q95f10.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2019787 3' similar to gb:M35718
3726	16327	28794	1.36	4.2E-02	P23091	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR BFR-2 PRECURSOR (HUMAN);
4410	16995	29437	1.03	4.2E-02	U26674.1	NT	TRANSFORMING PROTEIN MAF
4410	16995	29438	1.03	4.2E-02	U26674.1	NT	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
4854	17432	29863	0.69	4.2E-02	BF342895.1	EST_HUMAN	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
							602017105F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4152672 5'
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450
5802	18427	31145	1.49	4.2E-02	AF280107.1	NT	polypeptide 5 (CYP3A5) gene, partial cds
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450
5802	18427	31148	1.49	4.2E-02	AF280107.1	NT	polypeptide 5 (CYP3A5) gene, partial cds
7534	20054	32927	5.29	4.2E-02	AF276752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
8745	21284	34206	3.5	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10069	22584	35558	1.17	4.2E-02	Q16650	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56)
10919	23438	36459	3.12	4.2E-02	AA976118.1	EST_HUMAN	on33b11.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558461 3' similar to gb:M65280
11167	23692	36739	2.3	4.2E-02	BE815822.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
							PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11187	23692	36740	2.3	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11379	23831	36894	2.06	4.2E-02	AF176458.1	NT	PRRS isolate PRRSV38 envelope glycoprotein gene, complete cds
12226	25023		3.4	4.2E-02	A1983494.1	EST_HUMAN	w49g10.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
536	13167	25648	0.7	4.1E-02	AF200629.1	NT	Homo sapiens HPS1 gene, intron 5
2701	15258	27826	2.87	4.1E-02	AE002330.2	NT	Chlamydia muridarum, section 60 of 85 of the complete genome
4571	17154		8.95	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-180-400-164-f06 NN0012 Homo sapiens cDNA
5295	17857		0.69	4.1E-02	X65880.1	NT	L monocytogenes type 3 partial lap gene (strain 443)
5824	18448	31170	0.98	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
5924	18448	31171	0.98	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
6982	19539		0.97	4.1E-02	X75881.1	NT	A. thaliana mRNA for plasma membrane intrinsic protein 1a
7158	19698	32632	1.92	4.1E-02	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
7522	20042	32911	1.76	4.1E-02	7682347	NT	Homo sapiens KIAA0867 protein (KIAA0867), mRNA
							Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit?
7742	20260	33143	3.14	4.1E-02	AF026198.1	NT	CUTICLE COLLAGEN 34
8577	21116	34036	0.56	4.1E-02	P34687	SWISSPROT	EST04291 Cclon adenocarcinoma IV Homo sapiens cDNA 5' end
9081	21617	34552	0.85	4.1E-02	AA372398.1	EST_HUMAN	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
12572	25024	30618	24.9	4.1E-02	AJ271909.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3281	15892	28371	3.71	4.0E-02	AB040904.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
3868	16466	28929	0.98	4.0E-02	L11910.1	NT	Homo sapiens PTS gene for 8-pyruvyltetrahydropterin synthase, complete cds
5296	17859	30284	0.58	4.0E-02	AB042287.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5581	18212	30661	5.51	4.0E-02	AF280107.1	NT	7a52h07.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:O75296 O75296
6362	18966	31744	1.66	4.0E-02	BF110434.1	EST_HUMAN	R29124.1
							Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7678	20188	33078	5.8	4.0E-02	L29838.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7743	20251	33144	0.87	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7743	20251	33145	0.87	4.0E-02	AB000381.1	NT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8651	21190	34108	2.64	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9562	22062		0.84	4.0E-02	BF079376.1	EST_HUMAN	602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
9586	22086	35051	3.35	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thioi fumarate reductase subunit A

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9855	22392		1.28	4.0E-02	D43949.1	NT	Human mRNA for KIAA0082 gene, partial cds
11608	24051		1.62	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Ca++ ATPase
11841	24834	30798	18.69	4.0E-02	AJ001036.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1159	13762	26273	3.8	3.9E-02	BF516149.1	EST_HUMAN	UI-H-BW.1-anx-h-08-Q.U.1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1390	13984	26510	1.88	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
2004	14585	27145	2.67	3.9E-02	AJ403386.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2728	15283		1.85	3.9E-02	4508862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5325	17887	30303	0.6	3.9E-02	AW392417.1	EST_HUMAN	RC6-ST02358-171199-021-C09 ST0258 Homo sapiens cDNA
5344	17905	30320	1.14	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO11163 (PRO11163), mRNA
5344	17905	30321	1.14	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO11163 (PRO11163), mRNA
5687	18313	30810	0.73	3.9E-02	D50608.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5687	18313	30811	0.73	3.9E-02	D50608.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5905	18528	31254	1.24	3.9E-02	BE668841.1	EST_HUMAN	601649874F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3933642 5'
6018	18637	31377	0.68	3.9E-02	BF675203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
7118	19458	32273	1.01	3.9E-02	BE271437.1	EST_HUMAN	601140728F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7781	20324	33229	0.93	3.9E-02	BF239613.1	EST_HUMAN	601906848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
8004	20546	33449	0.56	3.9E-02	AJ228041.1	NT	Homo sapiens 959 kb contig between AML 1 and CBR1 on chromosome 21q22, segment 1/3
8004	20546	33450	0.56	3.9E-02	AJ228041.1	NT	Homo sapiens 959 kb contig between AML 1 and CBR1 on chromosome 21q22, segment 1/3
11287	20289	33186	1.6	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
11691	24981		7.19	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12373	24543		1.73	3.9E-02	U68081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV18S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TORBD1, TORBD1, TCRBJ1S1, TCRBJ1S2.>
12503	24902		64.84	3.9E-02	AL049866.2	NT	Mus musculus chromosome X contigB: X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnx28orf
1895	14577	27137	1.24	3.9E-02	BE985137.1	EST_HUMAN	601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5'
4997	17571	30015	0.99	3.9E-02	BE93275.1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3826757 5'
4997	17571	30016	0.99	3.9E-02	BE93275.1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3826757 5'
5062	17635	30078	0.93	3.9E-02	AU124122.1	EST_HUMAN	AU124122 NT2RM2 Homo sapiens cDNA clone NT2RM2001698 5'
5632	18261	30733	1.19	3.9E-02	M11228.1	NT	Human protein C gene, complete cds
6237	18846	31617	1.07	3.9E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOX-B4 (HOX-2.6)
7359	19895	32748	1.43	3.9E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8598	21137		1.3	3.8E-02	M80875.1	NT	Human von Willebrand factor gene, exons 23 through 34
10508	23000		0.47	3.8E-02	AE001329.1	NT	Chlamydia trachomatis section 56 of 87 of the complete genome
10532	23069	36082	2.17	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
1029	13639	26154	3.69	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1432	14025	26553	1.15	3.7E-02	L14501.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2278	14852	27430	4.49	3.7E-02	A1984806.1	EST_HUMAN	wr65e08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2613	15175	27743	0.93	3.7E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3085	15701	28174	0.97	3.7E-02	P79944	SWISSPROT	EOMESODERMIN
3088	15703	28175	4.74	3.7E-02	BF312963.1	EST_HUMAN	601896233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
7138	25118		0.73	3.7E-02	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 8/7
9828	22424		0.89	3.7E-02	AA782516.1	EST_HUMAN	ai55c09.s1 Scores_parathyroid_tumor_NbHPA Homo sapiens cDNA clone 1360912 3'
11735	24139	37156	7.89	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12435	24866	30707	3.02	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3715	16316	28784	0.82	3.6E-02	X73221.1	NT	H. vulgare Ss1 gene for sucrose synthase
3723	16324	28791	0.87	3.6E-02	AL098806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10(10q26.3) cl Homo sapiens
5620	18248	30701	0.77	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5620	18249	30717	0.77	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
6808	19399	32213	5.32	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6808	19399	32214	5.32	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
7143	19676	32516	1.68	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Cyt2 precursor (sgp2) gene, complete cds
7347	19873	32739	3.52	3.6E-02	AA714521.1	EST_HUMAN	hw20e05.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_rna2
7629	20141	33020	0.88	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
9313	21827	34776	1.87	3.6E-02	U20508.1	NT	Dictyostellium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9313	21827	34777	1.87	3.6E-02	U20508.1	NT	Dictyostellium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9530	22030	34989	0.72	3.6E-02	BF347586.1	EST_HUMAN	602020453F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156116 5'
928	13541	26059	1.57	3.5E-02	U09508.1	NT	Drosophila melanogaster tiggerin mRNA, complete cds
1046	13654	26166	2.29	3.5E-02	AF263417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds

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1610	14203	28736	1.49	3.5E-02	BF676085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1610	14203	28737	1.49	3.5E-02	BF676085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4293	16879	29326	1.91	3.5E-02	AE001773.1	NT	Thermotoga maritima section 85 of 136 of the complete genome
4406	16991	29435	1.16	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6370	18974	31752	2.11	3.5E-02	J01238.1	NT	Maize actin 1 gene (Mact), complete cds
7918	20460		0.82	3.5E-02	H28951.1	EST_HUMAN	yp44a05.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190256 5' similar to contains Alu repetitive element;
8558	21097	34018	3.5	3.5E-02	BE958970.1	EST_HUMAN	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928737 3'
9931	22427	35401	2.44	3.5E-02	X76842.1	NT	L lactis MG1363 grpE and dnaK genes
9977	22472	35455	0.49	3.5E-02	BE661042.1	EST_HUMAN	601344681F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11367	23819	36880	1.82	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-H03 CT0326 Homo sapiens cDNA
11367	23819	36881	1.92	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-H03 CT0326 Homo sapiens cDNA
12357	24534		1.39	3.5E-02	AF009663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV85SP to TCRBV21S2A2 region
12429	24913		4.38	3.5E-02	BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
604	13233	25706	1.18	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
604	13233	25707	1.18	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
605	13233	25706	3.27	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
605	13233	25707	3.27	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1089	13694	26203	3.22	3.4E-02	AW274020.1	EST_HUMAN	x26d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW: C211 HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR :
1248	13845		6.54	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2435	15002	27574	1.82	3.4E-02	T57160.1	EST_HUMAN	yc20e06.r1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3478	16084	28558	1.11	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3843	16442	28803	0.68	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-050700-011-d10 FN0155 Homo sapiens cDNA
3983	16591	29063	4.28	3.4E-02	AW794652.1	EST_HUMAN	RC8-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4703	17285	29730	3.17	3.4E-02	X59799.1	NT	M.musculus S-anigen gene promoter region
5217	17782		2.61	3.4E-02	Q26457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5237	17801	30220	1.47	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6353	18958		0.68	3.4E-02	BF131628.1	EST_HUMAN	601820445F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052434 5'
6938	18046	30468	4.63	3.4E-02	U24383.1	NT	Human lysyl oxidase-like protein gene, exon 3
8204	20745		3.76	3.4E-02	AI868629.1	EST_HUMAN	wf99d04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2433031 3'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8882	21221	34141	1.64	3.4E-02	AA684888.1	EST_HUMAN	nu70708.s1 NCL_CGAP_A1v1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element; contains element MER25 MER25 repetitive element;
							zq04f11.s1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:628749 3' similar to
8848	21387		5.71	3.4E-02	AA194306.1	EST_HUMAN	TR:G1017425 G1017425
9693	22192		0.53	3.4E-02	A1092719.1	EST_HUMAN	IPISGKPLPKVTLSDRGVPLKATMRNFTEITAENLTINLKESVTADAGRYEITAANSSGTTKAFINIVLDRPG
395	13041		11.74	3.3E-02	AA398735.1	EST_HUMAN	PPT GPVVISDITEESVTLKWEPPKYDGGQVNTYLLKRETSVAVTEVSA TVARTNMKV/MKL ...;
1209	13809	26322	18.12	3.3E-02	AB035867.1	EST_HUMAN	oz98h08.x1 Soares_papillary_thyroid_tumor_NbHFA Homo sapiens cDNA clone IMAGE:1683519 3'
1681	14273	26806	1.29	3.3E-02	AF110763.1	NT	z175e08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1775	14365		1.28	3.3E-02	AF110763.1	NT	Orbicularis griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
2131	14709		2.05	3.3E-02	R09112.1	EST_HUMAN	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3408	16015	28494	0.85	3.3E-02	H02389.1	EST_HUMAN	Aquifex aerophilus section 32 of 109 of the complete genome
4256	14273	26806	2.91	3.3E-02	AF110763.1	NT	y25c09.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:127888 5'
4566	17149	29596	2.15	3.3E-02	6755862	NT	y35h02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150771 5'
6561	19159	31856	26.84	3.3E-02	BF245995.1	EST_HUMAN	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
6561	19159	31857	26.84	3.3E-02	BF245995.1	EST_HUMAN	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
9246	21772	34721	0.73	3.3E-02	BF115621.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
9246	21772	34722	0.73	3.3E-02	BF115621.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
9345	21859	34807	0.59	3.3E-02	AA488202.1	EST_HUMAN	7m92d04.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3'
9345	21859	34808	0.59	3.3E-02	AA488202.1	EST_HUMAN	7m92d04.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3'
10491	22985		0.5	3.3E-02	H38109.1	EST_HUMAN	ad08f09.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
11000	23514	36548	3.5	3.3E-02	BF091107.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
11932	24268		2.14	3.3E-02	T96543.1	EST_HUMAN	ad08f09.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
12089	24358		2.06	3.3E-02	M81890.1	NT	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
137	12802	25281	1.87	3.2E-02	AJ002005.1	NT	ad08f09.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
1165	13767	26277	19.04	3.2E-02	AF098275.1	NT	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
1165	13767	26278	19.04	3.2E-02	AF098275.1	NT	yp51f11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190989 3'
1808	14398	26843	1.36	3.2E-02	AF128894.1	NT	60224717F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4332497 5'
2865	12802	25281	0.59	3.2E-02	AJ002005.1	NT	ye48f11.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:121101 5'
3168	15782	28253	12.01	3.2E-02	BE867363.1	EST_HUMAN	Human Interleukin 11 (IL11) gene, complete mRNA
							Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
							Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
							Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
							Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
							LARGE TEGUMENT PROTEIN
							Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
							601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3776	16376	28842	1.3	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4289	16885		20.05	3.2E-02	X94768.1	NT	H. sapiens RP3 gene (XLRP gene 3)
4882	17457	28909	3.35	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5728	18352	31055	1.45	3.2E-02	X68709.1	NT	S. griseocaneum whiG-Stv gene
5728	18352	31056	1.45	3.2E-02	X68709.1	NT	S. griseocaneum whiG-Stv gene
6646	19242	32045	2.59	3.2E-02	M32437.1	NT	Rat/polymavirus left junction in cell line W98.14
6847	19243		27.51	3.2E-02	T89367.1	EST_HUMAN	y433h12.s1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
6722	19316	32119	3.78	3.2E-02	AF173845.1	NT	Alu repetitive element contains LTR1 repetitive element ;
7739	20247	33140	0.85	3.2E-02	11424049	NT	Sagunius oedipus tissue kallikrein gene, complete cds
8242	20783	33702	13.06	3.2E-02	6680565	NT	Homo sapiens cytochrome P450, subfamily 1B (phenobarbital-inducible) (CYP2B), mRNA
8871	21410		0.69	3.2E-02	AF109718.1	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
9152	21687	34630	1.06	3.2E-02	A1278971.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
9152	21687	34631	1.08	3.2E-02	A1278971.1	EST_HUMAN	qm17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
9969	22484		4.05	3.2E-02	AA179795.1	EST_HUMAN	qm17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
10260	22755	35743	0.95	3.2E-02	U96762.1	NT	z954b12.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to
1303	13897		1.8	3.1E-02	4503416	NT	gbL08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
1348	13943	26466	1.28	3.1E-02	P18845	SWISSPROT	Macaca mulatta chemokine receptor CCR5 mRNA, complete cds
1836	14520	27076	1.52	3.1E-02	6671564	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
2017	14598		1.14	3.1E-02	Z50097.1	NT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
5207	17772		0.87	3.1E-02	BE091869.1	EST_HUMAN	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
5331	17892		3.09	3.1E-02	AL161550.2	NT	Drosophila melanogaster mRNA for headcase protein
5371	16916		0.98	3.1E-02	AU119008.1	EST_HUMAN	IL2-BT0733-130400-067-A06 BT0733 Homo sapiens cDNA
5468	18102	30421	1.13	3.1E-02	U78104.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5563	18184		2.32	3.1E-02	AA278478.1	EST_HUMAN	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5829	18453	31178	0.8	3.1E-02	BF887742.1	EST_HUMAN	zs81a06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
9944	22439	35417	3.63	3.1E-02	AF034779.1	NT	602068783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085789 5'
12667	24737		2.24	3.1E-02	AW468414.1	EST_HUMAN	Enterococcus faecalis surface protein precursor, gene, complete cds
1664	14257		2.3	3.0E-02	AF187125.1	NT	na37f07.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2921221 3'
2621	15183	27749	0.9	3.0E-02	AA402242.1	EST_HUMAN	Pityokines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
3623	18226	28704	1.24	3.0E-02	M94176.1	NT	z85h03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727253 5'
							Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3714	16315	28783	3.07	3.0E-02	AF247844.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3808	18407		0.79	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0296-150200-040-009 ST0296 Homo sapiens cDNA
4021	16619		0.74	3.0E-02	AA364003.1	EST_HUMAN	EST74530 Pineal gland II Homo sapiens cDNA 5' end
5000	17573	30017	1.04	3.0E-02	BE782850.1	EST_HUMAN	601472331F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3875503 5'
5208	17773	30185	7.49	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5208	17773	30186	7.49	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5303	17865	30289	1.1	3.0E-02	BE968917.1	EST_HUMAN	601849872R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933928 3'
5590	18221		3.82	3.0E-02	AB046793.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
6402	19005	31784	0.78	3.0E-02	N99815.1	EST_HUMAN	za39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element
6402	19005	31785	0.78	3.0E-02	N99815.1	EST_HUMAN	za39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element
6884	19619	32453	2.93	3.0E-02	AJ242906.1	NT	Cyprinus carpio mRNA for Inducible nitric oxide synthase (iNOS gene)
6987	19485	32306	3.15	3.0E-02	BE888948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6987	19485	32307	3.15	3.0E-02	BE888948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7131	19471	32290	1.93	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7131	19471	32291	1.93	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7282	19810	32656	1.32	3.0E-02	M86524.1	NT	Human dystrophin gene
7583	20098		0.76	3.0E-02	BF246361.1	EST_HUMAN	601854981F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074548 5'
8575	21114	34033	0.79	3.0E-02	BF553889.1	EST_HUMAN	IL5-HT0704-290600-108-c04 HT0704 Homo sapiens cDNA
8728	21267		1.77	3.0E-02	AF275654.1	NT	Ornithine decarboxylase X mRNA, complete cds
10357	22851	35845	1.46	3.0E-02	AE001787.1	NT	Thermotoga maritima section 109 of 138 of the complete genome
10441	22835	35944	0.46	3.0E-02	Z21211.1	EST_HUMAN	HSAAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam tes1244 (b)
11111	23621	36682	4.11	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11538	23988	37057	8.47	3.0E-02	AA483218.1	EST_HUMAN	ne8704.s1 NCL_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911263
12043	25078	30515	2.58	3.0E-02	R32019.1	EST_HUMAN	Y63d04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3'
12417	24570		18.42	3.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
12460	25089		3.53	3.0E-02	AF048687.1	NT	Rattus norvegicus UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
2479	15467	27614	1.05	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
3021	15637	28114	1.11	2.9E-02	BE565644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3021	15637	28115	1.11	2.9E-02	BE565644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
3616	16219	28698	0.84	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
4003	16601	29075	0.69	2.9E-02	H72805.1	EST_HUMAN	yu07610.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
5272	18016		62.36	2.9E-02	R09112.1	EST_HUMAN	yf25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
6213	18823	31594	1.31	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6434	18037	31824	6.5	2.9E-02	BF032233.1	EST_HUMAN	60145268F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856598 5'
7288	19824	32683	10.37	2.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7455	18979	32845	0.67	2.9E-02	D29214.1	EST_HUMAN	HUMNK262 Human epidermal keratinocyte Homo sapiens cDNA clone 262
7940	20482	33393	0.91	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlechtendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
7940	20482	33394	0.91	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlechtendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
9577	22077	35040	2.16	2.9E-02	AW875978.1	EST_HUMAN	CM3-PT0014-071289-051-c04 PT0014 Homo sapiens cDNA
9577	22077	35041	2.18	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071289-051-c04 PT0014 Homo sapiens cDNA
9788	22266		0.59	2.9E-02	AW976597.1	EST_HUMAN	EST388706 MAGC resequences, MAGN Homo sapiens cDNA
10247	22742	35732	0.94	2.9E-02	AP000064.1	NT	Aeropyrum pernix genomic DNA, section 7/7
10925	16219	28698	1.73	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12045	24979		1.88	2.9E-02	AU135817.1	EST_HUMAN	AU135817 PLACE1 Homo sapiens cDNA clone PLACE1002962 5'
591	13221		0.99	2.8E-02	AF970153.1	EST_HUMAN	EST382234 MAGC resequences, MAGK Homo sapiens cDNA
3414	16022	28502	1.62	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3414	16022	28503	1.62	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
4401	16986		0.71	2.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5337	17898	30313	0.92	2.8E-02	N87073.1	EST_HUMAN	L2083F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone L2083 5' similar to TRNA-
5679	18308	30802	11.28	2.8E-02	BE741083.1	EST_HUMAN	GUANINE TRANSGLYCOSYLASE
6900	19634	32472	1.14	2.8E-02	T78980.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948067 5'
8270	20811	33732	1.6	2.8E-02	AJ005820.1	NT	yd21b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108855 5'
8947	21485	34407	0.74	2.8E-02	AA280762.1	EST_HUMAN	Craterostigma plantaginum mRNA for homeodomain leucine zipper protein (hb-1)
9135	21670	34612	0.91	2.8E-02	AF187872.1	NT	zs96c06.r1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711466 5'
9237	21763	34709	0.64	2.8E-02	AE001092.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds
10498	22992	36002	1.81	2.8E-02	BF527244.1	EST_HUMAN	Archaeoglobus fulgidus section 15 of 172 of the complete genome
3479	16085	28559	4.18	2.7E-02	AL161494.2	NT	602039477F2 NCJ_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4177267 5'
4280	18866	29312	1.91	2.7E-02	N47258.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4280	18866	29313	1.91	2.7E-02	N47258.1	EST_HUMAN	y986h12.r1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:280487 5'
							y986h12.r1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:280487 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5633	18262	30734	1.11	2.7E-02	R12245.1	EST_HUMAN	yf33d08.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP:JC2264.JC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS:
6061	18678	31420	0.7	2.7E-02	X61670.1	NT	T.aeslivum pTTH20 mRNA for wheat type V thionin
6713	19307		0.9	2.7E-02	X87580.1	NT	A.bisporus poka gene
7127	19467	32285	2.06	2.7E-02	AA93571.1	EST_HUMAN	af98h03.s1 Soares_tctal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624681 3'
8295	20836		1.21	2.7E-02	A1377036.1	EST_HUMAN	tc28g08.x1 Soares_tctal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2065982 3' similar to contains Alu repetitive element;
597	13228	25700	1.52	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2404	14972	27544	2.79	2.6E-02	AA490021.1	EST_HUMAN	ab02b02.s1 Strabegene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2406	14974	27546	7.33	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2408	14974	27547	7.33	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2940	15558		1.17	2.6E-02	AF109806.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and smRNP genes, complete cds; GTA gene, partial cds; and unknown genes
5031	17605	30048	4.74	2.6E-02	L12032.1	NT	Chicken dorsalin-1 mRNA, complete cds
5224	17789	30208	1.58	2.6E-02	AE002014.1	NT	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5254	17817	30241	2.34	2.6E-02	AW241154.1	EST_HUMAN	xa52b04.x1 NCI_CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN
6368	18972		6.32	2.6E-02	AI206030.1	EST_HUMAN	Q15041 HYPOTHETICAL PROTEIN KIAA0069;
6556	19154	31850	2.28	2.6E-02	BE621748.1	EST_HUMAN	qg27f11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
6815	19574	32402	0.75	2.6E-02	Z99084.1	NT	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
6815	19574	32403	0.75	2.6E-02	Z99084.1	NT	Vaccinia virus ORF1L, strain Wyeth
6990	19488	32310	6.45	2.6E-02	6981271	NT	Vaccinia virus ORF1L, strain Wyeth
8442	20982	33897	0.77	2.6E-02	AA860946.1	EST_HUMAN	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
9282	21882	34827	1.41	2.6E-02	11432020	NT	ak22f04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406719 3'
9630	22130	35094	0.6	2.6E-02	AF114952.1	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
9630	22130	35095	0.6	2.6E-02	AF114952.1	NT	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10302	22786	35787	4.1	2.6E-02	AL163303.2	NT	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
11265	23783		2.44	2.6E-02	AA278351.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
11437	23887	36955	1.63	2.6E-02	AW500547.1	EST_HUMAN	zs84c02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5'
11865	25080	30512	1.26	2.6E-02	BF343827.1	EST_HUMAN	U1HF-BN0-ak-q-10-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077488 5'
12083	24354		1.28	2.6E-02	11422836	NT	G02015501F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150944 5'
557	13188	25668	1.76	2.5E-02	AI793130.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10724 (FLJ10724), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
557	13188	25667	1.76	2.5E-02	A1793130.1	EST_HUMAN	on2606.y5 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
842	13458	25967	19.88	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
902	13516	26034	4.46	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
2791	15344		2.84	2.5E-02	U12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2983	15599	28078	3.52	2.5E-02	X98697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
2983	15599	28079	3.52	2.5E-02	X98697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4119	18005	29187	0.77	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4119	18005	29188	0.77	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4284	16870	29316	5.25	2.5E-02	AW592114.1	EST_HUMAN	h36h08.x1 Soares_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:2934015 3'
5889	18512	31238	0.7	2.5E-02	A1732776.1	EST_HUMAN	z683c10.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810354 3'
6340	18946		4.9	2.5E-02	BE670128.1	EST_HUMAN	7e30e09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.11 L1 repetitive element;
8357	18981		4.3	2.5E-02	BE746888.1	EST_HUMAN	601576333F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
6478	19079	31862	0.72	2.5E-02	L29028.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7660	20172	33058	1.52	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCL CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213406 5'
7660	20172	33059	1.52	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCL CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213406 5'
7920	20462	33368	0.48	2.5E-02	BE252469.1	EST_HUMAN	601108291F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3344278 5'
8759	21298	34219	0.93	2.5E-02	Q91713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
8804	21432	34355	0.45	2.5E-02	AW025821.1	EST_HUMAN	wu08c10.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2516370 3'
9978	22473		0.8	2.5E-02	X71303.1	NT	D. radicum 28S ribosomal RNA, D2 domain
10475	22869	35978	0.73	2.5E-02	A147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
10869	23219	36231	2.04	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
10869	23219	36232	2.04	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Aalpha) and major histocompatibility protein class II beta chain (EBeta) genes, complete cds;
10761	23285		4.04	2.5E-02	AF050157.1	NT	butyrophilin-like (NG9), butyrophilin-lp>
11602	24045		1.73	2.5E-02	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
11922	24993		3.33	2.5E-02	11420078	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC63634), mRNA
12115	24855		1.53	2.5E-02	U60169.1	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
12215	24438		2.17	2.5E-02	U60169.1	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
12242	24454	30957	1.31	2.5E-02	BE973327.1	EST_HUMAN	Dicotyledon discoidium putative protein kinase Mica (mika) gene, complete cds
185	12848	25332	0.75	2.4E-02	A1378582.1	EST_HUMAN	601652365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
1642	14234	26768	2.09	2.4E-02	H65984.1	EST_HUMAN	ic72c07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2070158 3'
2088	15457	27239	2.02	2.4E-02	P01901	SWISSPROT	y7511.11 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:211149 5'
							H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2088	15457	27240	2.02	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4458	17044	29487	1.89	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4619	17202	29650	1.63	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4619	17202	29651	1.63	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
6363	18987	31745	0.84	2.4E-02	W86980.1	EST_HUMAN	zh63h04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416791 3'
7273	19801	32658	1.08	2.4E-02	Z20573.1	EST_HUMAN	HSAAACKVX T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7287	19815	32672	0.95	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7287	19815	32673	0.95	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7831	20373		0.69	2.4E-02	AW813007.1	EST_HUMAN	RC3-ST0186-230300-019-h06 ST0186 Homo sapiens cDNA
7884	20426		0.6	2.4E-02	M16780.1	NT	Human retrotransposon 3' long terminal repeat
8379	20919		0.88	2.4E-02	H78376.1	EST_HUMAN	yu12c05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233576 3' similar to contains Alu repetitive element; contains A3R repetitive element
8468	21008	33925	10.74	2.4E-02	N69442.1	EST_HUMAN	za95g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:284596 3' similar to gb K02809 RATSR7K Rat (RNA); contains A3R.b1 A3R repetitive element
8917	21455	34375	0.54	2.4E-02	AE001125.1	NT	Borrelia burgdorferi (section 11 of 70) of the complete genome
							zu91c06.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb J04422 ISLET AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR XTR repetitive element
8939	21477	34398	0.75	2.4E-02	AA625680.1	EST_HUMAN	
9720	22218	35193	2.76	2.4E-02	AV692954.1	EST_HUMAN	AV692954 GKC Homo sapiens cDNA clone GKCD5003 5'
							nh07b12.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element PTR5 repetitive element
9891	22388	35368	2.9	2.4E-02	AA493894.1	EST_HUMAN	
11447	23897	36962	1.9	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70i gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
11447	23897	36983	1.9	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70i gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
11718	24127		3.56	2.4E-02	9627909	NT	Bacteriophage b1L87, complete genome
11868	24222	31044	2.48	2.4E-02	6753635	NT	Mus musculus Dmb1 homolog 1 (E. coli) (Dmb1), mRNA
11924	24259	31013	1.36	2.4E-02	BE928869.1	EST_HUMAN	MRO-FT0175-310800-202-e06 FT0175 Homo sapiens cDNA
11984	24284	30981	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds
11984	24284	31025	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12184	24404		8.87	2.4E-02	AB008589.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
12191	24422		2.11	2.4E-02	N42980.1	EST_HUMAN	Y03a06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270610 5'
12197	24425		1.55	2.4E-02	BF679477.1	EST_HUMAN	602153281.F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294173 5'
12362	24927	30795	1.48	2.4E-02	AA179693.1	EST_HUMAN	zp13h01.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609361 5'
1913	14498		5.46	2.3E-02	W05340.1	EST_HUMAN	zs84g08.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299294 5'
1931	14515		21.68	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2053	14634	27205	0.96	2.3E-02	AW797355.1	EST_HUMAN	CM2-UM0038-290400-172-b11 UM0038 Homo sapiens cDNA
2389	14957	27529	2.31	2.3E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
3745	16346	28814	6.21	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH.P, Human foetal Brain Whole tissue Homo sapiens cDNA
3777	16377		0.82	2.3E-02	L23429.1	NT	Canis beta-galactosides-binding lectin (LGALS3) mRNA, 3' end
4230	16818	29286	0.75	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4511	17095	29542	1.21	2.3E-02	AW899107.1	EST_HUMAN	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4546	17130	28574	0.91	2.3E-02	BE935225.1	EST_HUMAN	CM4-NN0080-290400-160-b04 NN0080 Homo sapiens cDNA
4548	17130	28575	0.91	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4547	18006	28576	1.05	2.3E-02	AW593693.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4547	18008	28577	1.05	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4698	17280	29726	2.96	2.3E-02	BF028487.1	EST_HUMAN	xs25d08.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4698	17280	29727	2.96	2.3E-02	BF028487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5'
5192	17748	30177	0.93	2.3E-02	AW844307.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5'
5398	17928	30342	2.72	2.3E-02	AI038076.1	EST_HUMAN	RC2-CN0051-290100-011-a07 CN0051 Homo sapiens cDNA
5578	18209	30659	3.34	2.3E-02	U88303.1	NT	ox21c10.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1656978 3' similar to gp.X69908_rna1 ATP SYNTHASE LIPOID-BINDING PROTEIN P2 PRECURSOR (HUMAN);
6733	19327	32132	4.43	2.3E-02	AL161505.2	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds
7056	18075	30428	0.88	2.3E-02	BE141475.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7817	20360	33266	6	2.3E-02	U63610.1	NT	MR0-HT0080-011099-002-c09 HT0080 Homo sapiens cDNA
8407	20947	33867	0.74	2.3E-02	AJ298105.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
8407	20947	33868	0.74	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8630	21169	34085	0.83	2.3E-02	AJ685380.1	EST_HUMAN	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8630	21169	34086	0.83	2.3E-02	AJ685380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9065	21602	34532	0.81	2.3E-02	P41998	SWISSPROT	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9773	22271	35256	0.72	2.3E-02	P50532	SWISSPROT	HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR CHROMOSOME ASSEMBLY PROTEIN XCAP-C

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8943	22438	35415	1.4	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
8943	22438	35416	1.4	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10661	23183	36208	2.37	2.3E-02	P08840	SWISSPROT	GLUCOAMYLASE S/SZ PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
11828	24070		1.87	2.3E-02	AF159132.1	NT	Melapneumoniae ensis fushi tarazu-factor 1 mRNA, complete cds
11846	24843		5.2	2.3E-02	BE278331.1	EST_HUMAN	601178958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3548567 5'
12282	24485	30940	1.69	2.3E-02	BF528482.1	EST_HUMAN	602043628F1 NCI_CGAP_Bn87 Homo sapiens cDNA clone IMAGE:4181454 5'
12282	24485	30941	1.59	2.3E-02	BF528482.1	EST_HUMAN	602043628F1 NCI_CGAP_Bn87 Homo sapiens cDNA clone IMAGE:4181454 5'
12392	24552	30907	2.2	2.3E-02	U39394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12447	25100		3.04	2.3E-02	U11077.1	NT	Dictyostellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
12660	24940		1.73	2.3E-02	11426388	NT	Homo sapiens dead ringer (Drosophila)-like 1 (DRIL1), mRNA
767	13386	25885	3	2.2E-02	AF018267.1	NT	Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1783	14373		1.03	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
2058	14639	27212	1.33	2.2E-02	Z82001.1	NT	S.pneumoniae pcpA gene and open reading frames
3482	16088		2.1	2.2E-02	AA577785.1	EST_HUMAN	nm24g04.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3708	16309		3.58	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3920	16518	28984	1.11	2.2E-02	AW601317.1	EST_HUMAN	PMO-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
3992	16590	29062	0.85	2.2E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
5225	17790	30209	0.92	2.2E-02	Z73597.1	NT	S.cerevisiae chromosome XVI reading frame ORF YPL241c
7294	19822	32681	3.52	2.2E-02	AV699721.1	EST_HUMAN	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'
8312	20853	33778	2.56	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8312	20853	33779	2.56	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8744	21283	34205	0.75	2.2E-02	X78488.1	NT	P.vulgaris alpha tub 2 mRNA
8574	22074	35036	0.57	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPAse 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9574	22074	35037	0.57	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPAse 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9804	22104	35066	1.88	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9604	22104	35067	1.88	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10106	22601		0.86	2.2E-02	6678140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
12120	24379		3.95	2.2E-02	AA503553.1	EST_HUMAN	ne47h07.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:500541 3' similar to contains Alu repetitive element;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
444	13077		4.45	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
474	13107		5.21	2.1E-02	AF029726.1	NT	Dicotyledonum discolorum histidine kinase C (dhkc) mRNA, complete cds
1308	13900	26420	8.15	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1430	14022	26550	1.48	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1430	14022	26551	1.48	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
2842	13428	25934	3.37	2.1E-02	N28286.1	EST_HUMAN	Y44307.1 Scars melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:264541 5'
3184	14660	27231	0.83	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0548-120100-001-111 BT0546 Homo sapiens cDNA
3184	14660	27232	0.83	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0548-120100-001-111 BT0546 Homo sapiens cDNA
3843	16248	28721	1.47	2.1E-02	AA481271.1	EST_HUMAN	z63b09.r1 Scars, fetal, fetus, Nb2HF8 9w Homo sapiens cDNA clone IMAGE:786121 5'
4211	16800	29249	0.77	2.1E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4398	16983	29428	0.83	2.1E-02	BF343855.1	EST_HUMAN	502013306F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4151161 5'
4340	17124	29588	1.64	2.1E-02	U4914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds, and unknown genes
4552	17135	29583	1.3	2.1E-02	A168127.1	EST_HUMAN	wg81d11.x1 Scars, NSF_F8 9w OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4820	17398	29852	5.95	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4836	17414	29867	0.57	2.1E-02	AA665737.1	EST_HUMAN	eg55g12.s1 Gessler Wills tumor Homo sapiens cDNA clone IMAGE:1126918 3'
4944	17519	29861	0.83	2.1E-02	A1823432.1	EST_HUMAN	wh54805.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
5321	17883		1.52	2.1E-02	S82470.1	NT	BB1-malignant cell expression-enhanced gene/tumor progression-enhanced gene [human, UIM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt]
5821	18445	31187	0.8	2.1E-02	AW379528.1	EST_HUMAN	GM4-HT0244-111199-040-h05 HT0244 Homo sapiens cDNA
7126	19466	32284	0.74	2.1E-02	BF086199.1	EST_HUMAN	QV3-GN0058-120900-329-a12 GN0058 Homo sapiens cDNA
8456	20996	33914	0.66	2.1E-02	9790238	NT	Mus musculus sorting nexin 1 (Snx1), mRNA
9422	21831	34879	0.56	2.1E-02	AA984288.1	EST_HUMAN	am83e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element; contains element MER11 repetitive element ;
9549	22049	35010	2.41	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9549	22049	35011	2.41	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9894	22391	35369	1.22	2.1E-02	L29324.1	NT	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds; and unknown genes
9973	22468	35452	0.57	2.1E-02	AA984288.1	EST_HUMAN	am83e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element; contains element MER11 repetitive element ;
12089	18030		11.53	2.1E-02	Y19213.1	NT	Homo sapiens putative psih-bA pseudogene for hair keratin, exons 2 to 7
12141	24839	30798	1.31	2.1E-02	L34170.1	NT	Human garmline UBETL gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
12552	24655	30871	16.83	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmaA precursor (omaA) gene, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
20	12699	25155	1.34	2.0E-02	BF002832.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13
21	12700	25156	9.6	2.0E-02	AW895365.1	EST_HUMAN	MER1 repetitive element:
280	12937	25422	2.31	2.0E-02	6753635	NT	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
317	12971	25480	2.42	2.0E-02	AA456538.1	EST_HUMAN	Mus musculus DnB homolog 1 (E. coli) (DnB1), mRNA
831	13448	25955	1.2	2.0E-02	6753635	NT	aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
1128	13729	26240	1.32	2.0E-02	AL066805.1	NT	Mus musculus DnB homolog 1 (E. coli) (DnB1), mRNA
1241	13839	26356	0.79	2.0E-02	8922391	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1 [p36.33] of Homo sapiens
1241	13839	26357	0.79	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1914	14499	27053	2.3	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1914	14499	27054	2.3	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2824	15378		3.19	2.0E-02	AL161532.2	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
3115	12699	25155	1.84	2.0E-02	BF002832.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3178	15791		1.38	2.0E-02	7305474	NT	7g51c08.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13
3284	15876		1.57	2.0E-02	AF095688.1	NT	MER1 repetitive element:
4078	16874	29135	1.54	2.0E-02	M18095.1	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA
5288	17830	30255	1.12	2.0E-02	AF189368.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
6056	18673	31414	0.87	2.0E-02	L35321.2	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
7553	20072	32847	1.28	2.0E-02	AP000004.1	NT	Ajellomyces capsulatus catalase isozyme A (CATA) mRNA, complete cds
7553	20072	32848	1.28	2.0E-02	AP000004.1	NT	Dictyostelium discoideum class VII unconventional myosin (myo) gene, complete cds
9781	22289		2.5	2.0E-02	U70408.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)
10284	22759	35746	1.63	2.0E-02	A1840342.1	EST_HUMAN	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)
10522	23060	36070	2.05	2.0E-02	Z73968.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
11250	23780	36836	2.85	2.0E-02	D88184.1	NT	wa17b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298315 3'
11530	23978	37047	1.58	2.0E-02	10947055	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162
11530	23978	37048	1.58	2.0E-02	AA456538.1	EST_HUMAN	Equus caballus DNA for 17alpha-hydroxylase/17 20-lyase, complete cds
11654	18034	30494	1.91	2.0E-02	AL161532.2	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12138	15376		1.94	2.0E-02	AL161532.2	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12835	24711		8.4	2.0E-02	T80037.1	EST_HUMAN	aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
722	13342	25832	1.83	1.9E-02	AA572764.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
							yd04c09.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24675 5'
							mf19e07.s1 NCI_CGAP_P71 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.t1 L1
							repetitive element:

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1658	14251	26785	0.96	1.9E-02	P18488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
2083	14684	27234	1.96	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2083	14684	27235	1.96	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2549	15113	27683	0.9	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2830	15546	28021	8.7	1.9E-02	AA713856.1	EST_HUMAN	nm004005.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
2980	15596	28076	1.58	1.9E-02	AV648669.1	EST_HUMAN	AV648669 GLC Homo sapiens cDNA clone GLOCBLH07 3'
3298	15809		0.75	1.9E-02	AB033611.1	NT	Urothuchus talpoides mitochondrial gene for cytochrome b, complete cds
3671	16272		1.09	1.9E-02	N52250.1	EST_HUMAN	yz28b02.s1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:284331 3'
3766	16367		6.81	1.9E-02	BE738088.1	EST_HUMAN	601572682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3838964 5'
4121	16714	26170	1.48	1.9E-02	AF141940.1	NT	Mycoplasma imitans VihA1 precursor (vihA1) and VihA2 precursor (vihA2) genes, partial cds
4271	16857	28305	1.57	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4271	16857	28306	1.57	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4639	17221	28675	3.21	1.9E-02	AI452999.1	EST_HUMAN	t46d04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
5157	15113	27683	2.73	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5519	18151	30565	0.83	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5680	18287	30765	1.38	1.9E-02	L47572.1	NT	Meleagris gallopavo paraxonase-2 (PON2) mRNA, complete cds
5959	18581		0.81	1.9E-02	AB019507.1	NT	Drosophila kanekoi gene for glyceral-3-phosphate dehydrogenase, complete cds
7158	18690	32534	1.41	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7158	18690	32535	1.41	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8506	21045		1.06	1.9E-02	AL162754.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 3/7
9254	21780	34732	0.94	1.9E-02	BF316129.1	EST_HUMAN	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125482 5'
9629	22128	35093	0.66	1.9E-02	L10114.1	NT	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
9858	22453	35435	1.04	1.9E-02	BF695832.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076263 5'
10054	22549	35543	0.49	1.9E-02	N39160.1	EST_HUMAN	y46h08.s1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:276639 3'
10151	22846	35639	0.56	1.9E-02	D64001.1	NT	Synechocystis sp. PCC6803 complete genome, 20/27, 2539000-2644794
11878	24847	30801	4.28	1.9E-02	AF101085.1	NT	Hirudo medicinalis intermediate filament gilaen mRNA, complete cds
12477	24818		1.27	1.9E-02	L11068.1	NT	Candida albicans lambda Cas3B fragment
12587	24680	30879	1.7	1.9E-02	X68271.1	NT	H. sapiens MUC18 gene exon 16
368	13017	25500	1.84	1.8E-02	AW771104.1	EST_HUMAN	hm52d06.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element ;
714	13335	25821	2.26	1.8E-02	BF308122.1	EST_HUMAN	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
1202	13802	28315	1.51	1.8E-02	X17064.1	NT	H.francisci mRNA for myelin basic protein (MBP)
1484	14077	26815	2.3	1.8E-02	AF243382.1	NT	Drosophila melanogaster cytoplasmic protein encore (enc) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2704	15261	27828	1.22	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PA01, section 105 of 528 of the complete genome
3247	15859		0.72	1.8E-02	AB05829.1	EST_HUMAN	hs52a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'
3956	16554	29023	1.07	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3956	16554	29024	1.07	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4160	16752		1.41	1.8E-02	AA861448.1	EST_HUMAN	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3'
4521	17105	29551	1.67	1.8E-02	AW936363.1	EST_HUMAN	QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA
5090	17663	30103	1.08	1.8E-02	Q60810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
6901	19635	32473	4.27	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION
8071	20613	33527	0.81	1.8E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds
8404	20944	33886	0.91	1.8E-02	AW905327.1	EST_HUMAN	QV2-NN1073-220400-159-h09 NN1073 Homo sapiens cDNA
8449	20989	33607	0.75	1.8E-02	6678943	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
9413	21922	34870	0.45	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9413	21922	34871	0.45	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9560	22060		2.41	1.8E-02	AA897543.1	EST_HUMAN	aj2009.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb:L11672 ZINC FINGER PROTEIN 91 (HUMAN);
9975	22470	35453	1.72	1.8E-02	BE778274.1	EST_HUMAN	601463545F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866963 5'
10126	22621	35611	1.12	1.8E-02	X86933.1	NT	L.stagnalis mRNA for myomodulin neuropeptide precursor
11313	23011	36019	1.79	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11313	23011	36020	1.79	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11480	23930	37001	1.73	1.8E-02	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1186001-1485000 nt, position (817)
11489	23938	37008	3.88	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
839	13552	28068	0.77	1.7E-02	BE394869.1	EST_HUMAN	601310526F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632180 5'
1827	14416	26963	1.89	1.7E-02	AW573183.1	EST_HUMAN	hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element;
1827	14416	26984	1.89	1.7E-02	AW573183.1	EST_HUMAN	hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element;
1912	14497		3.27	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2159	14736		12.81	1.7E-02	AB004816.1	NT	Oryzotagus cuniculus mRNA for mitsugumin29, complete cds
2332	14903	27474	4.64	1.7E-02	S74186.1	NT	(microsatellite INRA41) [Ovis aries=sheep, Genomic, 361 nt, segment 1 of 2]
3028	15644	28123	0.94	1.7E-02	AI147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3562	16166		4.33	1.7E-02	AW827368.1	EST_HUMAN	hm45a04.x1 NCI CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element;
3687	16288		0.65	1.7E-02	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4248	16836		1.08	1.7E-02	AA669618.1	EST_HUMAN	ac19f04.s1 Stratagene ovary (H937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element
4278	16864		2.52	1.7E-02	R02506.1	EST_HUMAN	ye88f08.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:124647 5'
4551	17134	28582	0.61	1.7E-02	A1305279.1	EST_HUMAN	qm08g07.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4628	17209	28659	1.44	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2633740 3' similar to contains L1.11 L1 repetitive element
4824	17402	28655	1.78	1.7E-02	V00641.1	NT	Messenger RNA for anglerfish (Lophius americanus) somatostatin II
4938	17511		5.99	1.7E-02	A1015076.1	EST_HUMAN	ov51e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
6274	18982	31650	1.8	1.7E-02	A1769247.1	EST_HUMAN	wg35f09.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element
6693	19289	32091	1.98	1.7E-02	A1038280.1	EST_HUMAN	ov51e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
7112	19452	32268	1.05	1.7E-02	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7255	19783	32639	1.96	1.7E-02		NT	Homo sapiens nebulin (NEB), mRNA
7394	19919	32783	1.07	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7394	19919	32784	1.07	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7724	20232		1.7	1.7E-02	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
8957	20296	33195	0.97	1.7E-02	U21854.1	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
8915	22115	35079	1.31	1.7E-02	AL040554.1	EST_HUMAN	DKFZp43410314_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp43410314 5'
12482	25025	30619	3.35	1.7E-02	AW903482.1	EST_HUMAN	GM4-NN1030-040-00-130-006 NN1030 Homo sapiens cDNA
537	13168		3.38	1.6E-02	AL021626.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 13/162
1696	14289	28825	1.05	1.6E-02	Y18889.1	NT	Treponema mallophilum flaB2, flaB3 and flhD genes for flagellin subunit proteins and CAP protein homologue
2290	14894	27438	2.13	1.6E-02	Q84176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2290	14894	27439	2.13	1.6E-02	Q84176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2600	15182	27730	0.88	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQT1 gene
2669	15227	27799	1.82	1.6E-02	AA484872.1	EST_HUMAN	ne81d08.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2718	15275		1.14	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3052	15688	28148	0.73	1.6E-02	AF11282.1	NT	Laccase sp. isolate 1bD cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product
3578	16182	28664	5.61	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
3914	16512	28974	0.62	1.6E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4254	16942		1.77	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4388	16974	28424	1.26	1.6E-02	AW875407.1	EST_HUMAN	QV2-PT0012-140100-030-107 PT0012 Homo sapiens cDNA
4901	17476	29932	3.69	1.6E-02	AI769132.1	EST_HUMAN	wg34b09.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2368989 3'
5306	17668		0.61	1.6E-02	N80156.1	EST_HUMAN	z65607.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:297444 3'
5807	18432	31153	1.26	1.6E-02	6671715	NT	Mus musculus CD5 antigen (Cd5), mRNA
6752	18345	32152	2	1.6E-02	AB015281.1	NT	Candida albicans CaGCR3 gene, complete cds
7011	19509	32328	1.22	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7011	19509	32330	1.22	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7696	20205	33092	0.9	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8064	20606	33518	0.78	1.6E-02	AJ277662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8119	20660		1.55	1.6E-02	X05151.1	NT	Human apC-II gene for preproapolipoprotein C-II
9953	22448		2.32	1.6E-02	AF079764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10317	22811	35805	1.17	1.6E-02	AA572818.1	EST_HUMAN	n18q03.s1 NCI CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
10317	22811	35806	1.17	1.6E-02	AA572818.1	EST_HUMAN	P29294 TELOKIN. [1]:
10788	24800	35319	2.38	1.6E-02	Z94828.1	NT	n18q03.s1 NCI CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
11090	23602	36840	2.5	1.6E-02	AL161508.2	NT	G gallus microsatellite DNA (LEI0260) (=T16iIE11)
11090	23602	36841	2.5	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11365	23837	36899	2.38	1.6E-02	AJ373558.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11855	14894	27438	3.63	1.6E-02	Q84176	SWISSPROT	qz96e10.x1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone IMAGE:2042442 3'
11855	14894	27439	3.63	1.6E-02	Q84176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
781	13400		51.07	1.5E-02	8923734	NT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2187	14763	27332	4.36	1.5E-02	N39521.1	EST_HUMAN	Homo sapiens transcription factor (HSA130894), mRNA
2219	14784	27387	1.76	1.5E-02	AL161594.2	NT	y27b07.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:243925 3'
3097	15712	28183	0.99	1.5E-02	AJ006216.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3097	15712	28184	0.99	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3787	16387	28853	0.96	1.5E-02	BF092942.1	EST_HUMAN	Homo sapiens CACNA1F gene, exons 1 to 48
4222	16810	29257	0.86	1.5E-02	AA160967.1	EST_HUMAN	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA
5160	17729		0.78	1.5E-02	M13879.1	NT	zq40g10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632228 5'
5405	17863	30374	1.14	1.5E-02	AW770341.1	EST_HUMAN	Human interleukin 2 gene, exons 1 and 2
							n176h11.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3007173 3'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8436	19039	31828	1.31	1.5E-02	Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
7360	19888		1.62	1.5E-02	11487282	NT	Cyanophora paradoxa cyanelle, complete genome
7432	19956	32821	1.36	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
7815	20358	33265	1.44	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7822	20364	33273	4.16	1.5E-02	11417739	NT	Homo sapiens valyl-tRNA synthetase 2 (VARS2), mRNA
8764	21303	34224	1.62	1.5E-02	BF345554.1	EST_HUMAN	602019135F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154504 5'
8989	21812		0.51	1.5E-02	AF098774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
8490	21946	34895	1.64	1.5E-02	D44606.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
9725	22223	35199	1.08	1.5E-02	R32687.1	EST_HUMAN	Yn54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
9725	22223	35200	1.08	1.5E-02	R32687.1	EST_HUMAN	Yn54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
10697	23227		1.71	1.5E-02	D26547.1	NT	Rice gene for thiredoxin h, complete cds
11047	23560	36597	2.32	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds
12076	24892		2.25	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
12636	24712		1.55	1.5E-02	AI763127.1	EST_HUMAN	w06h03.x1 NCI CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389493 3' similar to contains Alu repetitive element; contains element MER26 MSR1 repetitive element
442	13075		1.41	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 58 of 94 of the complete genome
1157	13760	26270	4.22	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1299	13893		1.29	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1341	13936		3.36	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1564	14156		1.09	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBA-H11 5'
3249	15861	28342	1.91	1.4E-02	AF160969.2	NT	Bifidobacterium longum Na+/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosaminohexose repressor protein (nagC/xyfR) gene, partial cds
3445	16053	28530	0.98	1.4E-02	AW074212.1	EST_HUMAN	xb09d09.x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3'
3531	16136	28616	5.67	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3531	16136	28617	5.67	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3571	16175	28657	0.68	1.4E-02	4503623	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3717	16318	28766	6.27	1.4E-02	6996918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-B), mRNA
4587	17170	29614	8.88	1.4E-02	AW962698.1	EST_HUMAN	EST374761 MAGC resequences, MAGG Homo sapiens cDNA
4587	17170	29615	8.88	1.4E-02	AW962698.1	EST_HUMAN	EST374761 MAGC resequences, MAGG Homo sapiens cDNA
4767	17348	29787	1.2	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4767	17348	29788	1.2	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
5003	17576	30020	6.64	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5003	17578	30021	6.64	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
6547	19145	31941	4.61	1.4E-02	AA559030.1	EST_HUMAN	n111c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
6547	19146	31942	4.61	1.4E-02	AA559030.1	EST_HUMAN	n111c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
8081	20623		1.97	1.4E-02	AL020273.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/182
8829	21368	34282	1.24	1.4E-02	M81702.1	NT	Candida boidinii methyl oxidase (AOD1) gene, complete cds
9082	21618	34553	0.99	1.4E-02	AJ27285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9321	21835	34786	2.48	1.4E-02	BE544581.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
10451	22945		0.81	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11765	24156	36772	12.78	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12134	24387		3.62	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12433	24574		2.32	1.4E-02	11426968	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1905	14490		1.18	1.3E-02	BE739283.1	EST_HUMAN	601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 5'
1998	14580	27138	2.55	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3250	15862	28343	1.91	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3250	15862	28344	1.91	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
4041	16639		1.66	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
5455	18090	30447	1.46	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
5455	18090	30448	1.48	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
6312	18919	31694	1.4	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
6345	18951	31729	0.88	1.3E-02	M62962.1	NT	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7041	18061	30449	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
7041	18061	30450	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7578	20094	32971	4.78	1.3E-02	AI031593.1	EST_HUMAN	ow05g05.x1 Soares_parathyroid_tumor_NBHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;
8418	20958	33876	1.63	1.3E-02	AF156961.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10108	22603	35593	1.71	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10178	22673	35665	0.77	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
10871	23392	36406	4.07	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2815036 3'
10871	23392	36407	4.07	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2815036 3'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11742	25051		2.12	1.3E-02	X51780.1	NT	Yeast ABP1 gene for actin binding protein
12139	25039		2	1.3E-02	Z88117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2598451 to 2812870
12246	24457		2.77	1.3E-02	9833089	NT	Human herpesvirus 6B, complete genome
12438	24813		47.13	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
228	12888		20.25	1.2E-02	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, iPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
377	13025	25511	3.79	1.2E-02	AA059299.1	EST_HUMAN	zf65g01.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element
478	13111	25501	1.71	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3REGION
768	13397	25886	8.37	1.2E-02	A1183522.1	EST_HUMAN	qdb8a12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.L1 L1 repetitive element
2221	14798	27389	1.85	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2223	14798	27371	1.15	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2487	15052	27624	1	1.2E-02	AW172350.1	EST_HUMAN	X37609.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2542	15108	27678	1.05	1.2E-02	BE638310.1	EST_HUMAN	601068406FT NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2542	15108	27679	1.05	1.2E-02	BE638310.1	EST_HUMAN	601068406FT NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
3135	15749		7.58	1.2E-02	AA075418.1	EST_HUMAN	zm88e03.r1 Strategene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5'
3327	15937	28413	2.02	1.2E-02	R62805.1	EST_HUMAN	y111b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
4938	17513	28959	0.61	1.2E-02	AL161593.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
5040	17613	30057	2.65	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NP T3) gene, complete cds
5194	17759		1.61	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CpUbigT mRNA, partial cds
5244	17808	30230	2.01	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5927	18549	31275	1.78	1.2E-02	D78588.1	NT	Rana rugosa mRNA for calreticulin, complete cds
7078	18650	32489	5.21	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7334	18861	32725	1.06	1.2E-02	H02197.1	EST_HUMAN	y34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3'
7353	19879	32744	19.46	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBUC09 5'
7939	20481	33392	2.3	1.2E-02	Q11205	SWISSPROT	CMP-N-ACETYLEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA 2) (SIAT4-B)
8133	20674	33585	1.2	1.2E-02	AF193812.1	NT	Homo sapiens fringe protein mRNA, partial cds
8133	20674	33586	1.2	1.2E-02	AF193812.1	NT	Homo sapiens fringe protein mRNA, partial cds
8822	21361		1.06	1.2E-02	T76987.1	EST_HUMAN	y072c08.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:113774 3'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9557	22057	35018	2.7	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
9589	22089	35053	1.74	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
12446	24582		4.73	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-557G06 5'
1312	13806	26428	1.49	1.1E-02	AA070364.1	EST_HUMAN	zn69e11.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3'
1744	14334	26880	1.91	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1744	14334	26881	1.91	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2082	14863	27233	5.42	1.1E-02	BF345283.1	EST_HUMAN	602018037F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153808 5'
2902	15519		4.2	1.1E-02	N99523.1	EST_HUMAN	zn40905.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:295040 5'
3575	16178	28662	2.88	1.1E-02	A1653508.1	EST_HUMAN	IQ95b10.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XPf_HUMAN
4094	16889		2.1	1.1E-02	BE144637.1	EST_HUMAN	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4183	16773		0.61	1.1E-02	AW813796.1	EST_HUMAN	PM3-HT0175-300999-001-108 HT0175 Homo sapiens cDNA
4956	17531	29973	2.09	1.1E-02	AL048383.2	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
							DKFZp586650924_s1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp586E0924
6298	18906	31677	1.03	1.1E-02	U68480.1	NT	Bacillus subtilis SpoVK (spvK), YnbA (ynbA), YnbB (ynbB), GlnR (glnR), glutamine synthetase (glnA), YnaA (ynaA), YnaB (ynab), YnaC (ynac), YnaD (ynad), YnaE (ynae), YnaF (ynaf), YnaG (ynag), YnaH (ynah), YnaI (ynai), YnaJ (ynaj), xylan beta-1,4-xylosyl
7594	20108	32983	2.55	1.1E-02	BE149611.1	EST_HUMAN	RC1-HT0256-100300-016-107 HT0256 Homo sapiens cDNA
8189	20740	33652	0.49	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8189	20740	33653	0.49	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8574	21113	34032	0.64	1.1E-02	AW996160.1	EST_HUMAN	QV3-BN0045-220300-128-102 BN0045 Homo sapiens cDNA
8756	21295	34215	0.69	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC4040
8833	21372	34297	7.39	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
9842	22340	35322					
10006	22501	35492	2.07	1.1E-02	AA082578.1	EST_HUMAN	zn24601.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5'
10858	23378	36398	3.78	1.1E-02	AA314685.1	EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
					11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
11702	24115		2.67	1.1E-02	AA668239.1	EST_HUMAN	ab7711.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
12512	16773		1.87	1.1E-02	AW813796.1	EST_HUMAN	Alu repetitive element
7	12898	25144	6.97	1.0E-02	AW846120.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
1570	14163	26694	2.33	1.0E-02	AW368128.1	EST_HUMAN	MR3-CT0176-111099-003-e10 CT0176 Homo sapiens cDNA
2606	15168		1.9	1.0E-02	AA806389.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
3126	15740	26209	3.7	1.0E-02	BE835556.1	EST_HUMAN	oc22108.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495 3'
3302	15913	26391	1.41	1.0E-02	BE968969.1	EST_HUMAN	RCO-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
							601649867R1 NH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3558	16162		0.83	1.0E-02	AW845621.1	EST_HUMAN	MRO-CT0060-081099-003-110 CT0060 Homo sapiens cDNA
3950	16548	28016	0.88	1.0E-02	AI065086.1	EST_HUMAN	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
4891	17466	29921	5.12	1.0E-02	6753821	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
4970	17544	29986	5.03	1.0E-02	R66567.1	EST_HUMAN	yq54h01.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:189633 5'
5221	17786	30204	1.01	1.0E-02	AF218910.1	NT	Homo sapiens atracrin precursor (ATRIN) gene, exon 25 and complete cds, alternatively spliced
5317	17879	30298	0.98	1.0E-02	P06899	SWISSPROT	EXTENSIN PRECURSOR
5394	17952		16.85	1.0E-02	AV723678.1	EST_HUMAN	AV723678 HTB Homo sapiens cDNA clone HTBAPF08 5'
5445	18000		3.87	1.0E-02	D34632.1	NT	Arabidopsis thaliana acc2 gene for acetyl-CoA carboxylase, partial cds
5610	18239	30688	0.8	1.0E-02	H52861.1	EST_HUMAN	yq36h11.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:235941 5'
5921	18543	31269	0.7	1.0E-02	AF309388.1	NT	Mus musculus transcription complex subunit NF-A-Tc4 (Nfalc4) gene, exons 1 and 2
6264	18872	31642	0.99	1.0E-02	AF257303.1	NT	Mus musculus synaptotagmin II (Sy2) gene, complete cds
6328	18934	31709	2.67	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6328	18934	31710	2.67	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6859	19593	32425	2.22	1.0E-02	Z29642.1	NT	Zmays U3snRNA pseudogene
8240	20781		0.46	1.0E-02	Z28107.1	NT	S. cerevisiae chromosome XI reading frame ORF YKL107w
9314	21828	34778	4.29	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
9314	21828	34778	4.29	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
							Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11143	23651		2.17	1.0E-02	AF157559.1	NT	
11246	23776	36833	2.02	1.0E-02	AV760016.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
11785	25110		2.18	1.0E-02	Q82203	SWISSPROT	SPLICOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
11847	24862	30705	4.64	1.0E-02	AW635521.1	EST_HUMAN	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
11861	24922		6.07	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12254	24898		1.53	1.0E-02	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12422	24982		4.42	1.0E-02	X62694.1	NT	H. sapiens gene for Me491/CD63 antigen
							WH4209.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
826	13539	26057	3.16	9.0E-03	AI796126.1	EST_HUMAN	MER22 MER22 repetitive element
1307	13901		1.26	9.0E-03	BE781889.1	EST_HUMAN	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3673346 5'
2439	15006	27578	3.82	9.0E-03	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2449	15016	27598	0.87	9.0E-03	AF099634.1	NT	Mus musculus MHC class III protein RP1 (Rp1) mRNA, partial cds
2831	15547	28022	0.61	9.0E-03	AI251744.1	EST_HUMAN	qh90109.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
2831	15547	28023	0.61	9.0E-03	AI251744.1	EST_HUMAN	qh90109.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3731	16332	28798	0.8	9.0E-03	J05184.1	NT	S. acidocaldarius thermophilin gene, complete cds
5978	18588		1.17	9.0E-03	AI809792.1	EST_HUMAN	wf77104.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361631 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6741	19335		4.24	9.0E-03	BE745988.1	EST_HUMAN	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'
7487	20010	32878	0.73	9.0E-03	8922570	NT	Homo sapiens hypothetical protein FLJ10850 (FLJ10850), mRNA
7818	20359		0.83	9.0E-03	AL039991.1	EST_HUMAN	DKFZp434L0412_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0412 5'
8191	20732		0.56	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9759	22257	35240	0.5	9.0E-03	P26011	SWISSPROT	INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M290 IEL ANTIGEN)
9778	22274	35259	1.26	9.0E-03	P20908	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
10865	23386		1.8	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
10891	23412	36431	1.71	9.0E-03	BE3395380.1	EST_HUMAN	601310881F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632181 5'
11505	23954	37022	1.58	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
11505	23954	37023	1.58	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
12001	25111		1.79	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-409 HT0452 Homo sapiens cDNA
12221	25105		36.8	9.0E-03	BE348385.1	EST_HUMAN	hw17609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
12319	24508	30843	1.38	9.0E-03	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
12539	24649		31.87	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-409 HT0452 Homo sapiens cDNA
527	13159		2.87	8.0E-03	AA723007.1	EST_HUMAN	zh30e03.e1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413598 3' similar to contains Alu repetitive element;
1026	13637	26152	35.57	8.0E-03	AF106656.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2203	14779	27351	1.26	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3351	15959	28436	0.98	8.0E-03	BE171225.1	EST_HUMAN	RC1-HT0545-120200-011-b09 HT0545 Homo sapiens cDNA
3404	16013	28482	0.89	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3738	16339	28605	1.77	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3738	16339	28606	1.77	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4343	16930	29371	1.19	8.0E-03	BE840049.1	EST_HUMAN	QV0-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4472	17058	28505	6.36	8.0E-03	BF363327.1	EST_HUMAN	GM4-NN0118-300600-223-b05 NN0118 Homo sapiens cDNA
5378	17937	30350	1.02	8.0E-03	U02970.1	NT	Prototheca wickerhamii 263-11 complete mitochondrial DNA
5410	17987	30376	0.88	8.0E-03	P01871	SWISSPROT	IG MU CHAIN C REGION
5714	18340	30846	2.89	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lapasin, RajGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
6346	24762	31730	1.34	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (217)
6846	19436	32251	4.45	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
6999	19497		1.72	8.0E-03	V01109.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7259	19787	32643	1.8	8.0E-03	M17197.1	NT	A. californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7547	20087		1.84	8.0E-03	AB038287.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
8816	21355	34279	0.62	8.0E-03	P98160	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
8841	21380	34304	3.73	8.0E-03	AW808692.1	EST_HUMAN	PRECURSOR (HSPG) (PERLECAN) (PLC)
8910	21448	34370	0.68	8.0E-03	9789956	NT	MR1-ST0111-111199-011-h06 ST0111 Homo sapiens cDNA
9859	22358		4.76	8.0E-03	BE086509.1	EST_HUMAN	Mus musculus fusion 2 (human) (Fus2), mRNA
10864	23385		3.01	8.0E-03	Z48652.1	NT	QV1-BT0877-040400-131-q03 BT0877 Homo sapiens cDNA
11259	23789	36845	1.97	8.0E-03	AA828817.1	EST_HUMAN	S. cerevisiae chromosome X reading frame ORF YJR152w
11259	23789	36846	1.97	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCL CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
11562	24009	37079	4.96	8.0E-03	AF084589.1	NT	cd80a09.s1 NCL CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
11713	24123		2.81	8.0E-03	M68035.1	NT	Homo sapiens melanoma-associated antigen (IMAGE-C1) gene, complete cds
11761	24154		5.99	8.0E-03	AB038181.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
723	13343	25833	14.03	7.0E-03	AF097183.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
723	13343	25834	14.03	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1012	13622	26137	5.78	7.0E-03	AF243376.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1155	13758	26268	3.21	7.0E-03	AV731712.1	EST_HUMAN	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1408	14001		1.28	7.0E-03	Q61060	SWISSPROT	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1439	14032	26560	4.09	7.0E-03	AA668298.1	EST_HUMAN	FORKHEAD BOX PROTEIN D3 (HNF3/TFH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFH-2)
1550	14142	26675	3.14	7.0E-03	AW303599.1	EST_HUMAN	ab78b09.s1 Stratiogene fetal retina 837202 Homo sapiens cDNA clone IMAGE:853145 3'
2297	15462	27447	2.12	7.0E-03	P04929	SWISSPROT	xv21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
3614	16217	28696	0.58	7.0E-03	AI150273.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3830	16430	28892	0.91	7.0E-03	AW444463.1	EST_HUMAN	q734h02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'
3885	16483	28945	1.01	7.0E-03	AF196344.1	NT	UI-H-B13-akb-c-10-0-UI.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4091	16430	28892	0.63	7.0E-03	AW444463.1	EST_HUMAN	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4704	17286		1.1	7.0E-03	AW630888.1	EST_HUMAN	UI-H-B13-akb-c-10-0-UI.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
5125	17697		2.08	7.0E-03	AL163278.2	NT	hh89a05.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969836 5'
5985	18605		0.79	7.0E-03	H71106.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
6280	24760		5.32	7.0E-03	AW861059.1	EST_HUMAN	yr82g01.r1 Soares_fetal_liver_spleen_1NFSL Homo sapiens cDNA clone IMAGE:211824 5' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN)
6456	19057	31842	1.45	7.0E-03	W68251.1	EST_HUMAN	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA
6658	19254	32056	2.88	7.0E-03	AA327129.1	EST_HUMAN	zd33f10.r1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:342475 5'
							EST30874 Colon1 Homo sapiens cDNA 5' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value :	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6881	19277	32080	0.92	7.0E-03	BE6857385.1	EST_HUMAN	7q34b10.x1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
7139	19519	32341	2.12	7.0E-03	BE928133.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 384D8_2; contains TAR1;2 TAR1 TARI repetitive element;
7528	20049	32921	5.78	7.0E-03	Z35838.1	NT	Q13387 HYPOTHETICAL PROTEIN 384D8_2; contains TAR1;2 TAR1 TARI repetitive element;
7529	20049	32922	5.78	7.0E-03	Z35838.1	NT	S cerevisiae chromosome II reading frame ORF YBL077w
7789	20332	33238	0.54	7.0E-03	AJ229043.1	NT	S cerevisiae chromosome II reading frame ORF YBL077w
7789	20332	33239	0.54	7.0E-03	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8055	20597	33504	2.36	7.0E-03	BE175687.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8318	21832		0.6	7.0E-03	AF111168.2	NT	RC5-HT0582-160300-011-002 HT0582 Homo sapiens cDNA
9513	22013	34972	0.87	7.0E-03	N52378.1	EST_HUMAN	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
9636	22136	35101	2.48	7.0E-03	P48982	SWISSPROT	yv49c10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains
9636	22136	35102	2.48	7.0E-03	P48982	SWISSPROT	Alu repetitive element;
10207	22702		0.99	7.0E-03	AV687379.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10381	22875		0.93	7.0E-03	AI799734.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10706	23235	36248	3.48	7.0E-03	AB008852.1	NT	AV687379 GKC Homo sapiens cDNA clone GKCAFC07 5'
10780	23304	36311	1.61	7.0E-03	AJ004882.1	NT	we37609.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2320840 3'
10780	23304	36312	1.61	7.0E-03	AJ004882.1	NT	Bos taurus mRNA for NDP52, complete cds
10930	23448		1.66	7.0E-03	AJ242804.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
12273	25095		1.83	7.0E-03	H94065.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12281	24484		1.58	7.0E-03	BE263253.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12382	24549		1.88	7.0E-03	Y17455.1	NT	Sporobolus stiptianus mRNA for putative glycine and proline-rich protein
12527	25092		1.38	7.0E-03	AL163300.2	NT	yv15h01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains
12664	24734		3.16	7.0E-03	AW868110.1	EST_HUMAN	Alu repetitive element;
1283	13878	26400	10.8	6.0E-03	AW511148.1	EST_HUMAN	G01145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
1283	13879	26401	10.8	6.0E-03	AW511148.1	EST_HUMAN	Homo sapiens LSFR2 gene, penultimate exon
2800	15352	27921	1.82	6.0E-03	AF112374.1	NT	Homo sapiens chromosome 21 segment HS21C100
2916	15533	28004	3.54	6.0E-03	AA759135.1	EST_HUMAN	RCO-SN0052-110400-021-a04 SN0052 Homo sapiens cDNA
2916	15533	28005	3.54	6.0E-03	AA759135.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
3283	15894		2.17	6.0E-03	H75690.1	EST_HUMAN	SW:PXN_HUMAN O75469 ORPHAN NUCLEAR RECEPTOR PXR;
							SW:PXN_HUMAN O75469 ORPHAN NUCLEAR RECEPTOR PXR;
							Danio rerio odorant receptor gene cluster
							ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
							ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
							y77h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'

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3344	15954		0.79	6.0E-03	AF190338.1	NT	Notoncus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3429	16037	28518	1.14	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3429	16037	28519	1.14	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3600	16204		1.13	6.0E-03	W37985.1	EST_HUMAN	zc13a1.1 r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3721	16322	28789	2.6	6.0E-03	BF510986.1	EST_HUMAN	UI-HB14-apm-c-06-0-UI.s1 NCJ_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3757	16358	28828	1.53	6.0E-03	BE077356.1	EST_HUMAN	RC1-B10606-260400-014-a07 BT0908 Homo sapiens cDNA
3845	16444	28905	1.14	6.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnp1), mRNA
3995	16593	29066	0.83	6.0E-03	AW847284.1	EST_HUMAN	RC0-CT0204-240998-021-b10 CT0204 Homo sapiens cDNA
4030	16628		0.92	6.0E-03	BE250108.1	EST_HUMAN	600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959513 5'
4419	17004		1.1	6.0E-03	N56946.1	EST_HUMAN	yy62h10.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278179 3'
4454	17040		1.58	6.0E-03	A016833.1	EST_HUMAN	ox33c11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4805	17363	29833	8.21	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' and similar to EST containing Alu repeat
5280	17852		0.92	6.0E-03	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
6301	24761	31680	0.72	6.0E-03	9827521	NT	Variola virus, complete genome
6908	19840	32476	0.73	6.0E-03	O14994	SWISSPROT	SYNAPSIN III
6939	18047	30469	0.72	6.0E-03	BE253748.1	EST_HUMAN	601112333F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7642	20154	33040	0.76	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
7774	20283	33180	24.22	6.0E-03	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55 ow13a04.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element;
7799	20342	33251	6.91	6.0E-03	A033980.1	EST_HUMAN	RC0-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
7915	20457	33363	2.45	6.0E-03	AW799337.1	EST_HUMAN	601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858626 5'
7990	20532		1.59	6.0E-03	BF038186.1	EST_HUMAN	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
9473	21872	34821	8.46	6.0E-03	D10548.1	NT	tt22c02.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
9956	22451		2.15	6.0E-03	A1432661.1	EST_HUMAN	P40429 60S RIBOSOMAL PROTEIN L13A ;
10067	22562	35557	0.73	6.0E-03	AJ011849.1	NT	Bacillus subtilis fnd gene
10197	22692		0.91	6.0E-03	AF084555.1	NT	Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10303	22797	35788	0.63	6.0E-03	X68366.1	NT	M.thermoformicum complete plasmid pFV1 DNA
10823	23155	36168	2.04	6.0E-03	AW982164.1	EST_HUMAN	EST374237 IMAGE resequences, MAGG Homo sapiens cDNA
10890	23220		2.23	6.0E-03	11545814	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10726	23252	36289	2.16	6.0E-03	A1420786.1	EST_HUMAN	te91c12.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.
10726	23252	36270	2.16	6.0E-03	A1420786.1	EST_HUMAN	te91c12.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.
10851	23382		2.08	6.0E-03	U14556.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
10852	23383	36401	2.4	6.0E-03	BE737895.1	EST_HUMAN	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
11630	24072	37134	1.57	6.0E-03	H70296.1	EST_HUMAN	y95f01.1f Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213049 5' similar to SP-6PGD_PIG P14332 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING ;
11828	24195		3.52	6.0E-03	AF010496.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
11956	24848		5.1	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450296 (section 39 of 148) of the complete genome
12039	24914		3.02	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pog1) gene, complete cds
12088	24357		1.61	6.0E-03	Q62209	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
12402	24561		1.49	6.0E-03	BE789019.1	EST_HUMAN	601482621F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885388 5'
12418	24571		1.52	6.0E-03	AJ245480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
12556	24942		1.6	6.0E-03	X74807.1	NT	R. norvegicus VEGP2 gene
229	12889	25375	5.16	5.0E-03	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, JPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQ82 and RING8, 9, 13 and 14 genes
697	13320	25806	1.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
697	13320	25807	1.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
698	13320	25806	2.74	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
698	13320	25807	2.74	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
1151	13754	26284	0.91	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
2706	15263	27830	2.77	5.0E-03	AB033008.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2952	15578	28057	0.66	5.0E-03	BE266057.1	EST_HUMAN	601194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5'
3170	15784	28256	4.54	5.0E-03	T87623.1	EST_HUMAN	yc81f09.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22395 3'
3189	15801		2.22	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3202	15814	28289	1.15	5.0E-03	R71794.1	EST_HUMAN	y86g02.s1 Soares breast 2NDHBst Homo sapiens cDNA clone IMAGE:155666 3'
3316	15928		0.86	5.0E-03	AJ297357.1	NT	Homo sapiens partial LMD1 gene for LIM domains containing protein 1 and KIAA0851 gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3728	18328	28795	5.04	5.0E-03	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
3762	16363	28831	4.88	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds
3822	18422	28884	0.68	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4043	16641		1.78	5.0E-03	AA289675.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4204	18793	29239	0.57	5.0E-03	AJ002125.1	NT	Matrix domestica Zfx type gene
4392	16978	29425	0.88	5.0E-03	H78355.1	EST_HUMAN	yu78g10.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:240066 5'
4394	18422	28884	0.71	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4670	17252	29704	0.68	5.0E-03	U46691.1	NT	Human putative chromatin structure regulator (SUPT6H) mRNA, complete cds
4714	17265	29739	0.8	5.0E-03	AJ131016.1	NT	Homo sapiens SOL gene locus
4828	17406	29860	1.72	5.0E-03	AI752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
5087	17840	30083	1.02	5.0E-03	P15285	SWISSPROT	SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
5381	17949	30382	0.95	5.0E-03	AF171666.1	NT	Bos taurus acidic alpha-glucosidase gene, exons 2 through 20 and complete cds
5954	18598	31320	7.68	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
							PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLSTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
6195	18805	31574	2.33	5.0E-03	O00507	SWISSPROT	Chlamydomonas reinhardtii AR39, section 62 of 94 of the complete genome
6230	18839		0.91	5.0E-03	AE002234.2	NT	600944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860871 3'
6708	18302		10.88	5.0E-03	BE300091.1	EST_HUMAN	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
6832	18040	30483	6.39	5.0E-03	AB025024.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7106	18446		0.85	5.0E-03	AB038267.1	NT	RC3-CT0255-031099-011-407 CT0255 Homo sapiens cDNA
7595	20109		1.16	5.0E-03	AW854327.1	EST_HUMAN	Homo sapiens MASL1 mRNA, complete cds
7744	20252	33146	7.43	5.0E-03	AB016816.1	NT	RC6-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8162	20703	33618	1	5.0E-03	AW855907.1	EST_HUMAN	RC6-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8181	20722	33636	2.26	5.0E-03	P48992	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8548	21087		6.38	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
8742	21281	34204	1.47	5.0E-03	D80723.1	NT	Escherichia coli genomic DNA, (19.1 - 19.4 min)
8870	21409	34333	0.69	5.0E-03	M25090.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
9503	22003	34960	0.45	5.0E-03	P33750	SWISSPROT	SOF1 PROTEIN
9753	22251	35234	0.82	5.0E-03	L21710.1	NT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds
9881	22378	35354	0.77	5.0E-03	AW821888.1	EST_HUMAN	RC0-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
10082	22557	35552	0.49	5.0E-03	AA533143.1	EST_HUMAN	h46h10.s1 NC1_CGAP_Pf8 Homo sapiens cDNA clone IMAGE:995587

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10236	22731	35722	0.92	5.0E-03	7662557	NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10599	23133		10.33	5.0E-03	T19586.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
10631	23163	36175	2.28	5.0E-03	D26273.1	NT	Unknown nitrogen-fixing bacteria nifD gene encoding alpha subunit of dinitrogenase (MoFe protein)
10819	23340	36354	2.94	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCEC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1, L2 L1 repetitive element ;
10819	23340	36355	2.94	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCEC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1, L2 L1 repetitive element ;
10820	23439	36460	2.02	5.0E-03	T49163.1	EST_HUMAN	y09e04.r1 Stratagene placenta (#337225) Homo sapiens cDNA clone IMAGE:70686 5'
11212	23715		3.91	5.0E-03	BE048055.1	EST_HUMAN	tz46c04.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291622 5'
11972	25054		8.12	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12111	24372		21.73	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
12217	24440		1.81	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12250	24481		1.78	5.0E-03	AA456597.1	EST_HUMAN	zx75e03.s1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:809548 3' similar to SW.DX.A2 MOUSE P14685 PROBABLE DIPHENOL OXIDASE A2 COMPONENT ;
12283	24856		5.46	5.0E-03	BF572332.1	EST_HUMAN	60207774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
12473	24598	30883	2.21	5.0E-03	AW449109.1	EST_HUMAN	UIH-BJ3-akf-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'
12499	24932		1.42	5.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN)(LC COLLAGEN)
253	12813	25397	2.58	4.0E-03	AW500196.1	EST_HUMAN	UIHF-BN0-akc-h-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078831 5'
343	12895	25480	1.77	4.0E-03	R46482.1	EST_HUMAN	y051e04.s1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:35988 3'
468	13101	25594	0.69	4.0E-03	P54675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE)(PTDINS-3-KINASE)(PI3K)
629	13256	25730	3.12	4.0E-03	AA938339.1	EST_HUMAN	on75g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562566 3'
910	13523	26043	1.75	4.0E-03	R46482.1	EST_HUMAN	y051e04.s1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:35988 3'
944	13557		3.19	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-f01 BT0333 Homo sapiens cDNA
1180	13791	26302	25.91	4.0E-03	AA099777.1	EST_HUMAN	zib1e08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
1211	13811	26325	1.71	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1346	13941	28463	1.4	4.0E-03	AA284374.1	EST_HUMAN	zaf59a01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1630	14222		1.06	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAKB06 5'
1779	14369	26913	2.74	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-46 mRNA, complete cds
2062	14642	27217	14.12	4.0E-03	AA099777.1	EST_HUMAN	zib1e08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
2289	14863		1.62	4.0E-03	BE410556.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2317	14889	27464	2.63	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA

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2608	15170	27737	1.6	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2608	15170	27738	1.6	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2715	15272	27838	3.14	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2715	15272	27839	3.14	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2721	15277	27842	1.25	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3282	15874	28355	1.07	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-h08 HT0340 Homo sapiens cDNA
3282	15874	28356	1.07	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-h08 HT0340 Homo sapiens cDNA
3583	16187	28689	0.85	4.0E-03	AW188426.1	EST_HUMAN	x9804.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2665279 3'
3583	16187	28690	0.85	4.0E-03	AW188426.1	EST_HUMAN	x9804.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2665279 3'
3695	16286	28755	0.63	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 51 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3696	16297	28767	0.63	4.0E-03	AV646253.1	EST_HUMAN	AV646253 GLC Homo sapiens cDNA clone GLCALD02 3'
4087	16983		1.93	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
4323	16909	28350	1.88	4.0E-03	AJ768727.1	EST_HUMAN	w87a06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400274 3'
5307	17869	30281	2.1	4.0E-03	AW103719.1	EST_HUMAN	xe83d03.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2814469 3' similar to contains L1.1 L1 L1 repetitive element
5354	17914	30329	1.17	4.0E-03	AA699895.1	EST_HUMAN	z68b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:436009 3'
5433	17899	30395	1.19	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5480	18114	30523	1.36	4.0E-03	AF005859.1	NT	Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds
5586	18228	30873	21.16	4.0E-03	AF168825.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5963	18585	31319	3.31	4.0E-03	P04196	SWISSPROT	(HPRG)
5965	18587	31321	1.56	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELLED TROPHOZOITE ANTIGEN PRECURSOR
6042	18661	31400	0.97	4.0E-03	AL133871.1	EST_HUMAN	DKFZp7611014_j1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7611014 5'
6235	18844		3.41	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
6381	18985	31765	0.98	4.0E-03	AW590572.1	EST_HUMAN	hg46c07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2948652 3'
6451	19052	31837	1.95	4.0E-03	BE548453.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6775	19367	32179	1.04	4.0E-03	AA813222.1	EST_HUMAN	g82111.s1 Soares_testis_NHT Homo sapiens cDNA clone 1382045 3'
6872	19608	32440	1.51	4.0E-03	U76408.1	NT	Lycopodium obscurum knotted 3 protein (TKn3) mRNA, complete cds
7130	19470	32288	1.13	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7130	19470	32289	1.13	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7249	19778	32633	5.45	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)

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7459	19982	32847	1.14	4.0E-03	AI681483.1	EST_HUMAN	b37g12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7481	19984	32849	0.95	4.0E-03	BE670170.1	EST_HUMAN	7e31b02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7883	20425	33334	0.63	4.0E-03	Q9TT92	SWISSPROT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5)
7892	20534	33438	4.22	4.0E-03	AF111944.1	NT	(ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
8145	20686	33598	1.84	4.0E-03	7682087	NT	Dictyostelium discoideum AX4 development protein DG1122 (DG1122) gene, partial cds
8848	21187	34105	6.89	4.0E-03	AI553983.1	EST_HUMAN	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
8821	21360		4.46	4.0E-03	AL163209.2	NT	le48b1.1, x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element
8830	21369	34293	3.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C009
8840	22338	35319	0.78	4.0E-03	H30684.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
10278	22773	35782	0.7	4.0E-03	AL161555.2	NT	yp42g12.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190150 5'
11009	23523	36557	6.06	4.0E-03	AL163206.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
11393	23845	36906	1.69	4.0E-03	AI208703.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C006
11607	24050	37116	1.62	4.0E-03	AE002102.1	NT	qg56c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839176 3'
11938	25071		10.45	4.0E-03	BE815173.1	EST_HUMAN	qg56c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839176 3'
11982	24284		1.62	4.0E-03	BE268290.1	EST_HUMAN	Ureaplasma urealyticum section 3 of 59 of the complete genome
12047	24331		2.71	4.0E-03	AW504273.1	EST_HUMAN	PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA
12294	24493		3.86	4.0E-03	BF224125.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12341	24975		2.24	4.0E-03	AW614598.1	EST_HUMAN	UI-HF-BN0-dip-g-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12352	24532		3.01	4.0E-03	AW819141.1	EST_HUMAN	7q74c08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains Alu repetitive element; contains element MER31 repetitive element
394	13040	25531	1.73	3.0E-03	AF011920.1	NT	hh02c07.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR5 repetitive element
812	13525	26044	5.57	3.0E-03	AF011920.1	NT	RC3-ST0281-240400-015-f03 ST0281 Homo sapiens cDNA
1701	14294	26829	2.85	3.0E-03	AA468110.1	EST_HUMAN	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
2298	14871		1.76	3.0E-03	AF055066.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
2333	14904		4.14	3.0E-03	Z32521.1	NT	nc73c05.s1 NCL_CGAP_P22 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element
2334	14905	27475	1.03	3.0E-03	U48858.1	NT	Homo sapiens MHC class 1 region
2334	14905	27476	1.03	3.0E-03	U48858.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2448	15015	27587	1.13	3.0E-03	AF240786.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
							Mus musculus intestinal trefoil factor gene, partial cds
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3022	15638		0.68	3.0E-03	Y08006.1	NT	Arabidopsis thaliana poMt gene
3119	15733	28203	3.25	3.0E-03	BE378286.1	EST_HUMAN	601237862F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608933 5'
3186	15798	28270	3.21	3.0E-03	AW802687.1	EST_HUMAN	IL2-UM0076-240300-068-D03 UM0076 Homo sapiens cDNA
3464	16071	28544	2.13	3.0E-03	U34606.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3473	16079		7.31	3.0E-03	Y12500.1	NT	C.elegans semdc gene
4049	16846	29114	7.57	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4049	16846	29115	7.57	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4109	16703	29156	1.75	3.0E-03	AI792278.1	EST_HUMAN	an04f09.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4485	17070	29520	6.2	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4560	17143		0.71	3.0E-03	BE348739.1	EST_HUMAN	h68g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151634 3'
4616	17199	29647	5.73	3.0E-03	AI536141.1	EST_HUMAN	xu8.P10.H3 conorm Homo sapiens cDNA 3'
4960	17535	29877	2.45	3.0E-03	AI732754.1	EST_HUMAN	ab18a08.x5 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
4978	17553	29895	6.1	3.0E-03	BE787945.1	EST_HUMAN	601482715F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3885483 5'
5069	17842	30084	1.01	3.0E-03	AJ007044.1	NT	Oryctolagus Cuniculus sod gene
5069	17842	30085	1.01	3.0E-03	AJ007044.1	NT	Oryctolagus Cuniculus sod gene
5470	18104	30423	3.56	3.0E-03	8922499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5744	18370	31078	1.18	3.0E-03	AJ246981.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5809	18434	31155	13.97	3.0E-03	U35323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6670	19266	32070	10.41	3.0E-03	AA456701.1	EST_HUMAN	aat3f10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7256	19784	32640	1.45	3.0E-03	AJ011419.1	NT	Kluveromyces marxianus pep3 gene for purine-cytosine permease
7531	20051	32924	3.37	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
7879	20421	33329	0.91	3.0E-03	BF333058.1	EST_HUMAN	RC0-BT0812-250900-032-e07 B T0812 Homo sapiens cDNA
7879	20421	33330	0.91	3.0E-03	BF333058.1	EST_HUMAN	RC0-BT0812-250900-032-e07 B T0812 Homo sapiens cDNA
8097	20636	33549	4.71	3.0E-03	N92580.1	EST_HUMAN	zb27b04.s1 Soares_parathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:304783 3'
8257	20798		0.55	3.0E-03	M63498.1	NT	S. cerevisiae UGA35 gene, complete cds
8397	20937	33860	1.11	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8419	20959	33877	1.31	3.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
8622	21081		1.37	3.0E-03	Q9QM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
8922	21460		12.62	3.0E-03	AW613774.1	EST_HUMAN	hh80f10.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2669131 3' similar to contains L1.11 L1 repetitive element
8976	21513	34436	4.44	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8999	21536	34466	6.98	3.0E-03	A1016731.1	EST_HUMAN	0x03d12.x1 NCL_CGAP_K103 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_rna1
9008	21545	34474	0.92	3.0E-03	BF338078.1	EST_HUMAN	HISTONE H2B.2 (HUMAN);
9330	21844		1	3.0E-03	D90901.1	NT	602035980.F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183938 5'
9368	20307	33210	0.66	3.0E-03	BE154670.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
9554	22054		0.67	3.0E-03	P03355	SWISSPROT	PM3-HT03444-071299-003-d07 HT03444 Homo sapiens cDNA
9623	22123		5.92	3.0E-03	P08672	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
							CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
							RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;
9809	22307	35291	1.58	3.0E-03	P11389	SWISSPROT	ENDONUCLEASE]
9907	22404	35379	1.3	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10046	22541	35538	3.96	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10728	23254		4.26	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11257	23787	36843	2.21	3.0E-03	AF009222.1	NT	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds
11321	23019	36028	1.99	3.0E-03	AF266285.1	NT	Homo sapiens gadinin-like protein (GLP) gene, complete cds
11354	23808	36887	3.96	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11354	23808	36888	3.96	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11707	24869		2.32	3.0E-03	A1525056.1	EST_HUMAN	promrna-5.E07.r bvtumor Homo sapiens cDNA 5'
							0x77b10.s1 Soares_t0tal_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1622779 3' similar to
11743	24142	36763	1.31	3.0E-03	AA993154.1	EST_HUMAN	contains L1.13 MER26 repetitive element;
11804	25007		1.81	3.0E-03	AB009668.1	NT	Homo sapiens gene for GMP-N-acetylneuraminic acid hydroxylase, partial cds
11988	24298	30984	2.67	3.0E-03	AJ298282.1	NT	Rattus norvegicus mRNA for connexin38 (cx36 gene)
541	13172	25651	0.8	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
541	13172	25652	0.8	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
818	15426		11.05	2.0E-03	T70874.1	EST_HUMAN	yJ15h03.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:108341 5'
1407	14000	28529	2.25	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1410	14003	26531	1.35	2.0E-03	AA661805.1	EST_HUMAN	nu86f01.s1 NCL_CGAP_AVI1 Homo sapiens cDNA clone IMAGE:1217593
1418	14011	26540	20.86	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRG2 (DRG2) gene, complete cds
							PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN
1536	14128	26664	1.04	2.0E-03	P48509	SWISSPROT	SFA-1) (CD151 ANTIGEN)
							Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome
1563	14155	26686	2.05	2.0E-03	4557836	NT	type VI) (PLOD) mRNA
1563	14155	26687	2.05	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome
1635	14227		5.58	2.0E-03	P29400	SWISSPROT	type VI) (PLOD) mRNA
							COLLAGEN ALPHA 5(V) CHAIN PRECURSOR

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1807	14397	26942	1.01	2.0E-03	AA450138.1	EST_HUMAN	z42a10.1 Soares_tetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1922	14507		0.89	2.0E-03	BE144908.1	EST_HUMAN	CM2-HT0183-061099-018-003 HT0183 Homo sapiens cDNA
2038	14620	27188	1.25	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2291	14855	27440	0.97	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2816	15177		4.13	2.0E-03	AW137782.1	EST_HUMAN	UI-H-B11-adi-g-10-Q-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3463	16070	28543	4.95	2.0E-03	AA450138.1	EST_HUMAN	z42a10.1 Soares_tetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3470	16076	28549	0.76	2.0E-03	BF568955.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3729	16330	28796	5.87	2.0E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, PP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
4024	16622	29094	0.89	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4191	16780	29228	2.48	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
4302	16888		12.85	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4502	17086		1.09	2.0E-03	L35079.1	NT	Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds
4518	17102		1.34	2.0E-03	AW297380.1	EST_HUMAN	UI-H-BW0-air-g-03-Q-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3'
4523	17107	29553	0.86	2.0E-03	A1064746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4844	17228	29681	1.82	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4844	17228	29681	1.82	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4821	17399		1.92	2.0E-03	R87773.1	EST_HUMAN	yo45902.s1 Soares_adult_brain_N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
4848	17426	29878	5.2	2.0E-03	AA909466.1	EST_HUMAN	cl4105.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1523457 3'
5187	17736	30163	0.81	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5428	17985		0.9	2.0E-03	AF205087.1	NT	Desulfotrio desulfuricans cytochrome c3 precursor (cycA) gene, complete cds
5878	18305	30787	1.16	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5810	24749	31156	2.28	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0093 protein, partial cds
5887	18510	31236	2.11	2.0E-03	U63711.1	NT	Xenopus laevis xefilin mRNA, complete cds
6258	18867	31636	4.06	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6258	18867	31637	4.06	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6488	19087	31869	2.38	2.0E-03	Q85203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6488	19087	31870	2.38	2.0E-03	Q85203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6488	19089	31872	7	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6521	19121	31912	2.17	2.0E-03	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
8546	19144	31940	1.46	2.0E-03	X94451.1	NT	L. esculentum mRNA for lyses-tRNA synthetase (LysRS)

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6745	19309		2.03	2.0E-03	A1991089.1	EST_HUMAN	wu36h08.x1 Soares Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW/RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ; contains element MSR1 repetitive element ;
7038	18058	30480	0.89	2.0E-03	AB038502.1	NT	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
7104	19874	32513	1.54	2.0E-03	5031864	NT	Homo sapiens lipoma HMGIc fusion partner (LHFP) mRNA
7104	19874	32514	1.54	2.0E-03	5031864	NT	Homo sapiens lipoma HMGIc fusion partner (LHFP) mRNA
7141	19521	32343	3.59	2.0E-03	BE067886.1	EST_HUMAN	CM4-BT0368-061299-054-d01 BT0368 Homo sapiens cDNA
7198	19729	32580	0.7	2.0E-03	A1298883.1	EST_HUMAN	qm98d11.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898885 3'
7335	19882	32726	0.87	2.0E-03	T86569.1	EST_HUMAN	yd77g10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:114306 5'
7613	20126	33003	1.49	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
7995	20537	33440	2.47	2.0E-03	AW592004.1	EST_HUMAN	h37b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR.Q60976 Q60976 JERKY. ;
8159	20700	33614	5.96	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1 b2 L1 repetitive element ;
8159	20700	33615	5.96	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1 b2 L1 repetitive element ;
8208	20749	33662	0.52	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C6G9.05 IN CHROMOSOME 1
8229	20769	33688	0.94	2.0E-03	P19137	SWISSPROT	LAMIN ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8282	20823	33743	0.82	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8282	20823	33744	0.82	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8307	20848	33771	0.8	2.0E-03	AU136878.1	EST_HUMAN	AU136879 PLACE1 Homo sapiens cDNA clone PLACE1004839 5'
8358	20898		2.04	2.0E-03	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
9123	18508	31233	0.69	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9123	18508	31234	0.69	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9164	21699	34643	0.85	2.0E-03	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9445	21971	34920	0.99	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194296 3'
9445	21971	34921	0.99	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194296 3'
							TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEI) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
9477	21876	34823	2.57	2.0E-03	P24821	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9585	22085	35049	1.03	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9585	22085	35050	1.03	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9639	22139	35105	0.54	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9639	22139	35108	0.54	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9829	22327	35308	0.99	2.0E-03	AW884269.1	EST_HUMAN	QV3-OT0064-060400-144-e01 OT0064 Homo sapiens cDNA
9956	22450		4.55	2.0E-03	AA251376.1	EST_HUMAN	Zs10a06.e1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684764 3'
10894	23415		3.24	2.0E-03	M86524.1	NT	Human dystrophin gene
11361	20126	33003	2.13	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11417	23868		2.25	2.0E-03	BF330909.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11424	23875	36939	13.97	2.0E-03	Z11740.1	NT	H.sapiens variable number tandem repeat (VNTR) locus DNA
11687	24103		3.17	2.0E-03	A1625745.1	EST_HUMAN	Y65h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE
11705	24118	37151	4.77	2.0E-03	AF157516.2	NT	Q25932 VACUOLAR ATP SYNTHASE SUBUNIT G;
11730	24135	37155	1.94	2.0E-03	A1084325.1	EST_HUMAN	Homo sapiens SEL1L (SEL1L) gene, partial cds
11754	18032		8.96	2.0E-03	AJ245167.1	NT	oy43g06.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1668634 3' similar to
11967	25050		2.34	2.0E-03	AV697966.1	EST_HUMAN	TR:P97535 P97535 PS-PLA1 PRECURSOR.;
12062	24345	30984	1.49	2.0E-03	Y00508.1	NT	Camelus dromedarius cchp19 gene for immunoglobulin heavy chain variable region
							AV697966 GKC Homo sapiens cDNA clone GKCXGD05 5'
							H. sapiens M1 gene for muscarinic acetylcholine receptor
12372	24542		2.06	2.0E-03	AF129758.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b,
12551	24849		5.07	2.0E-03	AV697966.1	EST_HUMAN	CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
464	13098	25589	1.33	1.0E-03	H96471.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCXGD05 5'
862	13477	25992	1.47	1.0E-03	A1720263.1	EST_HUMAN	y88c08.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
							as70b08.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
862	13477	25993	1.47	1.0E-03	A1720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE.;
1134	13737	26246	2.21	1.0E-03	A1865788.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1154	13757	26287	1.31	1.0E-03	A1954572.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE.;
1208	13809	26321	1.67	1.0E-03	A1692616.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
2074	14654	27227	4.05	1.0E-03	P47808	SWISSPROT	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE.;
2199	14775	27348	9.99	1.0E-03	AJ131016.1	NT	wk86a08.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
3008	15624	28102	1.45	1.0E-03	AB033117.1	NT	wk86a10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
							wk86a01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu
							repetitive element;
							HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMWMI)
							Homo sapiens SCL gene locus
							Homo sapiens mRNA for KIAA1291 protein, partial cds
							CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED
							CARBONIC ANHYDRASE)(SALIVARY CARBONIC ANHYDRASE)
3225	15637	28315	1.81	1.0E-03	P18915	SWISSPROT	

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3225	15837	28316	1.81	1.0E-03	P16915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3341	15951	28427	0.79	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
3596	16200	28683	0.65	1.0E-03	U69061.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3596	16200	28684	0.65	1.0E-03	U69061.1	NT	Human MUC2 gene, promoter region
3727	16328		1.31	1.0E-03	AB044400.1	NT	Human MUC2 gene, promoter region
3997	16595	29087	0.75	1.0E-03	AW170552.1	EST_HUMAN	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4008	16606	29080	0.81	1.0E-03	Z49649.1	NT	contains TAR1.11 TAR1 repetitive element
4528	17112	29558	4.29	1.0E-03	BE939162.1	EST_HUMAN	S cerevisiae chromosome X reading frame ORF YJR149W
4574	17157	29601	5.77	1.0E-03	BE248538.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4770	17351	29803	0.83	1.0E-03	U29449.1	NT	TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4950	17525	29868	2.83	1.0E-03	A1073485.1	EST_HUMAN	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4950	17525	29867	2.83	1.0E-03	A1073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4951	17526		5.92	1.0E-03	BE154067.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
5236	17800	30219	11.45	1.0E-03	O48409	SWISSPROT	PM0-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5511	18144	30556	2.02	1.0E-03	AA290951.1	EST_HUMAN	APOLIPROTEIN A-IV PRECURSOR (APO-AIV)
5598	18228	30676	2.74	1.0E-03	AJ006345.1	NT	Zs44f01.11 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5647	18275	30749	1.7	1.0E-03	K03332.1	NT	Homo sapiens KVLQ11 gene
5647	18275	30749	1.7	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5647	18275	30750	1.7	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5761	18387	31101	0.92	1.0E-03	BE796491.1	EST_HUMAN	601589841F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954 5'
5766	18392	31105	1.72	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
6171	18783		2.62	1.0E-03	X07699.1	NT	Mouse nucleolin gene
6209	18819	31590	1.1	1.0E-03	BE963339.2	EST_HUMAN	601657519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875693 3'
6339	18945		8.29	1.0E-03	11528176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6476	19077	31860	1.21	1.0E-03	T87761.1	EST_HUMAN	yd83a11.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:115772 5'
6541	19140		1.4	1.0E-03	AW902585.1	EST_HUMAN	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA
6852	19441	32258	1.31	1.0E-03	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
7206	19737	32590	2.48	1.0E-03	D16826.1	NT	Human gene for fourth somatostatin receptor subtype
7498	20021		1.72	1.0E-03	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
7635	20147	33030	1.7	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrioleukodystrophy protein >

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7694	20203	33090	3.21	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7734	20242	33133	1.13	1.0E-03	BE880044.1	EST_HUMAN	601491081F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893276 5'
7830	20372	33279	0.57	1.0E-03	AF274581.1	NT	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
7891	20433	33342	5.79	1.0E-03	AJ251973.1	NT	Homo sapiens partial stearin-1 gene
8088	20627	33541	1.29	1.0E-03	AA122270.1	EST_HUMAN	z497c09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.11 L1 repetitive element;
8186	20727	33639	2.03	1.0E-03	AF153980.1	NT	Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8369	20909	33828	0.81	1.0E-03	U29397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
8530	21069	33988	0.52	1.0E-03	AA001613.1	EST_HUMAN	zh82e08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8530	21069	33989	0.52	1.0E-03	AA001613.1	EST_HUMAN	zh82e08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8873	21412		1.29	1.0E-03	Y11204.1	NT	V.carteri gene encoding volvoxopsin
8900	21438	34361	0.59	1.0E-03	AW840353.1	EST_HUMAN	CM3-LT0078-170200-092-e07 LT0079 Homo sapiens cDNA
9009	21549		0.68	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
9047	21584	34514	3.37	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9047	21584	34515	3.37	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9525	22025	34982	1.98	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
9525	22025	34983	1.96	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
9734	22232	35210	0.94	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE
10089	22563	35558	0.57	1.0E-03	AF003529.1	NT	PROTEOGLYCAN-II (DSPG)
10073	22588		0.75	1.0E-03	AF097485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10218	22713	35705	1.25	1.0E-03	AI024350.1	EST_HUMAN	ov75f08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643175 3' similar to contains MER39.b1 MER39 MER39 repetitive element;
10545	23082	36095	1.71	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
10545	23082	36096	1.71	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
10829	23161	36173	3.2	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
10703	23232		3.19	1.0E-03	AI583847.1	EST_HUMAN	tt73e12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR:Q26195 Q26195 PVA1 GENE;
11036	23550		3.78	1.0E-03	AV759949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
11682	24099	37149	4.46	1.0E-03	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12149	24392	30874	1.27	1.0E-03	9507208	NT	Rattus norvegicus transformation related protein 63 (Trp63), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12175	25030		5.99	1.0E-03	A1347355.1	EST_HUMAN	tc05h11.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element;
12282	25052	30510	5.72	1.0E-03	BE780372.1	EST_HUMAN	601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
5862	18484		1.63	9.0E-04	P08727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6612	19209	32017	1.08	9.0E-04	P02381	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1
9561	22061		1.56	8.0E-04	AB037203.1	NT	Glycyrrhiza glabra GgbAS1 mRNA for beta-amyrin synthase, complete cds
1535	14127		1.05	8.0E-04	X98469.1	NT	X laevis mRNA for C4SR protein
4289	16845		5.17	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4880	17455	26608	2.55	8.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11024	23538		2.15	8.0E-04	AA777084.1	EST_HUMAN	z124c10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377874 3'
11175	23682		2.5	8.0E-04	A1571089.1	EST_HUMAN	h85a08.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
12500	24626	30892	1.65	8.0E-04	AW575954.1	EST_HUMAN	PM2-H10353-130100-002-f10 HT0353 Homo sapiens cDNA
1867	14453	27012	0.99	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2442	16009	27681	0.92	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2739	15294	27861	1.75	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3319	15926	28406	1.23	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
6246	18855	31626	0.75	7.0E-04	AA518212.1	EST_HUMAN	ng65g12.s1 NCL_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1.b3 L1 L1 repetitive element;
6636	19232		2.63	7.0E-04	A1769331.1	EST_HUMAN	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
7279	19807		0.79	7.0E-04	AK024445.1	NT	Homo sapiens mRNA for FLJ00035 protein, partial cds
9719	22217	35191	0.57	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
9719	22217	35192	0.57	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11440	23890		3.42	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
11463	23913	36980	2.68	7.0E-04	Z40561.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12222	24443		11.57	7.0E-04	BE077941.1	EST_HUMAN	CM1-BT0614-110300-142-b12 B10614 Homo sapiens cDNA
12472	24597		4.94	7.0E-04	R17336.1	EST_HUMAN	yj13c06.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32298 5'
12505	24628		7.97	7.0E-04	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
2720	15276		0.93	6.0E-04	BF341380.1	EST_HUMAN	S02013339F1 NCL_CGAP_Bmf64 Homo sapiens cDNA clone IMAGE:4149297 5'
4033	16631	26100	1.61	6.0E-04	A1862525.1	EST_HUMAN	w15a11.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3'
4163	16754	29205	0.6	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4163	16754	29206	0.6	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4264	16850	29298	3.2	6.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
4538	17122	29867	0.93	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-f09 HT0560 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4538	17122	29588	0.93	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-180200-011-409 HT0560 Homo sapiens cDNA
5413	17970	30379	0.9	6.0E-04	AI906687.1	EST_HUMAN	RC-BT122-180399-057 BT122 Homo sapiens cDNA
5413	17970	30380	0.9	6.0E-04	AI906687.1	EST_HUMAN	RC-BT122-180399-057 BT122 Homo sapiens cDNA
7807	20350		3.04	6.0E-04	P46408	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
7858	20500		0.67	6.0E-04	H92947.1	EST_HUMAN	Y94c11.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231956 3' similar to contains LOR1 repetitive element
9890	22387		3.74	6.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586M2024
9924	22420		0.77	6.0E-04	AI858286.1	EST_HUMAN	w35g02.x1 NCI CGAP_U1 Homo sapiens cDNA clone IMAGE:2426830 3'
9992	22487	35475	2.18	6.0E-04	BE005850.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
10242	22737		0.64	6.0E-04	AF287478.1	NT	Lytichinus variegatus embryonic blastocoele extracellular matrix protein precursor (ECM3) mRNA, complete cds
11358	23812	36872	2.9	6.0E-04	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11441	23891	36958	5.11	6.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-aab-e-08-0-J1.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
11485	23944		2.28	6.0E-04	Q01768	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
11859	24928		3.55	6.0E-04	AW380519.1	EST_HUMAN	RC1-HT0269-261199-012-d08 HT0269 Homo sapiens cDNA
12871	24739		1.61	6.0E-04	AI817088.1	EST_HUMAN	wj78g11.x1 NCI CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element
678	13303	25785	8.64	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 29.3 KD PROTEIN (ORF92)
1549	14141		1.68	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-e07 CT0225 Homo sapiens cDNA
3460	16087	28540	1.53	5.0E-04	AA548531.1	EST_HUMAN	nk27e11.s1 NCI CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element
3778	16378	28843	1.02	5.0E-04	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5664	18291	30770	1.98	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6740	19334	32141	6.37	5.0E-04	AA156080.1	EST_HUMAN	zo33b08.r1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:588863 5'
7411	19936	32801	16.91	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
7898	20440	33346	4.97	5.0E-04	AI188382.1	EST_HUMAN	qd13f06.x1 Soares_placenta_8tc9weeks_2NbHP8c9W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN), contains Alu repetitive element
8245	20798	33705	0.91	5.0E-04	AA814519.1	EST_HUMAN	ob96602.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339228 3' similar to contains element MER22 repetitive element
9201	21718	34682	1.37	5.0E-04	AA846545.1	EST_HUMAN	ej56h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9293	21893	34840	0.6	5.0E-04	N83765.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPEITIVE ELEMENT
9437	21893	34912	0.65	5.0E-04	P29126	SWISSPROT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR
9527	22027	34986	4.43	5.0E-04	AW270938.1	EST_HUMAN	xs06602.xt NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2768858 3'
10855	23376		4.52	5.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586M2024
11559	18291	30770	11.05	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
11631	18936	32801	1.84	5.0E-04	M23604.1	NT	Corilla gorilla involucrin gene medium allele, complete cds
11809	24857		3.21	5.0E-04	AA568513.1	EST_HUMAN	n15h02.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:913875
12353	24883		1.77	5.0E-04	U83834.1	NT	Human KIT protein and alternatively spliced KIT protein (KIT) gene, complete cds
415	13050		0.64	4.0E-04	BF241482.1	EST_HUMAN	601876534F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5'
701	13323	.25810	1.12	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
880	13494	26012	1.46	4.0E-04	A1720263.1	EST_HUMAN	as70b08.x1 Barsstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
880	13494	26013	1.48	4.0E-04	A1720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
1514	14108	26842	9.82	4.0E-04	AW753356.1	EST_HUMAN	as70b08.x1 Barsstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
2130	14708	27280	1.59	4.0E-04	AL163278.2	NT	RC3-CT0254-130100-023-01 CT0254 Homo sapiens cDNA
2179	14756		1.34	4.0E-04	AL048704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
2656	15215	27787	1.83	4.0E-04	O96616	SWISSPROT	DKFZp434D059_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059 5'
3200	15812	28286	2.59	4.0E-04	AF281074.1	NT	SERPIN-2 (SILK GUM PROTEIN 2)
3405	16014	28493	0.58	4.0E-04	AV696624.1	EST_HUMAN	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3935	16533		0.94	4.0E-04	AL163267.2	NT	AV696624 GKC Homo sapiens cDNA clone GKCFFH07 5'
4415	17000	29442	3.2	4.0E-04	AA576331.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C067
4415	17000	29443	3.2	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCI_CGAP_Cot1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL
4635	17218	28671	1.94	4.0E-04	AA086324.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5249	17812	30235	6.04	4.0E-04	BE560660.1	EST_HUMAN	nh10a10.s1 NCI_CGAP_Cot1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL
7312	19840	32699	1.25	4.0E-04	P48442	SWISSPROT	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
7541	20081		2.42	4.0E-04	AL161568.2	NT	zn61c08.s1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:582670 3'
8473	21013	33929	1.42	4.0E-04	BF240712.1	EST_HUMAN	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
8481	21020	33935	1.85	4.0E-04	N25507.1	EST_HUMAN	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
							Arabisopsis thaliana DNA chromosome 4, contig fragment No. 66
							601875885F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089700 5'
							yx39e12.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:284142 5'

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Table 4
Single Exon Probes Expressed In Fetal Liver.

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9608	22108	35070	2.79	4.0E-04	AI025698.1	EST_HUMAN	ov87h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3'
9754	22552		1.22	4.0E-04	AF022855.1	NT	Mus musculus neupilin-2(a17) mRNA, alternatively spliced, complete cds
12188	24833		2.4	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
167	12830	25316	2.71	3.0E-04	AL119426.1	EST_HUMAN	DKFZp761J221_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221 5'
209	12870	25356	3.63	3.0E-04	P48259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
813	13526	26045	1.72	3.0E-04	U83591.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1879	14465	27022	5.5	3.0E-04	AI262100.1	EST_HUMAN	qz28d03.y1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
1894	14479		1.08	3.0E-04	AI399874.1	EST_HUMAN	ih23a02.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2119082 3'
3349	15958	28434	4.85	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR
4036	16634	29103	3.07	3.0E-04	P48448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4131	16723		1.37	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4167	16758		1.14	3.0E-04	BE140608.1	EST_HUMAN	RCO-HT0014-310599-028 HT0014 Homo sapiens cDNA
4941	17516		5.05	3.0E-04	BE153778.1	EST_HUMAN	PMO-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
5162	17731	30158	0.57	3.0E-04	Q09472	SWISSPROT	E1A-ASSOCIATED PROTEIN P300
6292	18900		5.93	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
6809	19568	32395	1.67	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7590	20105	32981	1.04	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8202	20743	33656	6.78	3.0E-04	P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
9834	22332	35313	1.46	3.0E-04	AA454055.1	EST_HUMAN	zx48d08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762
10080	22575	35570	0.5	3.0E-04	AI992139.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);
10356	22850	35844	8.78	3.0E-04	AA781201.1	EST_HUMAN	wt75a11.x1 Soares_thymus_NHFT Homo sapiens cDNA clone IMAGE:2513276 3'
11758	25072	30514	3.55	3.0E-04	AA228301.1	EST_HUMAN	gi24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 60S
12140	24909	30713	4.29	3.0E-04	AB018292.1	NT	nc38e04.r1 NCL_CGAP_P22 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1 repetitive element;
12574	24671		3.54	3.0E-04	AL134483.1	EST_HUMAN	Homo sapiens mRNA for KIAA0749 protein, partial cds
187	12848	25333	1.23	2.0E-04	AF217798.1	NT	DKFZp547L185_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547L185 5'
504	13136	25624	2.88	2.0E-04	AU146707.1	EST_HUMAN	Homo sapiens SCG10 like-protein, helicase-like protein NHL; M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
940	13553	26089	5.4	2.0E-04	M86524.1	NT	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
940	13553	26070	5.4	2.0E-04	M86524.1	NT	Human dystrophin gene
1221	13821		3.94	2.0E-04	AI286021.1	EST_HUMAN	Human dystrophin gene
							qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1228	13827		1.95	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1872	14458		1.12	2.0E-04	AF224288.1	NT	Mus musculus 5' flanking region of Pib3 gene
2227	14802		0.9	2.0E-04	AA478980.1	EST_HUMAN	zu39805.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element;
2810	15172	27740	6.83	2.0E-04	U86081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2.>
3016	15632	28109	1.13	2.0E-04	AI124528.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3377	15986	28484	0.76	2.0E-04	5174736	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3483	16089	28561	2.53	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0636-070500-194-b07 BT0636 Homo sapiens cDNA
3983	16561	28032	0.85	2.0E-04	AW878441.1	EST_HUMAN	EST390550 MAGE resequences, MAGP Homo sapiens cDNA
4224	16812		6.34	2.0E-04	U01026.1	NT	Phaseolus vulgaris nitrate reductase (PNR2) gene, complete cds
4776	17357	28609	1.34	2.0E-04	H96265.1	EST_HUMAN	yu01et1.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4776	17357	28810	1.34	2.0E-04	H96265.1	EST_HUMAN	yu01et1.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4913	17488		1.79	2.0E-04	U09226.1	NT	Gallus gallus probasome 28 kDa subunit homolog mRNA, complete cds
5216	17780	30199	1.44	2.0E-04	AB037697.1	NT	Danio rerio hegoromo gene, exons 1 to 6, partial cds
5733	18359	31065	1.92	2.0E-04	AV854352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLCDUH10 3'
5745	18371	31079	1.87	2.0E-04	AI690862.1	EST_HUMAN	tp03b11.x1 NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:2207709 3'
5924	18546	31272	0.87	2.0E-04	AA366652.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
6102	18718	31470	1.06	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6385	18989	31769	0.81	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7281	19809		2.44	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
7816	20129		13.08	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7826	20138	33017	1.28	2.0E-04	P64296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
7897	20439	33344	2.74	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
7897	20439	33345	2.74	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8226	20767	33685	0.97	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8226	20767	33698	0.97	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8500	21039	33960	1.77	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8678	21217	34137	0.56	2.0E-04	X57331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
9257	21783	34736	0.47	2.0E-04	AA725700.1	EST_HUMAN	ai22a12.s1 Soares testis NHT Homo sapiens cDNA clone 1343518 3'
9340	21854	34803	0.5	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLGCF26.1
9885	22382	35357	1.4	2.0E-04	BE149303.1	EST_HUMAN	RC3-HT0264-151099-011-b05 HT0264 Homo sapiens cDNA
9830	22426	35400	2.39	2.0E-04	AA405777.1	EST_HUMAN	zu66c11.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:742964 5'
10731	23257	36273	6.22	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAAA01 5'
11185	23690	36737	5.43	2.0E-04	AI440282.1	EST_HUMAN	ig01f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element
11303	23796	36854	2.72	2.0E-04	AW136740.1	EST_HUMAN	UJ-H-B11-adim-c-04-Q-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717180 3'
799	13416	25920	1.41	1.0E-04	H98646.1	EST_HUMAN	yx26c09.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:282864 3' similar to contains L1.1 L1 repetitive element ;
1113	13717	26227	2.57	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
1163	13756	26265	4.04	1.0E-04	AW013847.1	EST_HUMAN	UJ-H-B10-aab-e-09-Q-UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1153	13756	26268	4.04	1.0E-04	AW013847.1	EST_HUMAN	UJ-H-B10-aab-e-09-Q-UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1377	13870		3.95	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
							Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1669	14282	26785	2.57	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1669	14282	26785	2.57	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1901	14486	27047	2.44	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY38
2711	15268	27835	1.09	1.0E-04	BE218833.1	EST_HUMAN	hy45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
2711	15268	27836	1.09	1.0E-04	BE218833.1	EST_HUMAN	hy45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
3323	15933	28410	1.1	1.0E-04	Q82203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3799	16399	28864	2.7	1.0E-04	AI440282.1	EST_HUMAN	ig01f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element
4134	16726	29180	1.72	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4156	16748	29201	1.27	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLCBBD04 3'
5263	17825	30250	0.95	1.0E-04	A1357150.1	EST_HUMAN	qx62h04.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:2005975 3'
6021	18640	31380	1.5	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6569	19166	31962	0.97	1.0E-04	AA117711.1	EST_HUMAN	nc02e12.s1 NCI_CGAP_P3 Homo sapiens cDNA clone IMAGE:252

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6925	19584	32414	0.78	1.0E-04	AA564561.1	EST_HUMAN	nj26a04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:990486 3' similar to gb:M97252 KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element;
7237	19767	32623	14.09	1.0E-04	A1251880.1	EST_HUMAN	qv57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
7572	19767	32623	14.23	1.0E-04	A1251880.1	EST_HUMAN	qv57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
7937	20479	33389	1.02	1.0E-04	AA630453.1	EST_HUMAN	ab94g08.s1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:854654 3'
9260	21786	34736	2.34	1.0E-04	A1808220.1	EST_HUMAN	wf26e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9270	21786	34745	1.71	1.0E-04	O88969	SWISSPROT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
9346	21860		0.78	1.0E-04	T77153.1	EST_HUMAN	yf22c08.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:113774 5'
9594	22094	35023	2.2	1.0E-04	10863876	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10081	22578		2.87	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10116	22611	35601	0.83	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11218	23721		2.08	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11503	23982	37020	1.98	1.0E-04	AB032868.1	EST_HUMAN	Homo sapiens mRNA for KIAA1142 protein, partial cds
11540	23988	37059	2.1	1.0E-04	AW269081.1	EST_HUMAN	xv49g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
11570	24017	37086	1.87	1.0E-04	Q03698	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11570	24017	37087	1.87	1.0E-04	Q03698	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11670	24092		1.57	1.0E-04	BE696769.1	EST_HUMAN	OM0-CT0404-130700-475-h03 CT0404 Homo sapiens cDNA
11919	24878		1.99	1.0E-04	BE676399.1	EST_HUMAN	728a10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3286058 3' similar to contains L1.13 L1 repetitive element;
727	13347	25839	1.98	9.0E-05	AA718933.1	EST_HUMAN	ah45c11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1292468 3'
2047	14628	27188	0.92	9.0E-05	AW866218.1	EST_HUMAN	QV4-SN0023-070400-168-b04 SN0023 Homo sapiens cDNA
6117	18733	31486	1.45	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
9397	21820		2.71	9.0E-05	D85608.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
9399	21822	34771	2.79	9.0E-05	AF120882.1	NT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11017	23531	36587	2.86	9.0E-05	AW073078.1	EST_HUMAN	xa34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1 repetitive element;
11121	23628	36671	1.99	9.0E-05	A1287878.1	EST_HUMAN	qv23f08.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MIR repetitive element;
11483	18733	31486	3.89	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
11974	24939		4.26	9.0E-05	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1; DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
854	13470	25981	1.21	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
897	13511		9.89	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2977	15593		0.71	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4579	17162	29604	1.87	8.0E-05	AW044605.1	EST_HUMAN	wy78a04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
8683	21222	34142	0.49	8.0E-05	Y11686.1	NT	Mus musculus gene for hexokinase II, exon 1 (end joined CDS)
11030	23544	36581	2.32	8.0E-05	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
12813	24921		2.72	8.0E-05	AA276333.1	EST_HUMAN	zs88h01.s1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element ;
369	13018	25501	8.81	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
369	13018	25502	8.81	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
593	13223	25697	3.82	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
593	13223	25698	3.82	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1093	13698	26208	1.41	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYL TRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2744	15299	27865	3.67	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3194	15808	28279	4.69	7.0E-05	AB009080.1	NT	Dicotyledon discoidium gene for TRFA, complete cds
4462	17048	29492	1.73	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4543	17127	29570	0.58	7.0E-05	U60980.1	NT	Caenorhabditis elegans Skp1p homolog mRNA, complete cds
8167	20708	33624	1.11	7.0E-05	AA505582.1	EST_HUMAN	nh83g01.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:966096 3'
9472	21871	34820	3.74	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Stragene (cat#939206) Homo sapiens cDNA clone HFBED60
11040	23554		7.95	7.0E-05	10835046	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2073	14653	27225	2.03	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2073	14653	27226	2.03	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2624	15186	27753	1.34	6.0E-05	AI855241.1	EST_HUMAN	wb54h06.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309631 3' similar to gb.J03250 DNA TOPOISOMERASE I (HUMAN);
2709	15266	27833	0.9	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2709	15266	27834	0.9	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2840	13328	25815	2.88	6.0E-05	AF053630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5352	17912	30327	1.3	6.0E-05	AW962309.1	EST_HUMAN	EST374382 MAGG cDNAs, MAGG Homo sapiens cDNA
6071	18698	31432	3.12	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6071	18698	31433	3.12	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6535	19135	31928	1.45	6.0E-05	N72826.1	EST_HUMAN	yf50g11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246212 5'
7013	19511	32332	0.79	6.0E-05	AA897880.1	EST_HUMAN	q98a03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1504588 3'
8029	20571	33475	0.97	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
8029	20571	33476	0.97	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriplor
8381	20921	33841	0.65	6.0E-05	AA150482.1	EST_HUMAN	z108c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491726 3' similar to contains element MER28 repetitive element;
8385	20925	33845	2.3	6.0E-05	AW896628.1	EST_HUMAN	PM4-NN0050-310300-001-f10 NN0050 Homo sapiens cDNA
8516	21055	33978	0.62	6.0E-05	Q60401	SWISSPROT	COMPLEMENT DEACY-ACCELERATING FACTOR PRECURSOR
9178	21753	34699	1.09	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9178	21753	34700	1.09	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9440	21966	34915	1.13	6.0E-05	T94148.1	EST_HUMAN	ye28c12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119082 5'
9837	22137	35103	0.57	6.0E-05	AW627985.1	EST_HUMAN	h137603.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974444 3'
10627	23159	38172	3.98	6.0E-05	R75639.1	EST_HUMAN	y158408.s1 Soares_placenta Nb2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains L TR7 repetitive element;
11394	23846	38911	4.18	6.0E-05	AA044015.1	EST_HUMAN	z158f02.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
12193	24919	30716	10.26	6.0E-05	AW890110.1	EST_HUMAN	MR0-NT0038-250400-001-f09 NT0038 Homo sapiens cDNA
1449	14041	28569	18.37	5.0E-05	AW392086.1	EST_HUMAN	QV4-ST0234-241199-040-h11 ST0234 Homo sapiens cDNA
1603	14488		1.75	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC558895), mRNA
4051	16648	29116	3.86	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5716	18342	30848	11.26	5.0E-05	X58855.1	NT	Human ML C1emb gene for embryonic myosin alkaline light chain, 3'UTR
6144	18758	31516	2.97	5.0E-05	AV653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCDMA06 3'
6316	18923	31700	0.97	5.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7370	19896		1.22	5.0E-05	AB037964.1	NT	Mus musculus gene for calretinin, exon 1
11971	24460		5.73	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12249	24460		9.18	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2833	12906		3.49	4.0E-05	U12821.1	NT	Human renin (REN) gene, 5' flanking region
4580	17163	29605	1.37	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4580	17163	29608	1.37	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
5166	17735	30162	0.58	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
7020	19518	32340	0.75	4.0E-05	U01947.1	NT	Macaca mulatta haptoglobin (HP) gene, 5' region
9442	21968		7.26	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE];
9912	22408	35384	0.55	4.0E-05	P11369	SWISSPROT	ENDONUCLEASE
10305	22799	35780	0.73	4.0E-05	P23780	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
10648	23180	36183	5.05	4.0E-05	AW627946.1	EST_HUMAN	h136c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element;
11850	24210	31041	3.27	4.0E-05	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
11929	24284		1.38	4.0E-05	AW117560.1	EST_HUMAN	xd93c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605192 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
709	13330	25817	0.64	3.0E-05	A1248061.1	EST_HUMAN	qh64c10.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element ;
1097	13702	26212	1.49	3.0E-05	AW273851.1	EST_HUMAN	xx24c03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1170	13772	26280	1.51	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3885142 5'
1170	13772	26281	1.51	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3885142 5'
2748	15301	27867	1.17	3.0E-05	Q62234	SWISSPROT	SKLEMIN
3331	15941		0.69	3.0E-05	A1288919.1	EST_HUMAN	qj91g11.x1 Soares_NHhMPu_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:O08632
4471	17057	29503	7.22	3.0E-05	BE169211.1	EST_HUMAN	O08632 GLYCINE TYROSINE-RICH HAIR PROTEIN. ;
4471	17057	29504	7.22	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4565	17148	29594	1.06	3.0E-05	AA368679.1	EST_HUMAN	EST78998 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein
4565	17148	29595	1.06	3.0E-05	AA368679.1	EST_HUMAN	EST78998 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein
4692	17274		0.71	3.0E-05	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4728	17307	29751	0.75	3.0E-05	AF14973.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4983	13330	25817	0.65	3.0E-05	A1248061.1	EST_HUMAN	qh64c10.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element ;
5746	18372	31080	1.73	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Myc2pl), mRNA
6854	19442	32257	1.28	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL 1 gene, exons 6-8
6854	19442	32258	1.28	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL 1 gene, exons 6-8
7839	20381	33296	1.9	3.0E-05	BE733157.1	EST_HUMAN	601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842282 5'
8293	20834	33756	1.29	3.0E-05	AA284049.1	EST_HUMAN	zs60605.s1 Sratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
8824	21363	34288	1.78	3.0E-05	AW770982.1	EST_HUMAN	h194e08.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'
8928	21367	34291	1.22	3.0E-05	6912431	NT	Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
8932	21371	34296	0.47	3.0E-05	P43361	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
9058	21595		0.88	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9244	21770	34718	1.3	3.0E-05	AA372562.1	EST_HUMAN	EST94475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
9581	22081		2.97	3.0E-05	A1769331.1	EST_HUMAN	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10428	22922	35925	0.85	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
10428	22922	35926	0.85	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
12055	24358		1.48	3.0E-05	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12387	25101		1.52	3.0E-05	AW518689.1	EST_HUMAN	xs89d06.x1 NCJ_CGAP_U2 Homo sapiens cDNA clone IMAGE:2776811 3'
2362	14933	27506	1.55	2.0E-05	A1266021.1	EST_HUMAN	qh88e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element ;
2619	15181	27747	10.26	2.0E-05	M113792.1	NT	Human adenosine deaminase (ADA) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2738	15293		6.76	2.0E-05	AA160562.1	EST_HUMAN	zq46a12.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element;
3171	15785	28257	1.59	2.0E-05	BE066036.1	EST_HUMAN	RC3-BT0319-120200-014-h08 BT0319 Homo sapiens cDNA
3391	15999	28477	0.63	2.0E-05	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3416	16024	28506	1.04	2.0E-05	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
3541	16146		0.72	2.0E-05	X95465.1	NT	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3880	16478		0.67	2.0E-05	AL039107.1	EST_HUMAN	DKFZp5661064_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp5661064 5'
5010	17583	30026	0.63	2.0E-05	AJ131016.1	NT	Homo sapiens SCL gene locus
5176	17743		2.42	2.0E-05	L77569.1	NT	Homo sapiens DGeorge syndrome critical region, telomeric end
5933	18555	31282	1.64	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6125	18740	31492	1.4	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6125	18740	31493	1.4	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6305	18912	31688	0.73	2.0E-05	A1149272.1	EST_HUMAN	qc72a02.x1 Soares_placenta_8to9weeks_2NbpHP8ta9W Homo sapiens cDNA clone IMAGE:1715114 3'
6736	19330	32136	2.12	2.0E-05	AA714330.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element;
6982	19480	32301	2.2	2.0E-05	Y08926.1	NT	nm00612.s1 NCI CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
6994	19492	32313	1.34	2.0E-05	A1492860.1	EST_HUMAN	P. falciparum mRNA for AARP1 protein, partial
7002	19500		8.08	2.0E-05	A1891025.1	EST_HUMAN	qz47b06.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR:O02711
							O02711 PRO-POL-DUTPASE POLYPROTEIN;
							wu35h07.x1 Soares_Dieckgraebe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
7207	19738	32591	2.2	2.0E-05	AF224262.1	NT	Heterodentus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7207	19738	32592	2.2	2.0E-05	AF224262.1	NT	Heterodentus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7403	19928		0.91	2.0E-05	AF128947.1	NT	Homo sapiens Indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
7826	20368	33276	1.41	2.0E-05	A1381040.1	EST_HUMAN	tg20h05.x1 NCI CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2109369 3'
9191	21708	34651	0.49	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9191	21708	34652	0.49	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9837	22335	35317	0.48	2.0E-05	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10041	22536	35532	0.74	2.0E-05	BF055939.1	EST_HUMAN	775g09.y1 NCI CGAP_Brn20 Homo sapiens cDNA clone IMAGE:3340576 5'

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10482	22976	35984	2.62	2.0E-05	N41751.1	EST_HUMAN	yw91a08.r1 Soares_placenta_8to9weeks_2NBHP81069W Homo sapiens cDNA clone IMAGE:259570 5'
10482	22976	35985	2.62	2.0E-05	N41751.1	EST_HUMAN	yw91a08.r1 Soares_placenta_8to9weeks_2NBHP81069W Homo sapiens cDNA clone IMAGE:259570 5'
10524	19500		2.44	2.0E-05	A1991025.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgraefe_colon_NHOD Homo sapiens cDNA clone IMAGE:2522077 3'
11327	23025	36034	2.74	2.0E-05	BE175801.1	EST_HUMAN	RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
11983	24844		4.91	2.0E-05	BE348229.1	EST_HUMAN	hw21a03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832
12090	25018		13.02	2.0E-05	AW074604.1	EST_HUMAN	xa69a03.x1 NCL_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2573932 3' similar to contains L1.b3 L1 repetitive element
12144	24831		2.54	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12655	24727		2.35	2.0E-05	A1200970.1	EST_HUMAN	qf68g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755238 3'
2719	15475	27841	1.45	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3711	16312	28780	1.91	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lemto 120 Suppressor of Hairless (Su(H)) gene, partial cds
4039	16637	29105	11.9	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4252	16840	29289	0.98	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4364	16951	29381	1.89	1.0E-05	AA431119.1	EST_HUMAN	zw69g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4976	17550	29892	2.24	1.0E-05	AW418134.1	EST_HUMAN	xy49g11.x1 NCL_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
5395	17853		0.94	1.0E-05	AI733588.1	EST_HUMAN	os64d07.x5 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1810125 3' similar to contains Alu repetitive element
5426	17983	30389	0.91	1.0E-05	L27595.1	NT	Mus musculus bradykinin B2 receptor (B2R) gene, complete cds
6848	19438	32252	1.32	1.0E-05	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
7140	19520	32342	3.98	1.0E-05	AA641846.1	EST_HUMAN	ns18g02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1
7142	19675	32515	14.32	1.0E-05	4503844	NT	L1 repetitive element
7655	20167	33054	0.76	1.0E-05	BF222848.1	EST_HUMAN	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
7754	20282		2.22	1.0E-05	P19474	SWISSPROT	7p57d01.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3649945 3' similar to contains MER10.b3
8846	21385		2.56	1.0E-05	AL163227.2	NT	MER10 repetitive element
8990	21528	34457	2.18	1.0E-05	AA452578.1	EST_HUMAN	52 KD RO PROTEIN (SIOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
9211	21728	34671	13.74	1.0E-05	AA236110.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
9288	21888	34834	0.6	1.0E-05	AV732180.1	EST_HUMAN	zq35h12.s1 Soares_totat_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb:L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
							z805e11.1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu repetitive element; contains element TAR1 repetitive element
							AV732190 HTF Homo sapiens cDNA clone HTFBIH01 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9752	22250	35232	0.76	1.0E-05	AW510902.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.11 OFR repetitive element;
9752	22250	35233	0.76	1.0E-05	AW510902.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.11 OFR repetitive element;
9830	22328	35309	1.58	1.0E-05	AW291521.1	EST_HUMAN	UI-H-B12-egl-a-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
9830	22328	35310	1.58	1.0E-05	AW291521.1	EST_HUMAN	UI-H-B12-egl-a-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10087	22582		1.73	1.0E-05	AW468995.1	EST_HUMAN	ha07c10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1 repetitive element;
10798	23322	36332	2.32	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10799	23322	36333	2.32	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12493	25011	30618	1.67	1.0E-05	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2686	15253	27824	4.74	9.0E-06	AI583811.1	EST_HUMAN	tt73a06.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3130	15744	28213	5.23	9.0E-06	AI218983.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8to8weeks_2NbpHP8to8W Homo sapiens cDNA clone IMAGE:1759191 3'
3670	16271		3.37	9.0E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
6084	18681	31423	2.25	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
6947	19524	32346	0.84	9.0E-06	BE065042.1	EST_HUMAN	RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA
7466	18988	32853	0.85	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7751	20259	33156	12.47	9.0E-06	AI034370.1	EST_HUMAN	ox20g01.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1856912 3' similar to contains Alu repetitive element;
8400	20940	33863	1.18	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8913	21451	34372	2.48	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8913	21451	34373	2.48	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9149	21684	34628	4.6	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
10818	23339	36353	3.76	9.0E-06	Q10384	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2569	15469	27701	1.48	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201199-011-h11 CT0283 Homo sapiens cDNA
10424	22918	35919	0.64	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10424	22918	35920	0.64	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1015	13625		1.71	7.0E-06	AA669729.1	EST_HUMAN	ab00110.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.t1 MER20 repetitive element ;
1487	14080	26619	3.36	7.0E-06	7692177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2177	14754	27324	1.55	7.0E-06	AW593215.1	EST_HUMAN	hg11b12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2945279 3' similar to gb:X62048 cds1 WEE1-LIKE PROTEIN KINASE (HUMAN);
2897	15514		7.94	7.0E-06	AI388252.1	EST_HUMAN	qw16g09.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:1991296 3' similar to contains Alu repetitive element;
3620	16223		1	7.0E-06	AA385542.1	EST_HUMAN	EST99205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5874	18496		5.81	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0062-250400-173-H01 OT0062 Homo sapiens cDNA
5972	18593	31327	0.94	7.0E-06	N98645.1	EST_HUMAN	W65c07.r1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:278412 5' ;
8724	21263	34183	0.72	7.0E-06	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF68S1E), mRNA
9814	22312		2.32	7.0E-06	Q61147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
11710	25043	30506	1.82	7.0E-06	BF215972.1	EST_HUMAN	607881622F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4093972 5'
2942	15558	28032	1.29	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0378-010300-105-J11 BT0379 Homo sapiens cDNA
4855	15584	28085	2.03	6.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4875	17450	29901	1.47	6.0E-06	AI040099.1	EST_HUMAN	ox08a02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.L2 MER8 repetitive element ;
5552	18184	30599	1.3	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5605	18234	30685	1.15	6.0E-06	Q02040	SWISSPROT	PROTEIN XE7
9770	22268		1.67	6.0E-06	AW801912.1	EST_HUMAN	IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA
12602	24698	30881	1.47	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
5381	17921	30335	1.02	5.0E-06	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
6211	18821	31582	3.73	5.0E-06	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
6479	19080	31883	2.04	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met), complete cds
7284	18812	32688	1.11	5.0E-06	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
10013	22508	35499	6.57	5.0E-06	AA313620.1	EST_HUMAN	EST185496 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
10406	22900	35895	0.54	5.0E-06	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12482	24615	30890	13.8	5.0E-06	AI065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
675	13289	25780	6.05	4.0E-06	R16267.1	EST_HUMAN	ye48c03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element ;
879	13493	26011	6.94	4.0E-06	AW103354.1	EST_HUMAN	xc68g12.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1379	13972	28499	3.92	4.0E-08	A1334928.1	EST_HUMAN	ib33609.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2058168 3'
1379	13972	28500	3.92	4.0E-08	A1334928.1	EST_HUMAN	ib33609.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2058168 3'
1522	14114	26651	3.17	4.0E-06	BF365612.1	EST_HUMAN	QV2-NT0046-200600-250-107 NT0046 Homo sapiens cDNA
2305	14878	27454	1.68	4.0E-06	AW015401.1	EST_HUMAN	UI-H-B10-aat-f-05-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3099	15714	28188	1.26	4.0E-06	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3963	16561	29030	1.35	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4930	17505	28951	1.86	4.0E-06	A1886939.1	EST_HUMAN	w194c10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element
5053	17626	30070	2.12	4.0E-06	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
8438	20978	33890	0.53	4.0E-06	O16393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
8735	21274	34185	2.66	4.0E-06	AF008660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
9624	22124	35098	1.11	4.0E-06	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
11324	23022	36031	3.84	4.0E-06	AB007855.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
2208	14784	27337	1.31	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.t1 L1 repetitive element
2208	14784	27358	1.31	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.t1 L1 repetitive element
2307	14879		1.54	3.0E-06	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
2948	15564	28038	1.02	3.0E-06	AA668218.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13
3304	15915		2.41	3.0E-06	A1857779.1	EST_HUMAN	w22a05.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN ; contains L1.12 L1 repetitive element
3851	16449	28911	1.06	3.0E-06	BE047094.1	EST_HUMAN	hq84d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3851	16449	28912	1.06	3.0E-06	BE047094.1	EST_HUMAN	hq84d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4573	17158	29600	0.68	3.0E-06	T50266.1	EST_HUMAN	y678b10.r1 Stralagene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
4681	17243	29697	4.82	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
5045	17618	30063	0.94	3.0E-06	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
5045	17618	30064	0.94	3.0E-06	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
6308	18915	31689	0.78	3.0E-06	AU159412.1	EST_HUMAN	AU159412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
7280	18908		2.79	3.0E-06	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8027	20569	33473	0.72	3.0E-06	BE562864.1	EST_HUMAN	601336213FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690314 5'
8618	21157	34070	0.69	3.0E-06	P07743	SWISSPROT	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12162	24394		13.37	3.0E-06	AW385262.1	EST_HUMAN	RCO-LT0001-261199-011-A03 LT0001 Homo sapiens cDNA
216	12877		2.91	2.0E-06	P54366	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
1614	14207		4.46	2.0E-06	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2418	14986	27590	2.2	2.0E-06	A1872138.1	EST_HUMAN	wa04a03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2287068 3' similar to contains MER30 b1 MER30 repetitive element;
2506	15070	27643	1.78	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2601	15163	27731	1.34	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3570	16174	28656	1.04	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB05 3'
3825	16425	28897	1.85	2.0E-06	AA173518.1	EST_HUMAN	zp02a05.r1 Stratiogene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5'
3836	16435	28897	0.63	2.0E-06	AW450215.1	EST_HUMAN	UI-H-B13-aky-g-05-Q-U1.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736176 3'
3844	16443	28904	1.74	2.0E-06	AB030896.1	NT	Mus musculus gene for odorant receptor A16, complete cds
6239	18848		0.79	2.0E-06	AA974932.1	EST_HUMAN	on34h01.s1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558609 3' similar to contains Alu repetitive element;
6267	18875	31643	0.87	2.0E-06	A1539448.1	EST_HUMAN	le51f05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TR:Q13537
6570	19168	31985	4.94	2.0E-06	A1819424.1	EST_HUMAN	Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
7858	20400		0.89	2.0E-06	AW869223.1	EST_HUMAN	w90804.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
8033	20575	33480	0.75	2.0E-06	T12238.1	EST_HUMAN	MR3-SN0067-120400-002-f02 SN0067 Homo sapiens cDNA
8770	21309		0.59	2.0E-06	AA772497.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447 z127c11.s1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to TR:P70467 P70467 REVERSE TRANSCRIPTASE;
8782	21321	34245	1.54	2.0E-06	H62051.1	EST_HUMAN	y037c04.t1 Soares ovary tumor N8HOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929
9143	21678	34621	0.91	2.0E-06	AF003529.1	NT	KERATIN, TYPE II CYTOSKELETAL 6 (HUMAN);
9143	21678	34622	0.91	2.0E-06	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9617	22117	35080	0.72	2.0E-06	N30576.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9833	22331		0.63	2.0E-06	AV748969.1	EST_HUMAN	yw66a03.s1 Soares placenta_8tc9weeks_2NbhP8tc9W Homo sapiens cDNA clone IMAGE:257212 3'
12052	25046	30508	1.61	2.0E-06	P23249	SWISSPROT	AV748969 NPC Homo sapiens cDNA clone NPCAXD05 5'
12210	24434		6.63	2.0E-06	BE328232.1	EST_HUMAN	PROTEIN MOV-10 hs9202.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144699 3' similar to contains L1.12 L1 repetitive element;
36	12715	25174	1.77	1.0E-06	O76082	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH- AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
685	13309	25794	1.45	1.0E-06	AF084384.1	NT	Mus musculus D6Mm5e protein (D6Mm5e) mRNA, complete cds
1500	14092	26631	2.08	1.0E-06	P09125	SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8

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1571	14164	26695	1.12	1.0E-06	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1627	14220		1.54	1.0E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
2037	14819	27186	8.38	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2037	14819	27187	8.38	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4459	17045	29488	14.7	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5299	17831	30256	0.99	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5299	17831	30257	0.99	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5494	18128	30536	4.64	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA
5518	18150	30563	1.08	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5518	18150	30564	1.08	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5667	18294	30774	1.13	1.0E-06	O60613	SWISSPROT	15 KDA SELENOPROTEIN PRECURSOR
6954	19531	32356	5.96	1.0E-06	P02671	SWISSPROT	FIBRINOGEN ALPHA1(A) CHAIN PRECURSOR
7943	20485		0.68	1.0E-06	AA912623.1	EST_HUMAN	α28-08 s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524878 3'
8216	20757	33671	1.21	1.0E-06	AI347010.1	EST_HUMAN	qp54602.x1 NCL_CGAP_C08 Homo sapiens cDNA clone IMAGE:1926842 3'
8425	20965	33879	1.23	1.0E-06	AI287878.1	EST_HUMAN	qv2305.x1 NCL_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MIR repetitive element:
9228	21950	34899	0.98	1.0E-06	N74635.1	EST_HUMAN	za55601.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:298472 3'
9301	21801	34850	0.5	1.0E-06	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9800	22100	35082	3.34	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9800	22100	35083	3.34	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9843	22143	35111	4.36	1.0E-06	AA132811.1	EST_HUMAN	zo17e08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 5'
9703	22202		3.84	1.0E-06	AA449257.1	EST_HUMAN	z04d11.s1 Soares_total_fetus_Nb2H-F8_9w Homo sapiens cDNA clone IMAGE:785493 3' similar to gb:D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
10382	22876		1.61	1.0E-06	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11502	23951		6.24	1.0E-06	AW890941.1	EST_HUMAN	RC4-NT0054-120500-012-b03 NT0054 Homo sapiens cDNA
12067	24356	30966	7.83	1.0E-06	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
12195	14819	27186	1.67	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
12195	14819	27187	1.67	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
12603	14220		1.38	1.0E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
383	13030	25518	2.01	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
383	13030	25519	2.01	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8346	20887		0.57	9.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11126	23634	36675	2.95	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4885	17460	29912	5.02	8.0E-07	A1288596.1	EST_HUMAN	qB2g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4885	17460	28913	5.02	8.0E-07	A1288596.1	EST_HUMAN	qB2g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
6047	18666		7.49	8.0E-07	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
7944	20486		9.51	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11488	23935		8.73	8.0E-07	T07770.1	EST_HUMAN	EST05660 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBEN89
11630	24106		7.99	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1806	14491	27052	1.14	7.0E-07	AF107341.1	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
5710	18336	30841	0.69	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5710	18336	30842	0.69	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
10842	23174	36186	1.59	7.0E-07	BE976648.1	EST_HUMAN	7133g01.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296496 3' similar to TR:Q96897 Q96897
1956	14540	27096	2.56	6.0E-07	AW855558.1	EST_HUMAN	ENDOGENOUS RETROVIRUS-K, LTR U5 AND GAG GENE.;
2534	15098	27671	2.3	6.0E-07	AF010413.1	NT	CM3-CT0277-221099-024-e11 CT0277 Homo sapiens cDNA
4044	16642		1.76	6.0E-07	P41479	SWISSPROT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (BF), and complement component C2 (C2) genes.;
9088	21605	34536	1.94	6.0E-07	BF001867.1	EST_HUMAN	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
11625	24097	37131	1.83	6.0E-07	A1792850.1	EST_HUMAN	7g94f07.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920 4F5L.;
11949	24989		2.85	6.0E-07	AW903222.1	EST_HUMAN	cm87f05.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1554177 5'
348	12959		1.19	5.0E-07	A1831893.1	EST_HUMAN	CM4-NN1029-250300-121-h12 NN1029 Homo sapiens cDNA
1095	13700		2.21	5.0E-07	AA380630.1	EST_HUMAN	wh64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
3066	15691		0.64	5.0E-07	A1831893.1	EST_HUMAN	EST93615 Supt cells Homo sapiens cDNA 5' end
4751	17332	29775	1.32	5.0E-07	AF149774.1	NT	wh64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
6268	18876	31644	1.13	5.0E-07	U85087.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
7124	19494	32281	1.56	5.0E-07	A1393981.1	EST_HUMAN	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
7124	19494	32282	1.56	5.0E-07	A1393981.1	EST_HUMAN	tg08b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element ;
7386	19912	32776	16.07	5.0E-07	AW070895.1	EST_HUMAN	tg06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element ;
8217	20758	33672	0.82	5.0E-07	Q9WUQ1	SWISSPROT	xa31a02.x1 NCI_CGAP_B18 Homo sapiens cDNA clone IMAGE:2588362 3' similar to gb:X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
							ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1)(ADAMTS-1)(ADAM-TS1)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8427	20967		1.06	5.0E-07	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
10270	22765	35752	4.46	5.0E-07	A1908587.1	EST_HUMAN	CM-BT178-220499-014 BT178 Homo sapiens cDNA
10542	23079	36093	1.56	5.0E-07	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11391	23843	36907	4.94	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11452	23902		2.43	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12391	24889		2.85	5.0E-07	AW862537.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
4071	16667	29129	1.94	4.0E-07	AW009602.1	EST_HUMAN	ws84h05.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504697 3'
7230	19761		0.88	4.0E-07	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7311	19839	32687	1.35	4.0E-07	Q8Z2V8	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7311	19839	32698	1.35	4.0E-07	Q8Z2V8	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7863	20405	33312	0.65	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
8981	21519	34445	5.37	4.0E-07	AW419134.1	EST_HUMAN	xy48g11.x1 NCL_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
10228	22723	35715	0.5	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10817	23338	36351	4.05	4.0E-07	A1765528.1	EST_HUMAN	ws1808.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
10817	23338	36352	4.05	4.0E-07	A1765528.1	EST_HUMAN	ws1808.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
11100	23610		2.06	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
							Human microfilament-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
496	13100	25591	4.51	3.0E-07	U19719.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
609	13237	25711	2.64	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1417	14010	26539	1.65	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
1667	14260		1.95	3.0E-07	M84857.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele
2090	14670		3.87	3.0E-07	AA528763.1	EST_HUMAN	ni56b09.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1 & L1 repetitive element
2327	14898	27471	1.72	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
2508	15072	27845	6.56	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2508	15072	27846	6.56	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3069	15684	28156	0.79	3.0E-07	T84704.1	EST_HUMAN	yd5012.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:111695 5'
3195	15807	28280	2.03	3.0E-07	P38739	SWISSPROT	HYPOPHYSICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4788	17368		0.58	3.0E-07	P20740	SWISSPROT	OVOSTATIN PRECURSOR (OVOMACROGLOBULIN)
4834	17412	29865	7.74	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLOC001 3'
4878	17453	29905	0.71	3.0E-07	A1797236.1	EST_HUMAN	ws88b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347987 3'
5222	17787	30205	1.81	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb-M62882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5222	17787	30206	1.81	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5847	18471	31197	12.78	3.0E-07	Q88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6128	18743	31496	0.71	3.0E-07	Q42280	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6804	19395		5.41	3.0E-07	AA815175.1	EST_HUMAN	WNT-14 PROTEIN PRECURSOR
7519	20039	32908	3.22	3.0E-07	AW797168.1	EST_HUMAN	cc04c10.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890 3'
7659	20171		1.6	3.0E-07	AI591065.1	EST_HUMAN	QV1-JM0036-200300-115-g02 UM0036 Homo sapiens cDNA
11373	23825		1.68	3.0E-07	BE439409.1	EST_HUMAN	tw28111.x1 NCL CGAP_Ov45 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element ;
12641	24716		6.74	3.0E-07	AJ132352.1	NT	HTM1-025F1 HTM1 Homo sapiens cDNA
31	12710	25168	3.36	2.0E-07	AF262888.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
165	12828	25314	7.91	2.0E-07	L77569.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
165	12828	25315	7.91	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
194	12854	25338	45.63	2.0E-07	U38849.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
778	13397	25898	2.58	2.0E-07	AF003530.1	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds
778	13397	25898	2.58	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
791	13409		0.81	2.0E-07	P11369	SWISSPROT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
979	13591	26106	2.56	2.0E-07	AA223260.1	EST_HUMAN	zr08b07.s1 Stragene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
980	13592	26107	6.66	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:80760 3' similar to contains L1 repetitive element ;
1205	13805	26318	0.76	2.0E-07	Q26768	SWISSPROT	I/B AUTOANTIGEN
1644	14236	26771	1.88	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3679	16280		0.65	2.0E-07	BF131397.1	EST_HUMAN	601818916F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3751	16352	28820	22.38	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5547	18179	30593	1.81	2.0E-07	AW898066.1	EST_HUMAN	RC3-NN0068-280400-021-g11 NN0068 Homo sapiens cDNA
6769	19662	32171	1.59	2.0E-07	A1208715.1	EST_HUMAN	qq56d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
8405	20946		3.57	2.0E-07	AV729390.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAEG02 5'
8628	21197	34082	1.1	2.0E-07	AA035198.1	EST_HUMAN	z427g09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'
9876	22175		2.27	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10188	22663	35658	5.85	2.0E-07	AW892507.1	EST_HUMAN	GM4-NN0003-280300-124-e08 NN0003 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10383	22877	35868	0.75	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
10383	22877	35869	0.75	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
11642	24603		2.57	2.0E-07	BE163717.1	EST_HUMAN	PMO-HT0339-260100-008-H07 HT0339 Homo sapiens cDNA
11734	24890		3.58	2.0E-07	AI732482.1	EST_HUMAN	zn85h11.x5 Stragene lung carcinoma 937218 Homo sapiens cDNA IMAGE:565029 3' similar to contains THR.b2 THR repetitive element:
1141	13744		1.17	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2013	14595	27157	0.97	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2013	14595	27158	0.87	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2424	14992	27565	0.93	1.0E-07	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
2854	14162	26693	2.94	1.0E-07	P09256	SWISSPROT	GLYCOPROTEIN GPV
3907	13744		1.22	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4380	16967	29413	2.75	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLC/NF04 5'
4380	16967	29414	2.75	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLC/NF04 5'
6627	19223	32028	1.57	1.0E-07	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
6950	19527	32349	4.57	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291339 5'
6950	19527	32350	4.57	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291339 5'
7504	20026	32890	8.62	1.0E-07	N55081.1	EST_HUMAN	yw43c07.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:245484 3'
7644	20156	33042	0.82	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-Q30800-002-b05 TN0024 Homo sapiens cDNA
7844	20156	33043	0.82	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-Q30800-002-b05 TN0024 Homo sapiens cDNA
7669	20181	33068	1.35	1.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
8157	20688	33611	2.52	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8157	20688	33612	2.52	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8894	21422	34347	2.7	1.0E-07	AA693576.1	EST_HUMAN	z51e10.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:434346 3'
9194	21711	34654	1.05	1.0E-07	P57110	SWISSPROT	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
9535	22035	34695	0.49	1.0E-07	BE327843.1	EST_HUMAN	hu28h06.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
9849	22347	35329	2.51	1.0E-07	BF74524.1	EST_HUMAN	MER18 repetitive element:
9855	22353	35334	1.19	1.0E-07	AA386311.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
10362	22856		3.53	1.0E-07	AL163282.2	NT	EST185054 Brain IV Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C082

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12013	24860	30704	2.42	1.0E-07	BE048770.1	EST_HUMAN	h53c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:313212.3' similar to TR:095722 O95722
7325	18852	32714	0.87	9.0E-08	AI539362.1	EST_HUMAN	DJ1163J1.1;
6802	22300	35285	2.1	9.0E-08	AV734819.1	EST_HUMAN	te51b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195.3'
11061	23573	36610	3.41	9.0E-08	AI891052.1	EST_HUMAN	AV734819 cda Homo sapiens cDNA clone cdABFB08.5'
11519	23967	37039	4.51	9.0E-08	AL163301.2	NT	wn30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932.3' similar to contains OFR.12
11061	24263		2.98	9.0E-08	AJ251973.1	NT	OFR repetitive element;
635	15420		2.27	8.0E-08	AI811352.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
1088	13663		0.79	8.0E-08	BE785469.1	EST_HUMAN	Homo sapiens partial steirin-1 gene
3598	16202		1.05	8.0E-08	BE785469.1	EST_HUMAN	wd16b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273.3'
8674	21213	34133	3.54	8.0E-08	AI752367.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976.5'
8674	21213	34134	3.54	8.0E-08	AI752367.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976.5'
8545	22045	35006	3.32	8.0E-08	AW970693.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
11124	23632		2.81	8.0E-08	AF253417.1	NT	EST382776 MAGE resequences, MAGK Homo sapiens cDNA
84	12760	25243	2.82	7.0E-08	Q02357	SWISSPROT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1405	13998	26527	11.08	7.0E-08	X04809.1	NT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
3635	16238	28713	0.7	7.0E-08	P15305	SWISSPROT	Rat mRNA for ribosomal protein L31
3635	16238	28714	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
4002	16600	28073	0.89	7.0E-08	P01606	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
4002	16600	28074	0.89	7.0E-08	P01606	SWISSPROT	IG KAPPA CHAIN V-J REGION OU
10693	23223		6.5	7.0E-08	AI535743.1	EST_HUMAN	IG KAPPA CHAIN V-J REGION OU
11523	23971	37041	6.1	7.0E-08	U24070.1	NT	cong3.P11.A5 cohort Homo sapiens cDNA 3'
12450	16238	28713	3.59	7.0E-08	P15305	SWISSPROT	Rattus norvegicus Munc13-1 mRNA, complete cds
12450	16238	28714	3.59	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
850	13466	25974	3.81	6.0E-08	AL163248.2	NT	DYNEIN HEAVY CHAIN (DYHC)
850	13466	25975	3.81	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2401	14989	27543	2.01	6.0E-08	BE144398.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
4334	16921	26363	1.14	6.0E-08	AL163248.2	NT	MRO-HT0166-191199-004-g09 HT0166 Homo sapiens cDNA
7892	20434		0.68	6.0E-08	P08547	SWISSPROT	Homo sapiens chromosome 21 segment HS21C048
9251	21777		0.6	6.0E-08	AA827075.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							ab56c05.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1335368.3' similar to contains
							MER12.b3 MER12 repetitive element;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11283	23745	36802	2.61	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11407	23858		1.77	6.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
88	12764	25247	2.33	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2277	14851	27429	1.23	5.0E-08	AA493851.1	EST_HUMAN	rh03b09.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element;
11682	24107		7.32	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
11898	24233	31004	1.48	5.0E-08	AW851878.1	EST_HUMAN	QV0-CT0225-131099-034-a12 CT0225 Homo sapiens cDNA
1797	14387	26831	1.53	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1797	14387	26932	1.53	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2910	15527		1.49	4.0E-08	AL079581.1	EST_HUMAN	DKFZ434J0428_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434J0428 5'
3100	15715		1.01	4.0E-08	AI078417.1	EST_HUMAN	ox05602.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674458 3' similar to contains Alu repetitive element;
3986	16584	28055	0.67	4.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6537	19136	31928	1.14	4.0E-08	P52624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8733	21272	34192	0.57	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9066	21603	34533	0.92	4.0E-08	L42571.1	NT	Oricellus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
9563	22063		0.87	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10233	22728		0.71	4.0E-08	AI016342.1	EST_HUMAN	α78d12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622903 3'
10287	22782	35774	3.59	4.0E-08	AI050027.1	EST_HUMAN	an2d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
10782	23306		1.7	4.0E-08	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)
10968	23483	36510	3.7	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
10968	23483	36511	3.7	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4333300 5'
11697	25022		1.4	4.0E-08	W76159.1	EST_HUMAN	zdf5g03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element;
12378	24546		3.48	4.0E-08	AJ343353.1	EST_HUMAN	bs5a11.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3 MER18 MER18 repetitive element;
5795	18420	31136	3.12	3.0E-08	BE018348.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 SYNTAXIN 17.1;
7052	18071	30462	3.77	3.0E-08	AI792737.1	EST_HUMAN	qs78f11.y8 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:1944045 5'
7545	20085	32939	1.41	3.0E-08	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7730	20238		4.17	3.0E-08	AI436352.1	EST_HUMAN	th83h09.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
9812	22310		0.51	3.0E-08	AF055066.1	NT	Homo sapiens MHC class I region
11662	24087		38.65	3.0E-08	R18420.1	EST_HUMAN	y90204.r1 Soares Infant brain T1B1 Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element;
220	12881		6.74	2.0E-08	AW302996.1	EST_HUMAN	xr8706.x1 NCI_CGAP_L126 Homo sapiens cDNA clone IMAGE:2767139 3'
247	12907		6.48	2.0E-08	AA425598.1	EST_HUMAN	zw4807.r1 Soares total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element ;
522	13154	25637	2.59	2.0E-08	AF199349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
688	13312	25796	10.99	2.0E-08	AW888438.1	EST_HUMAN	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
688	13312	25797	10.99	2.0E-08	AW888438.1	EST_HUMAN	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1027	13638		22.68	2.0E-08	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1387	13961	26508	2.03	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1777	14367		1.3	2.0E-08	BE734871.1	EST_HUMAN	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3645189 5'
1895	14480		4.65	2.0E-08	AW270271.1	EST_HUMAN	xp43f11.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2462	15029	27597	0.97	2.0E-08	AA731948.1	EST_HUMAN	nw64h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1251409 3' similar to contains L1.13 L1 repetitive element ;
2590	15143		2.21	2.0E-08	K00216.1	NT	Sheep H1s-rRNA-GUG
3243	15855	28337	6.85	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3243	15855	28338	6.85	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3926	16524		1.93	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161099-012-603 ST0197 Homo sapiens cDNA
4152	18744	29198	0.57	2.0E-08	U92668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4494	17079		1.74	2.0E-08	AA459040.1	EST_HUMAN	aa28c07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element ;
5092	17665		3.83	2.0E-08	AW572881.1	EST_HUMAN	he17h08.x2 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element;
5817	18441	31163	0.87	2.0E-08	AA813204.1	EST_HUMAN	ai80h11.s1 Soares testis NHT Homo sapiens cDNA clone 1377189 3'
5998	18618	31354	0.87	2.0E-08	AW088924.1	EST_HUMAN	xd32c04.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18 b3 MER18 MER18 repetitive element ;
7946	20488	33398	1.07	2.0E-08	P10272	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8054	20596	33503	1.2	2.0E-08	AA490121.1	EST_HUMAN	ab02q06.s1 Strabagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3'
9014	21551		1.41	2.0E-08	AU139978.1	EST_HUMAN	AU139978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10413	22807	35904	0.78	2.0E-08	N78097.1	EST_HUMAN	y7202.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contig LTR1.b3 LTR1 repetitive element;
10413	22807	35905	0.78	2.0E-08	N78097.1	EST_HUMAN	y7202.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
11982	24293		1.74	2.0E-08	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
12559	25073		1.44	2.0E-08	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450
1812	14402	26947	0.89	1.0E-08	AF125348.1	NT	polypeptide 5 (CYP3A5) gene, partial cds
2095	14874		2.74	1.0E-08	BE141959.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5785	18410	31126	4.23	1.0E-08	AJ010770.1	NT	PM2-HT0130-150899-001-f12 HT0130 Homo sapiens cDNA
7748	20254	33148	1.14	1.0E-08	P19474	SWISSPROT	Homo sapiens hypericin gene, exons 1-50
7978	20520	33426	0.55	1.0E-08	AL163302.2	NT	52 KD RO PROTEIN (SJOGEREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8070	20612	33525	0.85	1.0E-08	AF224668.1	NT	Homo sapiens chromosome 21 segment HS21C102
8070	20612	33526	0.85	1.0E-08	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8484	21023	33940	1.84	1.0E-08	AI015304.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9132	21687	34608	0.75	1.0E-08	BE072572.1	EST_HUMAN	cds5a05.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1618736 3'
9876	22373	35350	1.16	1.0E-08	P79110	SWISSPROT	PM2-BT0548-210100-004-d02 BT0548 Homo sapiens cDNA
10449	22943	35953	0.64	1.0E-08	P68063	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
11195	23700	36751	3.79	1.0E-08	AF044083.1	NT	(TRICARBOXYLATE CARRIER PROTEIN)
12081	24353		2.27	1.0E-08	X51755.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
4327	16913	26356	3.93	8.0E-08	AL163278.2	NT	Homo sapiens major histocompatibility locus class III region
4327	16913	26357	3.93	8.0E-08	AL163278.2	NT	Human lambda-immunoglobulin constant region complex (germline)
9574	22469		0.49	9.0E-08	T97950.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
7308	19336	32684	8.83	8.0E-08	AI183500.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
7942	20484	33396	2.88	8.0E-08	AW900159.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
8919	21457		2.77	8.0E-08	AA938892.1	EST_HUMAN	q42e07.x1 Soares fetal heart NBH10W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.11 MSR1 repetitive element;
3687	16268		1.87	7.0E-08	D86842.1	NT	CMO-NN1004-100300-273-606 NN1004 Homo sapiens cDNA
4080	16676		1	7.0E-08	U50871.1	NT	op74408.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3'
							Homo sapiens DNA for 3-ketoadyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
							Human familial Alzheimer's disease (STM2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7843	20385		0.5	7.0E-09	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29 b2 MER29 repetitive element ;
7991	20533		0.78	7.0E-08	AA256200.1	EST_HUMAN	z780c05.r1 Soares_NhlHMPu_S1 Homo sapiens cDNA clone IMAGE:681992 5' similar to contains L1.12 L1 repetitive element ;
9184	21701	34644	2.89	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10086	22581	35574	1.3	7.0E-09	BE254850.1	EST_HUMAN	601111173F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3351834 5'
10248	22743		0.63	7.0E-08	AA058626.1	EST_HUMAN	z58e07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381156 3' similar to contains L1.12 L1 repetitive element ;
10552	23088		2.78	7.0E-08	T97950.1	EST_HUMAN	y658a12.s1 Soares fetal liver epsilon 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
2198	14774		1.16	6.0E-09	AL040439.1	EST_HUMAN	DKFZp434C0514_r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434C0514 5'
5116	17688	30128	5.44	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-180200-001-h05 HT0527 Homo sapiens cDNA
5246	17810	30232	1	6.0E-09	AW593471.1	EST_HUMAN	hg16112.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2945807 3' similar to gb:X53743 FIBULIN-1, ISOFORM C PRECURSOR (HUMAN);
5248	17810	30233	1	6.0E-09	AW593471.1	EST_HUMAN	hg16112.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2945807 3' similar to gb:X53743 FIBULIN-1, ISOFORM C PRECURSOR (HUMAN);
5582	18213	30662	12.11	6.0E-09	AW195784.1	EST_HUMAN	zn85h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8512	21051	33973	0.81	6.0E-09	BE161653.1	EST_HUMAN	MR3-HT0446-260300-201-h12 HT0446 Homo sapiens cDNA
9103	21639	34578	2.37	6.0E-09		NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10177	22872		3.89	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
10610	23143	36154	1.68	6.0E-09	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29 b2 MER29 repetitive element ;
1460	14052	26584	3.95	5.0E-09	BE149284.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
1893	14478	27038	0.83	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6542	19141	31933	2.29	5.0E-09	AA359454.1	EST_HUMAN	EST68746 Fetal lung II Homo sapiens cDNA 5' end
8521	21060	33983	0.59	5.0E-09	P37071	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
10007	22502	35493	2.27	5.0E-09	AW799667.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
547	13178		1.89	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1000	13611		1.99	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C085
1518	14110	26846	1.81	4.0E-09	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2473	15040	27608	4.54	4.0E-09	AA350878.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
7788	20331	33237	0.72	4.0E-09	AA495747.1	EST_HUMAN	zn04c08.r1 Soares_NhlHMPu_S1 Homo sapiens cDNA clone IMAGE:768298 5'
8459	20989	33915	0.82	4.0E-09	T64942.1	EST_HUMAN	y411a07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66804 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10998	23510		1.73	4.0E-09	AA195142.1	EST_HUMAN	z34a12.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665278 5' similar to gb:L07807 DYNAMIN-1 (HUMAN);
2390	14958	27530	6.63	3.0E-09	BE222239.1	EST_HUMAN	hu08e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element;
2589	15151	27717	0.95	3.0E-09	BE222239.1	EST_HUMAN	hu08e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element;
2677	15235	27802	1.22	3.0E-09	P23249	SWISSPROT	PROTEIN MOV-10
3372	15980	28437	1.05	3.0E-09	BE222239.1	EST_HUMAN	hu08e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element;
3423	16031		3.13	3.0E-09	AA442272.1	EST_HUMAN	z54a04.r1 Soares_leslis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4172	16763		3.54	3.0E-09	X16674.1	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
4517	17101	29548	5.18	3.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
4610	17193	29639	1.52	3.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
7841	20383	33287	1.29	3.0E-09	BE465780.1	EST_HUMAN	hx80a02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O55091 O55091 IMPACT PROTEIN.;
10146	22641	35631	1.98	3.0E-09	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10900	23420	36437	3.87	3.0E-09	BF109643.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
10900	23420	36438	3.87	3.0E-09	BF109643.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
845	13461		1.01	2.0E-09	X16674.1	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1301	13895	26417	6.02	2.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1698	14291		10.31	2.0E-09	AL116573.1	EST_HUMAN	DKFZp761B1710_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'
2384	14935	27507	2.79	2.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
4011	16609	29082	4.13	2.0E-09	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
4083	16679	29139	0.94	2.0E-09	AI283479.1	EST_HUMAN	q107d09.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1855793 3'
6876	19810		0.74	2.0E-09	AA357407.1	EST_HUMAN	EST66142 Kidney IX Homo sapiens cDNA 5' and similar to EST containing L1 repeat
7474	19996	32861	8.48	2.0E-09	AA461430.1	EST_HUMAN	z63h06.r1 Soares_tetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:796187 5' similar to contains Alu repetitive element;
7532	20052	32925	0.68	2.0E-09	W28834.1	EST_HUMAN	52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8646	21185	34104	1.72	2.0E-09	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
11634	24074		1.72	2.0E-09	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
12238	13461		27.08	2.0E-09	X16674.1	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
12310	25094		2.25	2.0E-09	AA226070.1	EST_HUMAN	nc11c02.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1032	13642		1.14	1.0E-09	W78152.1	EST_HUMAN	z790403.s1 Soares_telat_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346853 3' similar to
1148	13751	26260	2.3	1.0E-09	5031624	NT	gb:L02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1148	13751	26261	2.3	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2914	15531	28003	1.74	1.0E-09	U0017.1	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2952	15668	28042	3.98	1.0E-09	M28699.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory
2952	15668	28043	3.98	1.0E-09	M28699.1	NT	protein (naip) and survival motor neuron protein (smn) genes, complete cds
3073	15688	28160	0.77	1.0E-09	BE535440.1	EST_HUMAN	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
							Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
4916	17491		5.48	1.0E-09	AA719297.1	EST_HUMAN	601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
5694	18320	30819	0.87	1.0E-09	AL163283.2	NT	z835003.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains
5696	18816	31352	1.46	1.0E-09	U07000.1	NT	Alu repetitive element; contains element MER22 repetitive element ;
6293	18901	31871	3.17	1.0E-09	P26694	SWISSPROT	Homo sapiens chromosome 21 segment HS21C083
8329	20870	33794	0.87	1.0E-09	A1688474.1	EST_HUMAN	Human breakpoint cluster region (BCR) gene, complete cds
10216	22711		2.57	1.0E-09	AL163283.2	NT	CIRCUMSPOROZITE PROTEIN PRECURSOR (CS)
12136	25032	30620	3.3	1.0E-09	11418127	NT	wc39b05.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains
12593	24944		1.82	1.0E-09	AF260225.1	NT	MER25.11 MER25 repetitive element ;
1352	13947	26471	1.48	9.0E-10	AW867740.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
							Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2860	15479	27955	6.87	9.0E-10	A1870071.1	EST_HUMAN	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
6922	19581	32410	4.35	9.0E-10	A1452982.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
158	12821	25309	10.47	8.0E-10	U63630.2	NT	we78h03.x1 Soares_Dieckgraebe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to
3366	15995	28472	0.59	8.0E-10	BE080748.1	EST_HUMAN	SW:RL29_HUMAN_P47914 60S RIBOSOMAL PROTEIN L29 ; contains element PTR5 repetitive element ;
4279	16865	29311	4.11	8.0E-10	AA376832.1	EST_HUMAN	TR:000372 O00372 PUTATIVE P150. ;
6875	22372		2.34	8.0E-10	U36308.2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
730	13350	25844	24.84	7.0E-10	7706225	NT	QV1-BT0631-150200-071-f01 BT0631 Homo sapiens cDNA
730	13350	25845	24.84	7.0E-10	Q13342	SWISSPROT	EST89564 Small intestine [Homo sapiens cDNA 5' end
1663	14256	26791	2.13	7.0E-10	P08548	SWISSPROT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
2087	14847		1.31	7.0E-10	P08548	SWISSPROT	Homo sapiens TPA inducible protein (LOC51586), mRNA
2594	15156		13	7.0E-10	P08547	SWISSPROT	Homo sapiens TPA inducible protein (LOC51586), mRNA
							LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SPI100)
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOG

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3124	15738	28206	2.84	7.0E-10	X00856.1	NT	H sapiens DHFR gene, exon 3
6332	18938	31714	5.28	7.0E-10	AA345220.1	EST_HUMAN	EST51247 Gall bladder II Homo sapiens cDNA 5' end
7446	19970	32838	1.2	7.0E-10	BF352883.1	EST_HUMAN	IL3-HIT0618-110700-209-D12 HT0619 Homo sapiens cDNA
7652	20184		1.43	7.0E-10	P35084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7916	20453	33364	1.68	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
7916	20453	33365	1.68	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
10212	22707	35701	0.57	7.0E-10	L08895.1	NT	Homo sapiens MADSMF2-family transcription factor (MEF2C) mRNA, complete cds
11511	23959	37030	1.54	7.0E-10	AW778769.1	EST_HUMAN	h012902.x1 NCL_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3037202 3' similar to contains Alu repetitive element; contains MER7.b1 MER7 repetitive element;
946	13559	26072	3.68	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2702	15259	27827	1.89	6.0E-10	AI424405.1	EST_HUMAN	h02807.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2095021 3'
4847	17425		2.15	6.0E-10	AW853719.1	EST_HUMAN	RC3-C10254-031089-012-g12 C10254 Homo sapiens cDNA
8718	21257	34177	0.94	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
8718	21257	34178	0.94	6.0E-10	P33730	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
9552	22052	35015	0.52	6.0E-10	P98073	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
11731	24136		1.47	6.0E-10	AW971923.1	EST_HUMAN	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
792	13410		5.2	5.0E-10	AL048804.1	EST_HUMAN	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
3522	16127	28607	0.96	5.0E-10	Q01033	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
5002	17575	30018	1.05	5.0E-10	AW028877.1	EST_HUMAN	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
5002	17575	30019	1.05	5.0E-10	AW028877.1	EST_HUMAN	EST384012 MAGE resequences, MAGL Homo sapiens cDNA
5128	17700	30134	1.37	5.0E-10	AF181897.1	NT	DKFZp434N219_1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N219 5'
7363	19889		1.84	5.0E-10	BF105159.1	EST_HUMAN	HYPOTHETICAL GENE 48 PROTEIN
9455	21981	34932	1.65	5.0E-10	P34678	SWISSPROT	ww97b03.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542081 3' similar to contains MER10.11
9455	21981	34933	1.65	5.0E-10	P34678	SWISSPROT	ww97b03.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542081 3' similar to contains MER10.11
116	12787		1.02	4.0E-10	AI221083.1	EST_HUMAN	ww97b03.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542081 3' similar to contains MER10.11
607	13235	25709	0.73	4.0E-10	AA515260.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
2039	14621	27189	1.17	4.0E-10	AW594709.1	EST_HUMAN	801822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2608	15171	21739	4.19	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7228	19759	32814	22.35	4.0E-10	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10097	22592	35584	0.62	4.0E-10	AW203243.1	EST_HUMAN	U1-H-B12-ah1-a-07-Q.U1.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727061 3'
10342	22836	35831	1.01	4.0E-10	AL267342.1	EST_HUMAN	aq63h1.1.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035663
948	13560	26074	1.95	3.0E-10	N36113.1	EST_HUMAN	Y932F08.s1 Soares melanocyte 2NbhHM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1 L1 L1 repetitive element;
1395	13988		4.43	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
4633	17216	29687	1.07	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4633	17216	29688	1.07	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5846	18274	30748	0.92	3.0E-10	N50109.1	EST_HUMAN	yz11g08.s1 Soares_multiple sclerosis 2NbhMSP Homo sapiens cDNA clone IMAGE:282782 3'
6350	18955	31734	1.87	3.0E-10	P20350	SWISSPROT	RHOMBOLD PROTEIN (VEINLET PROTEIN)
6492	18993	31877	2.86	3.0E-10	BE302670.1	EST_HUMAN	ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2806319 5'
7737	20245	33136	2.3	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBG008 5'
7737	20245	33137	2.3	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBG008 5'
8665	21204	34122	1.08	3.0E-10	H87208.1	EST_HUMAN	ys74b12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element;
8978	21517	34442	1.61	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B08 CT0219 Homo sapiens cDNA
8978	21517	34443	1.61	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B08 CT0219 Homo sapiens cDNA
9264	21790		0.86	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10359	22853		2.13	3.0E-10	T65891.1	EST_HUMAN	yc11e12.1r1 Stradagene lung (#937210) Homo sapiens cDNA clone IMAGE:80398 5'
10485	22979		1.71	3.0E-10	AA769294.1	EST_HUMAN	n236g03.s1 NCL_CGAP_GCBT Homo sapiens cDNA clone IMAGE:1289908 3'
12415	24688	30911	3.44	3.0E-10	BE179517.1	EST_HUMAN	IL3-HT0618-110500-138-E07 HT0618 Homo sapiens cDNA
38	12717	25176	92.79	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
38	12717	25177	92.79	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1942	14526		2.33	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
3015	15631		0.66	2.0E-10	BF675047.1	EST_HUMAN	602136840FT NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5971	18592		7.24	2.0E-10	Q28640	SWISSPROT	(HPRG)
6398	19001	31779	1.42	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7414	19938	32803	7.79	2.0E-10	BE791082.1	EST_HUMAN	601596208FT NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7958	20498	33407	0.54	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
7956	20488	33408	0.54	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
9226	21742		0.85	2.0E-10	BF434585.1	EST_HUMAN	707808.x1 NCL CGAP_Kid111 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.13 L1 repetitive element ;
1558	14148		2.26	1.0E-10	AW667767.1	EST_HUMAN	MRO-SN0038-290300-001-r01 SN0038 Homo sapiens cDNA
1650	14242	26776	2.41	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCXA11 3'
2618	15180		1.78	1.0E-10	AW852001.1	EST_HUMAN	QV0-CT0225-191199-058-e08 CT0225 Homo sapiens cDNA
3548	16152	28634	0.73	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-181199-013-g10 TT0003 Homo sapiens cDNA
3593	16197		0.82	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3911	16197		0.88	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
4087	16883		6.83	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4207	16796	29243	5.77	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4207	16796	29244	5.77	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4214	16803	28253	1.95	1.0E-10	AB031069.1	NT	Homo sapiens POCX1 mRNA for protein containing CXXC domain 1, complete cds
4249	16837		2.53	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5343	17804		1	1.0E-10	AI797745.1	EST_HUMAN	we82f04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347815 3' similar to contains
8182	20723	33637	1.06	1.0E-10	AW408990.1	EST_HUMAN	MER31.11 MER31 repetitive element ;
8589	21128		1.03	1.0E-10	AI288340.1	EST_HUMAN	fb_6A4 Fetal brain library Homo sapiens cDNA
10103	22598		4.16	1.0E-10	AA081888.1	EST_HUMAN	qm04e10.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element ;
10793	23316	36325	3.47	1.0E-10	AI038280.1	EST_HUMAN	zn23g06.r1 Stralagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548314 5'
11672	18038		1.58	1.0E-10	X87344.1	NT	ov65h03.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1672681 3'
283	12839	25425	0.88	9.0E-11	BE145600.1	EST_HUMAN	H sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
2152	14729	27302	6.73	9.0E-11	AL134395.1	EST_HUMAN	IL2-HT0203-291099-016-c08 HT0203 Homo sapiens cDNA
2152	14729	27303	6.73	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
3430	16038	28520	2.33	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3430	16038	28521	2.33	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_11 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225 5'
4998	17182	29828	0.69	9.0E-11	AA775985.1	EST_HUMAN	ae7801.s1 Stralagene echizo brain S11 Homo sapiens cDNA clone IMAGE:970287 3'
5763	18389		3.77	9.0E-11	BE078780.1	EST_HUMAN	RC8-BT0827-140200-011-E08 BT0827 Homo sapiens cDNA
10058	22553	35548	0.88	9.0E-11	AA324950.1	EST_HUMAN	EST127872 Cerebellum II Homo sapiens cDNA 5' end
10058	22553	35548	0.98	9.0E-11	AA324960.1	EST_HUMAN	EST127872 Cerebellum II Homo sapiens cDNA 5' end
12059	24342	30989	3.52	9.0E-11	C16835.1	EST_HUMAN	C16835 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-508B08 5'
3150	15764						Yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;
4035	16633	29102	0.68	8.0E-11	H19791.1	EST_HUMAN	Im54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161938 3'
4117	16711	29185	5.2	8.0E-11	A1478617.1	EST_HUMAN	Yw46e06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
1497	14089	26629	2.94	7.0E-11	AA330642.1	EST_HUMAN	EST34392 Embryo, 6 week I Homo sapiens cDNA 5' end
3939	16537	29004	0.94	7.0E-11	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
8435	20975	33889	2.61	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10129	22824		1.1	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
12206	24430		1.52	7.0E-11	AV701656.1	EST_HUMAN	AV701656 ADB Homo sapiens cDNA clone ADBAC09 5'
437	13070	25586	5.57	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
437	13070	25567	5.57	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6822	19412	32229	1.03	6.0E-11	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
7680	20191	33080	3.29	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8305	20846	33769	3.25	6.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCASC06 5'
12	12891	25147	0.9	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3411	12691	25147	1.29	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4312	18998	28343	1.04	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
6639	19235	32037	3.02	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7537	20057	32931	12.3	5.0E-11	11418799	NT	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
1446	14038		1.41	4.0E-11	AA438042.1	EST_HUMAN	zu01b12.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
2816	15368	27837	8.36	4.0E-11	BE885900.1	EST_HUMAN	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908295 5'
2997	15913	28093	1.17	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4725	17306	28750	0.93	4.0E-11	D44666.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
6602	19199	32005	3.5	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7409	19934		4.06	4.0E-11	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9316	21830		1.44	4.0E-11	BE149425.1	EST_HUMAN	RC1-HT0256-210100-013-108 HT0256 Homo sapiens cDNA
9580	22080	35045	0.91	4.0E-11	AI609753.1	EST_HUMAN	tt82g12.x1 NCL CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105630 3' similar to WP:ZK353.1
12275	24479	30937	1.36	4.0E-11	11545732	NT	CE00385
1538	14130	26668	3.79	3.0E-11	6679077	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
4363	16950		1.47	3.0E-11	AA309248.1	EST_HUMAN	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nm2), mRNA
995	13607	26121	1.64	2.0E-11	AI150502.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
1227	13826	26342	5.04	2.0E-11	R24807.1	EST_HUMAN	q336c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
1227	13826	26343	5.04	2.0E-11	R24807.1	EST_HUMAN	MER10 repetitive element
1655	14247	26780	6.04	2.0E-11	L17432.1	NT	yg43e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1655	14247	26781	6.04	2.0E-11	L17432.1	NT	yg43e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1659	14252	26786	1.09	2.0E-11	AI126371.1	EST_HUMAN	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and epsilon-receptor-like protein
3230	15842	26323	6.98	2.0E-11	P10263	SWISSPROT	COR3 beta (COR3 beta) genes, complete cds
3368	15976	26453	0.76	2.0E-11	AI478617.1	EST_HUMAN	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and epsilon-receptor-like protein
3409	16018	26497	0.65	2.0E-11	Q10473	SWISSPROT	COR3 beta (COR3 beta) genes, complete cds
3544	16148		1.01	2.0E-11	AF020503.1	NT	q551c10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gb:L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1.11
4539	17123		0.89	2.0E-11	BE065537.1	EST_HUMAN	L1 repetitive element
4711	17293		0.65	2.0E-11	AI163227.2	NT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
5070	17643		1.37	2.0E-11	BE062558.1	EST_HUMAN	tm54c08.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161836 3'
6284	18892	31661	1.2	2.0E-11	AWB7806.1	EST_HUMAN	POLYPEPTIDE N-ACETYLGLYCOSAMINYL TRANSFERASE (PROTEIN-UDP
6452	18053	31838	2.02	2.0E-11	AA581028.1	EST_HUMAN	ACETYLGLYCOSAMINYL TRANSFERASE (UDP-GALNAC:POLYPEPTIDE, N-
7246	19775	32632	0.78	2.0E-11	BF592945.1	EST_HUMAN	ACETYLGLYCOSAMINYL TRANSFERASE (GALNAC-T1)
7823	20365		0.66	2.0E-11	P37072	SWISSPROT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (F-HIT) gene, exon 5
						NT	RC3-BT0316-170200-014-605 BT0316 Homo sapiens cDNA
						EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
						NT	Homo sapiens chromosome 21 segment HS21C027
						EST_HUMAN	QV2-BT0238-261099-014-601 BT0258 Homo sapiens cDNA
						EST_HUMAN	QV2-P10073-280300-109-108 PT0073 Homo sapiens cDNA
						EST_HUMAN	nc83h05.r1 NCL CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW:PR18_YEAST
						EST_HUMAN	P19938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16
						EST_HUMAN	7j97c03.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:3442565 3'
						SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR6

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9150	21685		1.27	2.0E-11	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
10184	22878	35671	4.6	2.0E-11	Q13608	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10409	22903	35899	0.79	2.0E-11	AW85874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10409	22903	35900	0.79	2.0E-11	AW85874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10992	23506	36538	2.41	2.0E-11	AA035369.1	EST_HUMAN	z627g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
10992	23506	36539	2.41	2.0E-11	AA035369.1	EST_HUMAN	z627g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11805	25020		2.8	2.0E-11	AA704196.1	EST_HUMAN	z177603.s1 Soares_fetal_liver脾脏_INFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
11836	24200		2.49	2.0E-11	AW842143.1	EST_HUMAN	RC00-GN0027-210100-011-c01 GN0027 Homo sapiens cDNA
11880	24218	31043	2.25	2.0E-11	BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12135	24388		2.03	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12263	24492		5.24	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12628	24707		3.57	2.0E-11	11417988	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
704	13325	25812	2.83	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
816	13434	25939	0.84	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1259	13856	26372	2.96	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1548	14138		1.66	1.0E-11	AF118914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2171	14748	27317	2.61	1.0E-11	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
3548	16150	28630	0.83	1.0E-11	BE004315.1	EST_HUMAN	CM0-BN0105-170300-292-412 BN0105 Homo sapiens cDNA
4905	17480		0.97	1.0E-11	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5535	18167	30581	15.03	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5997	18617	31353	0.8	1.0E-11	BF222646.1	EST_HUMAN	7p57d01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3648945 3' similar to contains MER10.b3
8143	20684	33598	3.16	1.0E-11	4885546	NT	MER10 repetitive element
8517	21056	33979	4.69	1.0E-11	R13174.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
8978	21516	34440	1.38	1.0E-11	BF365119.1	EST_HUMAN	y73d08.r1 Soares_infant_brain_1N1B Homo sapiens cDNA clone IMAGE:28166 5'
8978	21516	34441	1.38	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
11167	23674	36721	2.46	1.0E-11	BF680078.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
2979	15595	28075	0.67	9.0E-12	P20742	SWISSPROT	602154807F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4295977 5'
9713	22211	35184	5.63	9.0E-12	AL163300.2	NT	PREGNANCY ZONE PROTEIN PRECURSOR
9713	22211	35185	5.63	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9261	21787		1	8.0E-12	BE074720.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
11911	24249		4.51	8.0E-12	AJ271736.1	NT	IL5-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA
4766	17347	28786	1.86	7.0E-12	Q05904	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 2/2 34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11228	23759	38815	12.18	7.0E-12	AA704735.1	EST_HUMAN	z23g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
3601	16205		0.72	6.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF06 5'
4440	17026	29466	10.25	6.0E-12	AA732516.1	EST_HUMAN	n28f11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element
8928	21464	34380	0.92	6.0E-12	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
9395	21818		1.8	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER29.12
1081	13686	26198	2.85	5.0E-12	T08573.1	EST_HUMAN	MER29 repetitive element
3437	16045	28526	1.19	5.0E-12	BE047779.1	EST_HUMAN	EST04462 Fetal brain, Stralagene (cat#836206) Homo sapiens cDNA clone HFBDY33
3760	16390	28855	8.69	5.0E-12	AJ271736.1	NT	tz42b05.y1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291217 5'
6172	18784	31550	5.59	5.0E-12	AL163278.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6172	18784	31551	5.59	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6617	19214	32019	9.62	5.0E-12	AW974760.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
7099	19448	32264	1.12	5.0E-12	AL040739.1	EST_HUMAN	EST388850 IMAGE resequences, MAGN Homo sapiens cDNA
7108	19448	32264	1.14	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615.s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
8171	20712	33629	1.43	5.0E-12	AA033745.1	EST_HUMAN	DKFZp434B1615.s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
8602	21141		0.7	5.0E-12	AW887037.1	EST_HUMAN	z01g12.s1 Soares_fetal_liver_NbHH19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains L1.13 L1 repetitive element
8925	21463		0.56	5.0E-12	AL078581.1	EST_HUMAN	RC1-OT0086-220300-011-b07 OT0086 Homo sapiens cDNA
9037	21574	34504	2.42	5.0E-12	AJ271735.1	NT	DKFZp434J0426.r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0426 5'
9344	21858	34806	1.04	5.0E-12	P34982	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 1/2
10176	22871		4.17	5.0E-12	AL163303.2	NT	OLFATORY RECEPTOR 1D2 (OLFATORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFATORY RECEPTOR 17-4) (OR17-4)
10266	22761	35748	0.67	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C103
10461	22955	35966	2.12	5.0E-12	6978754	NT	Homo sapiens chromosome 21 segment HS21C102
265	12923	25409	3.53	4.0E-12	AA700326.1	EST_HUMAN	Rattus norvegicus Deleted in colorectal cancer (rat homolog) (Dcc) mRNA
266	12923	25409	4.43	4.0E-12	AA700326.1	EST_HUMAN	z74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460876 3'
4727	17308	29752	0.82	4.0E-12	AI689984.1	EST_HUMAN	z74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460876 3'
7615	20128		0.7	4.0E-12	BF445140.1	EST_HUMAN	bx29h05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE. ;
8185	20726		2.2	4.0E-12	AF109907.1	NT	nad21b03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MER7 b2
8821	21160	34075	1.2	4.0E-12	AB042815.1	NT	MER7 repetitive element ;
							Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
							Bos taurus Mch2 mRNA for mitochondrial carrier homolog 2, complete cds

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10961	23476	36501	4.25	4.0E-12	AJ228043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
12180	24418		1.61	4.0E-12	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
644	13267	25744	2.73	3.0E-12	AW341883.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517
644	13267	25745	2.73	3.0E-12	AW341883.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517
5843	18272	30748	1.18	3.0E-12	AF111188.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
8316	20857	33783	0.52	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSIN
8035	21572	34501	0.56	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSIN
10535	23072	36085	3.26	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
10535	23072	36086	3.26	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1693	14285	26820	1.05	2.0E-12	AW802131.1	EST_HUMAN	IL5-JM0071-120400-065-a05 UM0071 Homo sapiens cDNA
3513	16118	28598	0.87	2.0E-12	8754495	NT	Mus musculus keratin-associated protein 8.2 (Krtap8-2), mRNA
4192	16781	28228	0.9	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4192	16781	28230	0.9	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4512	17098		2.58	2.0E-12	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
6603	19200		1.54	2.0E-12	AW971857.1	EST_HUMAN	EST383948 IMAGE resequences, MAGL Homo sapiens cDNA
7227	19768	32613	2.97	2.0E-12	T08169.1	EST_HUMAN	EST06060 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
7382	18908	32773	1.21	2.0E-12	BE173035.1	EST_HUMAN	MRO-HT0559-200400-015-e08 HT0559 Homo sapiens cDNA
7656	20168	33055	2.38	2.0E-12	11422228	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
7894	20436		0.8	2.0E-12	AV693827.1	EST_HUMAN	AV693827 GKC Homo sapiens cDNA clone GKCZF804 5'
9232	21954		2.18	2.0E-12	AF196884.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
9898	22393		11.42	2.0E-12	BE165980.1	EST_HUMAN	MRS3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10408	22902	35898	0.69	2.0E-12	A1334130.1	EST_HUMAN	qq07f02.x1 Soares_NhlMPu_S1 Homo sapiens cDNA clone IMAGE:1931835 3' similar to TR:Q13538
11820	24190		2.46	2.0E-12	AL163283.2	NT	Q13538 ORF2: FUNCTION UNKNOWN ;
128	12796	25282	2.79	1.0E-12	AW627674.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
2031	14813		1.53	1.0E-12	A1871726.1	EST_HUMAN	h90a09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11
3106	15721	28191	1.33	1.0E-12	AF000991.1	NT	hm51f07.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1
3106	15721	28192	1.33	1.0E-12	AF000991.1	NT	repetitive element ;
3943	16541	28007	38.65	1.0E-12	AU132248.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
							Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
							AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3943	16541	29008	38.65	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
6121	18736		1.85	1.0E-12	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
6192	18802		1.95	1.0E-12	Q9Y2G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961
6653	19249	32051	0.7	1.0E-12	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
7170	19702	32549	1.74	1.0E-12	AF198864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7204	19735	32587	9.7	1.0E-12	A1248533.1	EST_HUMAN	qh66a04.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:U19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.t1 MER10 repetitive element;
7204	19735	32588	9.7	1.0E-12	A1248533.1	EST_HUMAN	qh66a04.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:U19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.t1 MER10 repetitive element;
							Human gamma T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
8426	20966	33880	0.54	1.0E-12	U66059.1	NT	ac28d05.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:857577 3'
8639	21178	34088	1.18	1.0E-12	AA782323.1	EST_HUMAN	EST374237 MAGG resequences, MAGG Homo sapiens cDNA
11723	24130	37154	4.65	1.0E-12	AW962164.1	EST_HUMAN	w133h08.x1 NCI CGAP_C016 Homo sapiens cDNA clone IMAGE:2392095 3'
11941	24273		1.6	1.0E-12	A1738592.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C088
12097	24900		2.72	1.0E-12	AL163268.2	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12424	24909		2.02	1.0E-12	AF224689.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
4019	16617	29092	0.81	8.0E-13	AB029600.1	NT	zab506.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:293851 3'
9519	22019		3.1	9.0E-13	N69653.1	EST_HUMAN	Homo sapiens prion protein (PrP) gene, complete cds
746	13368	25860	4.58	8.0E-13	U29185.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
746	13368	25861	4.58	8.0E-13	U29185.1	NT	wm31h09.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
1878	14464	27021	3.95	8.0E-13	U60017.1	NT	wm31h09.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8056	20598	33505	0.68	8.0E-13	A1894398.1	EST_HUMAN	Homo sapiens Brulon's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein
8056	20598	33506	0.68	8.0E-13	A1894398.1	EST_HUMAN	(L44L) and FTP3 (FTP3) genes, complete cds
10051	22546		2.58	8.0E-13	U78027.1	NT	

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11809	24052	37117	2.51	8.0E-13	U69060.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S6A3N2T, TCRBV13S6A2T, TCRBV6S9P, TCRBV6S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S6A2T, TCRBV6S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12>
8176	20717		0.63	7.0E-13	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12212	24435		37.61	7.0E-13	BE778223.1	EST_HUMAN	601463285F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866613 5'
12448	24583		1.71	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
2149	14728	27289	6.02	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3364	15972		0.78	5.0E-13	R78338.1	EST_HUMAN	y82704.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145759 5'
3444	16052		1.64	5.0E-13	AA435773.1	EST_HUMAN	z177a12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu
6958	19535	32359	0.68	5.0E-13	P08983	SWISSPROT	repetitive element/contains element MER22 repetitive element ; GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
10739	23264	36279	2.49	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1808	14493		3.69	4.0E-13	AW378814.1	EST_HUMAN	PM2-HT0224-221099-001-011 HT0224 Homo sapiens cDNA
2500	15064		1.71	4.0E-13	AF003528.1	NT	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
4858	17438		1.03	4.0E-13	AA454054.1	EST_HUMAN	z48407.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:795469 5'
5774	18398	31113	5.09	4.0E-13	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7257	19785	32841	1.07	4.0E-13	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
7807	20120	32887	0.81	4.0E-13	AA431528.1	EST_HUMAN	z476g12.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763 G452763 COR1 MRNA ;
7705	20214		1.84	4.0E-13	N44291.1	EST_HUMAN	Y33g05.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32895
8775	21314	34236	0.94	4.0E-13	AL043810.1	EST_HUMAN	A32895 t complex sterility protein - mouse ; DKFZp434A0128_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A0128 5'
8933	22429	35403	4.28	4.0E-13	AI269831.1	EST_HUMAN	q32d05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1899945 3' similar to contains Alu repetitive element;
11046	23559	36595	1.91	4.0E-13	AA435819.1	EST_HUMAN	z178g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
11046	23559	36598	1.91	4.0E-13	AA435819.1	EST_HUMAN	z178g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
192	12852		4.5	3.0E-13	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
898	13512		4.67	3.0E-13	AA430310.1	EST_HUMAN	z468g08.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'
2408	14978	27550	1.08	3.0E-13	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2519	15083		6.72	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2887	15245	27812	2.75	3.0E-13	BF372682.1	EST_HUMAN	CM3-FT0100-140700-242-h08 FT0100 Homo sapiens cDNA
3221	15833		3.1	3.0E-13	AA745844.1	EST_HUMAN	db18402.s1 NCI CGAP_Ki65 Homo sapiens cDNA clone IMAGE:1324035 3'
3551	18155	28637	1.04	3.0E-13	P18816	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
3551	18155	28638	1.04	3.0E-13	P18816	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
5730	18356	31060	0.7	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stralagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element;
5730	18356	31061	0.7	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stralagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element;
6143	18757	31515	0.68	3.0E-13	AW005839.1	EST_HUMAN	wz88c02.x1 NCI CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR:O75139 O75139 KIAA0644 PROTEIN;
7824	20368	33274	9.59	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
8021	20563	33484	0.68	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Re- reactive factor
8021	20563	33485	0.68	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Re- reactive factor
10556	23092		4.07	3.0E-13	AI064768.1	EST_HUMAN	HA0536 Human fetal liver cDNA library Homo sapiens cDNA
10924	23443	36484	2.91	3.0E-13	BE063508.1	EST_HUMAN	CMO-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
11469	23919	36988	2.49	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
161	12824	25312	2.58	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
260	12919	25406	2.22	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1313	13807	26427	8.84	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3038	15654	28133	0.58	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3038	15654	28134	0.58	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3320	15930	28407	1.2	2.0E-13	BF431899.1	EST_HUMAN	nab76f05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3555	16159	28642	1.14	2.0E-13	AF109807.1	NT	Homo sapiens S184 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4166	16776		1.9	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C0078
6271	18879	31647	5.27	2.0E-13	Q06852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6905	19639	32475	7.42	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
10355	22849	35843	4.58	2.0E-13	5031896	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
11893	24236		20.31	2.0E-13	AW892155.1	EST_HUMAN	CMO-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA
313	12967	25456	1.6	1.0E-13	S74129.1	NT	FGF-1=fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
921	13534	26052	4.35	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1381	13974	26502	1.01	1.0E-13	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
2088	14648	27220	1.6	1.0E-13	AA720574.1	EST_HUMAN	hw21g02.s1 NCL_CGAP_GC60 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 THR repetitive element ;
4116	16710		2.21	1.0E-13	AA324394.1	EST_HUMAN	EST27235 Cerebellum II Homo sapiens cDNA 5' and similar to EST containing L1 repeat
4696	17278	29724	1.51	1.0E-13	BF340987.1	EST_HUMAN	602038009F1 NCL_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4185866 5'
7851	20393	33298	0.77	1.0E-13	AA577812.1	EST_HUMAN	nm24d01.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element ;
7851	20393	33297	0.77	1.0E-13	AA577812.1	EST_HUMAN	nm24d01.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element ;
10002	22497		0.9	1.0E-13	O15481	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
10202	22697	35691	0.52	1.0E-13	AF300701.1	NT	Mus musculus osteotesticular protein tyrosine phosphatase mRNA, complete cds
11258	23786	36842	15.07	1.0E-13	BF108755.1	EST_HUMAN	745e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element ;
11714	24124		1.87	1.0E-13	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
12983	24553		4.28	1.0E-13	AJ271795.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
355	13004	25488	4.61	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element ;
358	13005	25489	2.07	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element ;
2545	15109		3.84	9.0E-14	AW881577.1	EST_HUMAN	RC4-CT0322-080100-013-009 CT0322 Homo sapiens cDNA
2627	15189	27757	1.41	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2627	15189	27758	1.41	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2782	15335	27905	3.29	9.0E-14	AB038182.1	NT	Homo sapiens TRF gene cluster for trefoil factor, complete cds
3145	15759	28225	4.32	9.0E-14	AW513266.1	EST_HUMAN	xs54h05.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707833 3'
3275	13004	25488	0.71	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element ;
3868	18464	28928	7.24	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4870	17448	28987	1.77	9.0E-14	AJ002153.1	NT	Seguinus codipus gene for seminal vesicle secreted protein semenogelin I

Table 4

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3545	16149		0.87	8.0E-14	BE492263.1	EST_HUMAN	h271c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
4028	16627		3.29	8.0E-14	R7629.1	EST_HUMAN	y172603.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144796 3'
9369	20308	33211	36.57	8.0E-14	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
9479	21878	34825	4.61	8.0E-14	AA219316.1	EST_HUMAN	zq17c10.s1 Stralagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:629970 3'
11310	23803		4.45	8.0E-14	BE062558.1	EST_HUMAN	QV2-BT0258-281099-014-a01 BT0258 Homo sapiens cDNA
12106	24368	30972	2.07	8.0E-14	AI688118.1	EST_HUMAN	wc92h08.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2328143 3'
1871	15447		2.78	7.0E-14	AW151673.1	EST_HUMAN	xd67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2823146 3' similar to contains MER10.12
8851	21390		0.54	7.0E-14	AL163285.2	NT	MER10 repetitive element ; Homo sapiens chromosome 21 segment HS21C085
390	13036	25525	14.21	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
9736	22234	35212	3.27	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region; diadenosine triphosphate hydrolase (FHIT) gene, exon 5
9738	22234	35213	3.27	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
646	13269	25747	5.28	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
5209	17774	30197	1.53	5.0E-14	AW073791.1	EST_HUMAN	xx03b05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1
5724	18350	31053	4.91	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1162	15434		1.61	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1920	14505	27062	3.86	4.0E-14	AJ007973.1	NT	Homo sapiens LGMD2B gene
3816	16416		0.84	4.0E-14	AA046502.1	EST_HUMAN	zk67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
4378	16966	29412	0.9	4.0E-14	N46328.1	EST_HUMAN	wy73c12.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.13 L1 repetitive element ;
7899	20441		0.49	4.0E-14	X87344.1	NT	H.sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, DOB, DQB2 and RING8, 9, 13 and 14 genes
11833	24073	37135	1.91	4.0E-14	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12457	25107		4.37	4.0E-14	AI886224.1	EST_HUMAN	wm08c03.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu
985	13597	28110	1.26	3.0E-14	X95468.1	NT	R.norvegicus mRNA for GPG2 protein
5059	17632	30075	0.74	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6832	19422	32237	1.08	3.0E-14	AI420786.1	EST_HUMAN	ts91c12.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ;
6832	19422	32238	1.08	3.0E-14	AI420786.1	EST_HUMAN	ts91c12.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ;
8722	21261	34181	0.96	3.0E-14	N42165.1	EST_HUMAN	y07b10.t1 Soares melanocyte 2NBM Homo sapiens cDNA clone IMAGE:270523 5'
10872	23393	36408	2.75	3.0E-14	BE889016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
11116	17632	30075	9.84	3.0E-14	AW265354.1	EST_HUMAN	xp45112.x1 NCL_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MERO repetitive element ;
12369	24904		1.84	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
413	13048	25539	2.51	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
413	13048	25540	2.51	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
719	15422	25828	9.8	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2431	14988		1.48	2.0E-14	AW372888.1	EST_HUMAN	RC5-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA
2504	15068		1.07	2.0E-14	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
2567	15131	27699	1.03	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2699	15256		0.88	2.0E-14	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5715	18341	30847	0.95	2.0E-14	BF380661.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5804	18429	31148	0.8	2.0E-14	AI312351.1	EST_HUMAN	ta78h01.x2 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.13 L1 repetitive element ;
5895	18517	31242	2.86	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
6963	19540		0.88	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-a06 BN0072 Homo sapiens cDNA
7328	19856	32719	1.12	2.0E-14	P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7518	20038	32806	20.34	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
7518	20038	32907	20.34	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
8831	22329	35311	0.54	2.0E-14	AI978795.1	EST_HUMAN	wf59g10.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element
10659	23181	36206	4.65	2.0E-14	AW139800.1	EST_HUMAN	UI-H-B11-adv-a-10-Q-JL.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
12366	24968		3.3	2.0E-14	AF008191.1	NT	Homo sapiens putative G6 protein (GR6) gene, complete cds
12617	15068		1.99	2.0E-14	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1105	13709	26218	1.89	1.0E-14	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
1452	14044	26572	6.89	1.0E-14	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
1452	14044	26573	6.89	1.0E-14	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
2044	14626	27195	7.63	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2228	14803	27374	5.33	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2453	15020	27591	5.89	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2971	15587	28069	1.51	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3203	15815	28260	3.91	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3203	15815	28261	3.91	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3955	16553	29022	2.1	1.0E-14	AA682994.1	EST_HUMAN	ee89c12.s1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4572	17155	29599	1.71	1.0E-14	AW275852.1	EST_HUMAN	xq39h10.x1 NCI CGAP Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
5977	18597	31332	2.03	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6778	24770	32183	12	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
6778	24770	32184	12	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
1620	14213	28744	1.19	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2217	14792		1.39	9.0E-15	AF198779.1	NT	Homo sapiens transcription factor IGEM enhancer 3, JM11 protein, JM4 protein, JM5 protein, TS4 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a7
7507	20029	32892	3.77	9.0E-15	P21416	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
7959	20501	33410	1.36	9.0E-15	BE903559.1	EST_HUMAN	601677750F1NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960156 5'
12560	24860		1.76	9.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2837	13138		1.17	8.0E-15	BE261482.1	EST_HUMAN	601148632F1NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
7233	19763	32619	1.29	7.0E-16	BF036327.1	EST_HUMAN	601498531F1NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
10331	22825		2.53	7.0E-15	AW241958.1	EST_HUMAN	xn77d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element
11776	24164		1.76	7.0E-15	AA284465.1	EST_HUMAN	zs57d08.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701583 5' similar to gb.L21834 STEROL O-ACYLTRANSFERASE (HUMAN); contains L1 L1 repetitive element
1031	13641	26156	6.29	6.0E-15	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6077	18694	31440	1.18	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
6077	18694	31441	1.18	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
11182	25128		1.88	6.0E-15	AW836943.1	EST_HUMAN	QV1-LT0036-150200-070-c10 LT0036 Homo sapiens cDNA
12648	24722		1.3	6.0E-15	BF432200.1	EST_HUMAN	nab81c12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
435	13068	25563	5.19	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2789	15342	27912	2.35	5.0E-15	U91928.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
3515	16120		1.08	5.0E-15	AW296817.1	EST_HUMAN	UI-H-BW0-ajb-g-10-0-UI.s1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731219 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5299	17891		1.28	5.0E-15	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
10555	23091		2.72	5.0E-15	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
452	12681	25137	2.33	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6771	19384	32173	0.79	4.0E-15	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
10940	20297	33184	2.54	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
10940	20297	33185	2.54	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4297	16983		7.28	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
5060	17633		0.57	3.0E-15	P92485	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5
5179	17746	30175	0.72	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library/Homo sapiens cDNA clone 7P01F03
5179	17746	30176	0.72	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library/Homo sapiens cDNA clone 7P01F03
6904	19638		1.41	3.0E-15	Q84625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7323	19850	32711	3.48	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7323	19850	32712	3.48	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
9839	22337		2.32	3.0E-15	AA807128.1	EST_HUMAN	cc36a07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.11 MER19 repetitive element;
10873	23205	36218	3.36	3.0E-15	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12114	24997		1.36	3.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
271	12928	25415	4.1	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
391	13037	25526	3.78	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
391	13037	25527	3.78	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2410	14978	27552	1.44	2.0E-15	BE350127.1	EST_HUMAN	h08g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
2410	14978	27553	1.44	2.0E-15	BE350127.1	EST_HUMAN	h08g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
3559	16163	28645	0.73	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3559	16163	28648	0.73	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4142	16734	29188	0.95	2.0E-15	AW239499.1	EST_HUMAN	xp26h01.x1 NCL_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741521 3' similar to contains L1.13 L1 repetitive element ;
4729	17310		2.72	2.0E-15	AI806335.1	EST_HUMAN	wf0706.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043 Q61043 NINEIN ;
5332	17893	30306	0.93	2.0E-15	P13993	SWISSPROT	REPETITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
5332	17893	30307	0.93	2.0E-15	P13993	SWISSPROT	REPETITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
6329	18935	31711	1.02	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
6329	18935	31712	1.02	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7168	19700		1.37	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7315	19842	32703	2.51	2.0E-15	AA704195.1	EST_HUMAN	z77603.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
7427	19951	32816	4.49	2.0E-15	W05064.1	EST_HUMAN	za76d10.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:298675 5' similar to WP:F44F4.8 CE02227 TRANSPOSASE ;
8837	21376	34300	2.62	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
9002	21539	34468	0.97	2.0E-15	AA397758.1	EST_HUMAN	z77g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9002	21539	34469	0.87	2.0E-15	AA397758.1	EST_HUMAN	z77g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9325	21839	34760	1.13	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
9325	21839	34761	1.13	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
10718	23246		3.59	2.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12487	16163	28845	2.97	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12487	16163	28846	2.97	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2803	15355		2.08	1.0E-15	AI689984.1	EST_HUMAN	b26h05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE ;
3046	15662	28143	1.24	1.0E-15	BE043584.1	EST_HUMAN	pk40602.y1 NCL_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2999162 5'
3176	15789	28261	1.05	1.0E-15	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6510	19110	31888	1.71	1.0E-15	T95763.1	EST_HUMAN	ye40e10.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER6 repetitive element ;
7080	19652		1.91	1.0E-15	BE074217.1	EST_HUMAN	QV3-BT0569-270100-074-g05 BT0569 Homo sapiens cDNA
7105	19445	32262	0.77	1.0E-15	P39057	SWISSPROT	DYNEIN BETA CHAIN, CILIARY
8174	20715	33631	0.89	1.0E-15	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8359	20899	33818	4.97	1.0E-15	AI200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8359	20899	33820	4.97	1.0E-15	AI200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8969	21507	34428	0.51	1.0E-15	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
8972	21510	34432	1.99	1.0E-15	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
9171	21748	34891	0.87	1.0E-15	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9550	22050	35012	1.18	1.0E-15	AA864653.1	EST_HUMAN	oh37c03.s1 NCI CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1459872 3' similar to contains L1.13 L1
10698	23228	38242	6.88	1.0E-15	AF044083.1	NT	repetitive element ;
12564	24820	30792	9.35	1.0E-15	A1783944.1	EST_HUMAN	Homo sapiens major histocompatibility locus class III region
4417	17002		0.83	9.0E-16	BF669487.1	EST_HUMAN	tr31c05.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219812 3' similar to contains Alu repetitive element;
4602	17185	29632	1.11	9.0E-16	4503168	NT	602120192F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4277422 5'
10873	23394	38409	2.66	9.0E-16	F08688.1	EST_HUMAN	Homo sapiens cut (Drosophila)-like 1 (CCAT displacement protein) (CUTL1) mRNA
5880	18502	31228	0.73	7.0E-16	4885120	NT	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
7379	19805	32769	1.36	7.0E-16	O88907	SWISSPROT	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
7379	19805	32770	1.36	7.0E-16	O88907	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
12509	24918		33.75	7.0E-16	T94149.1	EST_HUMAN	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
2186	14762		29.26	6.0E-16	AW972811.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
5436	17891	30387	0.94	6.0E-16	BF365702.1	EST_HUMAN	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
1539	14131	26667	1.21	5.0E-16	AJ251154.1	NT	ye28c12.1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:119082 5'
2705	15262	27829	2.6	5.0E-16	AA992176.1	EST_HUMAN	EST3784702 MAGL resequences, MAGL Homo sapiens cDNA
11396	23848	36914	3.76	6.0E-16	BF217368.1	EST_HUMAN	QV2-NT0048-160800-316-d12 NT0048 Homo sapiens cDNA
12606	24690		4.96	5.0E-16	11418127	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
2281	14855		1.23	4.0E-16	AB001523.1	NT	o80c04.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to
2419	14887	27561	1.88	4.0E-16	AW797168.1	EST_HUMAN	contains element L1 repetitive element ;
2419	14987	27562	1.88	4.0E-16	AW797168.1	EST_HUMAN	601885734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
3503	16108	28584	6.73	4.0E-16	Q16653	SWISSPROT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
4223	16811	29258	4.28	4.0E-16	BE083875.1	EST_HUMAN	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
4223	16811	29259	4.28	4.0E-16	BE083875.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
7698	20207	33094	37.48	4.0E-16	AL163284.2	NT	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
9219	21736	34678	1.44	4.0E-16	11423181	NT	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
11098	23608	36648	1.68	4.0E-16	AV730030.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
							PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C084
							Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
							AV730030 HTF Homo sapiens cDNA clone HTFAWA03 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11800	24180		1.34	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11887	24232		13.76	4.0E-16	C05947.1	EST_HUMAN	C05947 Human pancreatic islet Homo sapiens cDNA clone hbc5355
11897	24239	31008	2.91	4.0E-16	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12178	24414		1.8	4.0E-16	R18591.1	EST_HUMAN	yf6b11.11 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30489 5'
138	12803	25292	0.93	3.0E-16	AW022862.1	EST_HUMAN	af45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486378 5'
138	12803	25293	0.93	3.0E-16	AW022862.1	EST_HUMAN	af45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486378 5'
491	13124		1.24	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5'
501	13133		2.35	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1501	14093	26632	1.81	3.0E-16	Q26983	SWISSPROT	ZONADHESIN PRECURSOR
3004	15620	28097	4.2	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
4007	16605	29079	0.61	3.0E-16	T08169.1	EST_HUMAN	EST08060 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
4031	16629		1.07	3.0E-16	U03887.1	NT	Human BXP20 gene
4689	17271	28720	0.97	3.0E-16	AW160828.1	EST_HUMAN	au76b06.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782163 5' similar to SW:KID1_MOUSE Q61751 RENAL TRANSCRIPTION FACTOR KID-1;
5077	17650	30091	1.14	3.0E-16	AV661393.1	EST_HUMAN	AV661393 GLC Homo sapiens cDNA clone GLGSA01 3'
5482	18116		0.9	3.0E-16	AA077225.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5801	18426	31144	1.57	3.0E-16	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8592	21131	34047	4.08	3.0E-16	AI002836.1	EST_HUMAN	am98h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element;
9805	22303		0.84	3.0E-16	BF690617.1	EST_HUMAN	602246538F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
10027	22522	35518	5.15	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
12637	25078	30518	9.33	3.0E-16	AL043268.2	EST_HUMAN	DKFZp434L1623_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L1623 5'
1007	13618		1.38	2.0E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2429	14996		1.01	2.0E-16	AA621761.1	EST_HUMAN	af06d04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2713	15270		1.53	2.0E-16	J03081.1	NT	Human SSANV-related endogenous retroviral LTR-like element
4257	16843	29282	1.34	2.0E-16	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
5370	17830	30344	0.57	2.0E-16	BE091178.1	EST_HUMAN	RC3-BT0046-131199-003-H12 BT0046 Homo sapiens cDNA
6839	19429	32245	0.89	2.0E-16	Q31125	SWISSPROT	HISTIDINE-RICH PROTEIN KE4
7701	20210	33097	0.78	2.0E-16	AI470723.1	EST_HUMAN	ij16s11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element MER33 repetitive element;
7908	20450	33357	1.81	2.0E-16	AI732837.1	EST_HUMAN	nz47f06.x5 NCI_CGAP_Py12 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:O54849 O54849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905 ;contains MER7.1 MER7 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8099	20840	33551	0.7	2.0E-16	BE858026.1	EST_HUMAN	7182h09.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
8099	20840	33552	0.7	2.0E-16	BE858026.1	EST_HUMAN	7182h09.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
8484	21004	33921	0.6	2.0E-16	AW877214.1	EST_HUMAN	GM4-PT0034-180200-506-e01 PT0034 Homo sapiens cDNA
8484	21004	33922	0.6	2.0E-16	AW877214.1	EST_HUMAN	GM4-PT0034-180200-506-e01 PT0034 Homo sapiens cDNA
10808	23331	36343	2.71	2.0E-16	5902145	NT	Homo sapiens ubiquitin carrier protein E2-C (UBCH10), mRNA
197	12857	25339	2.56	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
405	13080		29.83	1.0E-16	AA628592.1	EST_HUMAN	af39g11.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.12 OFR repetitive element ;
2014	14596	27159	1.78	1.0E-16	BF327942.1	EST_HUMAN	QV0-BN0148-070700-293-a10 BN0148 Homo sapiens cDNA
5886	18518	31243	0.85	1.0E-16	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6565	19163		27.66	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
6688	19284	32087	2.77	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7556	19163		6.98	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
9207	21724	34667	1.15	1.0E-16	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
3802	18402	28966	2.48	9.0E-17	AW900048.1	EST_HUMAN	GM1-NN1003-200300-153-e01 NN1003 Homo sapiens cDNA
6824	19414		1.94	9.0E-17	A1392964.1	EST_HUMAN	ig22c11.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.12
8052	20584		4.65	9.0E-17	AW150257.1	EST_HUMAN	Mer28 repetitive element ;
10124	22619		2.1	9.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1056	13681		1.59	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
3981	18559		0.7	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5771	24748	31111	3.55	8.0E-17	BE172081.1	EST_HUMAN	MRO-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA
7319	19846		1.82	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
1505	14097		3.4	7.0E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBc2), mRNA
5528	18158		2.97	7.0E-17	AF216650.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6789	19380	32196	7.15	7.0E-17	AF228943.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
217	12878	25365	7.43	6.0E-17	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
6455	19056	31841	1.88	6.0E-17	AW682772.1	EST_HUMAN	hi81d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978695 3' similar to contains L1.12
10182	22687	35680	0.52	6.0E-17	AF20138	SWISSPROT	L1 repetitive element ;
							MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
446	12875	25131	2.78	5.0E-17	T64110.1	EST_HUMAN	yc05h08.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:79839 5'
7588	20101	32978	1.82	5.0E-17	T81043.1	EST_HUMAN	yd26b04.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:109327 5'
9284	21884	34828	1.12	4.0E-17	AW129165.1	EST_HUMAN	xf20e04.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618622 3' similar to contains Alu repetitive element; contains MER19 b1 MER19 repetitive element ;
11365	23817	36878	2.17	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
11816	24188		2.36	4.0E-17	A1073546.1	EST_HUMAN	ov43a04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR:Q16530
1540	14132		1.03	3.0E-17	D14547.1	NT	Q16530 PMS3 MRNA ; contains MER10.12 MER10 repetitive element ;
2146	14723	27295	1.28	3.0E-17	AW119123.1	EST_HUMAN	Human DNA, SINE repetitive element
3227	15838		1.41	3.0E-17	P35410	SWISSPROT	xd89c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2804784 3'
3704	16305	28773	1.24	3.0E-17	BE326522.1	EST_HUMAN	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3704	16305	28774	1.24	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
5181	17747		1.02	3.0E-17	BF511268.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
8212	20753	33687	1.09	3.0E-17	N68451.1	EST_HUMAN	UI-H-B14-adj-c-08-Q-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085043 3'
9618	22118	35081	4.54	3.0E-17	AB026898.1	NT	za14b02.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:292491 3' similar to contains PTR5.13 PTR5 repetitive element ;
10282	22777	35787	0.65	3.0E-17	BF327012.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10282	22777	35788	0.65	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
11775	24163		3.77	3.0E-17	11417868	NT	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
375	13024	25510	3.38	2.0E-17	A1270080.1	EST_HUMAN	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
376	13024	25510	2.68	2.0E-17	A1270080.1	EST_HUMAN	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
1025	13636		1.12	2.0E-17	AA722832.1	EST_HUMAN	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
2480	15055	27627	2.43	2.0E-17	Q28983	SWISSPROT	zg81d04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:399751 3'
2490	15055	27628	2.43	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2656	15572	28049	8.06	2.0E-17	P12036	SWISSPROT	ZONADHESIN PRECURSOR
5569	18200	30848	1.57	2.0E-17	M27685.1	NT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5569	18200	30849	1.57	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6410	18013		1.8	2.0E-17	AF050566.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6616	19213		1.58	2.0E-17	AL134881.1	EST_HUMAN	Homo sapiens MHC class 1 region
7773	20282	33179	0.85	2.0E-17	AB037839.1	NT	DKFZp762J0610_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762J0610 5'
							Homo sapiens mRNA for KIAA1418 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8028	20570	33474	1.64	2.0E-17	Q95156	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
8394	20934	33856	1.15	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' and similar to glycogenin
9783	22281	35287	2.45	2.0E-17	BE298888.1	EST_HUMAN	600944690F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860615 5'
9818	22316	35297	3.36	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9818	22316	35298	3.36	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10160	22655	35650	7.23	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10281	22778	35765	0.58	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10281	22778	35766	0.58	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10306	22800	35791	0.63	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10306	22800	35792	0.63	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
780	13399	25902	3.38	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1748	14338		1.2	1.0E-17	A127136.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
1804	14394	26939	2.89	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2162	14738	27309	2.11	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2373	14943	27515	1.86	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3625	16228		0.89	1.0E-17	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4217	16805		8.46	1.0E-17	R09942.1	EST_HUMAN	Y30a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5'
6759	19352	32161	1.55	1.0E-17	A1185642.1	EST_HUMAN	q655b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6759	19352	32162	1.55	1.0E-17	A1185642.1	EST_HUMAN	q655b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
7146	19878	32520	1.28	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8528	21067	33986	1.23	1.0E-17	BE062744.1	EST_HUMAN	QV0-BT0283-101289-072-d07 BT0283 Homo sapiens cDNA
9918	22415	35390	0.94	1.0E-17	AW996338.1	EST_HUMAN	QV3-BN0046-220300-129-c10 BN0046 Homo sapiens cDNA
11295	23747	36805	1.82	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
2510	15074	27847	1.13	9.0E-18	AA174078.1	EST_HUMAN	zp18g12.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609882 3'
9418	21827		3.03	9.0E-18	A1472187.1	EST_HUMAN	j86d03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2149389 3'
3854	16452	28815	1.56	8.0E-18	4759977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
371	13020	25504	32.66	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb.L20888 60S
371	13020	25505	32.66	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb.L20888 60S
7499	19991	32854	0.96	7.0E-18	AW887542.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); RC3-OT0091-170300-011-d03 OT0091 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12306	13020	25504	5.26	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
12306	13020	25505	6.26	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
3334	15944	28419	1.36	6.0E-18	X71791.2	NT	Rattus norvegicus partial Gdn/Pn-1 gene for gila-derived nean/protease nexin I, enhancer region
4857	17435		3.95	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYL TRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
8192	20733		2.75	6.0E-18	11428155	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC83448), mRNA
8289	20830	33751	0.6	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11014	23528	38564	1.87	6.0E-18	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11209	23713	38767	1.9	6.0E-18	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, JPP2, LMP2, TAP1, LMP7, DOB, DOB2 and RING8, 9, 13 and 14 genes
11591	24034		2.22	6.0E-18	11429885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC83091), mRNA
12041	24328	30995	2.24	6.0E-18	U87929.1	NT	Human acetylcholinesterase (AChE) gene, exon 4
1187	13788	26289	11.3	5.0E-18	AI280214.1	EST_HUMAN	qm65p11.x1 Soares_placenta_8w6weeks_2NbHP8a9W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element;
5284	17848	30273	0.94	5.0E-18	D61517.1	EST_HUMAN	HUM411F05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-411F05 5'
5477	18111	30520	1.03	5.0E-18	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
8654	21193	34111	4.62	5.0E-18	BE143312.1	EST_HUMAN	MR0-HT0181-221089-002-c06 HT0161 Homo sapiens cDNA
10857	23378	36396	3.68	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
10857	23378	36397	3.68	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12170	24409		6.5	6.0E-18	AW867182.1	EST_HUMAN	MR1-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA
12531	24644		51.19	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCGA02 3'
130	12797	25283	1.96	4.0E-18	BE044076.1	EST_HUMAN	h036n04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
130	12797	25284	1.96	4.0E-18	BE044076.1	EST_HUMAN	h036n04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
1754	14344	28890	8.14	4.0E-18	AA621814.1	EST_HUMAN	h024f11.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1833	14517		0.92	4.0E-18	AI738592.1	EST_HUMAN	w133n08.x1 NCL_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2392095 3'
2242	14817	27390	1.23	4.0E-18	Q06430	SWISSPROT	N-ACETYLGLUCOSAMINIDE BETA-1,8-N-ACETYLGLUCOSAMINYL TRANSFERASE (N- ACETYLGLUCOSAMINYL TRANSFERASE) (L-BRANCHING ENZYME) (IGNT)

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2242	14817	27391	1.23	4.0E-18	Q06430	SWISSPROT	N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (GNT)
5568	18197	30843	2.32	4.0E-18	A017565.1	EST_HUMAN	ou23a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3
5568	18197	30844	2.32	4.0E-18	A017565.1	EST_HUMAN	ou23a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3
7787	20330		0.81	4.0E-18	AA746811.1	EST_HUMAN	nx84a08.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1268998 similar to contains L1.12 L1 repetitive element ;
10884	23405	36424	7.68	4.0E-18	AA371807.1	EST_HUMAN	EST T83633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
882	13496	26015	18.02	3.0E-18	AA814198.1	EST_HUMAN	ob23h11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581.3 similar to SW_RS5_HUMAN P46782 40S RIBOSOMAL PROTEIN S5. ;
965	13578	26091	2.25	3.0E-18	BE088634.1	EST_HUMAN	CMO-BT0660-210300-288-g07 BT0660 Homo sapiens cDNA
4022	16620	28093	1.25	3.0E-18	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6917	19578	32405	6.98	3.0E-18	BE001671.1	EST_HUMAN	PMO-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
12312	24504		8.85	3.0E-18	AW022015.1	EST_HUMAN	df31h12.y1 Marton Felal Cochlea Homo sapiens cDNA clone IMAGE:2485126.5
272	12829	25416	2.57	2.0E-18	AW839820.1	EST_HUMAN	QV1-LT0036-150200-070-e07 LT0036 Homo sapiens cDNA
1192	13793		197.1	2.0E-18	BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044.5
3157	15771	28238	1.15	2.0E-18	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
5606	18235		3.99	2.0E-18	AA868810.1	EST_HUMAN	ak53a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409852.3 similar to TR:O14577
5697	18323	30823	3.16	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE. ;
5697	18323	30824	3.16	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
6038	18657		1.98	2.0E-18	BF347229.1	EST_HUMAN	Human DNA, SINE repetitive element
6313	18920	31695	1	2.0E-18	X60459.1	NT	602021164F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670.5
6313	18920	31696	1	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6424	19027	31810	0.84	2.0E-18	BF352940.1	EST_HUMAN	Human IFNAR gene for interferon alpha/beta receptor
6460	19061	31847	7.53	2.0E-18	AW665853.1	EST_HUMAN	IL3-HT0819-220700-222-C12 HT0819 Homo sapiens cDNA
9660	22455	35437	1.39	2.0E-18	AW151673.1	EST_HUMAN	h194g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979984.3 similar to contains MER10.12
9660	22455	35438	1.39	2.0E-18	AW151673.1	EST_HUMAN	x67a10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146.3 similar to contains MER10.12
10854	23375	36394	4.96	2.0E-18	AW470791.1	EST_HUMAN	x67a10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146.3 similar to contains MER10.12
							h33d08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499.3 similar to contains THR.b3 THR repetitive element ;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11579	24025	37063	5.24	2.0E-18	AW151299.1	EST_HUMAN	xg47e09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2
11970	13703		20.18	2.0E-18	BE256097.1	EST_HUMAN	MER8 repetitive element ; 601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
4507	17091		0.85	1.0E-18	T95406.1	EST_HUMAN	ye43g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element ;
5558	18190	30606	1.91	1.0E-18	AV653405.1	EST_HUMAN	AV653405 GLC Homo sapiens cDNA clone GLCKE11 3'
5759	18385	31099	2.18	1.0E-18	D00066.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5759	18385	31100	2.18	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
6592	19180	31980	1.37	1.0E-18	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8380	20920	33840	1.22	1.0E-18	AI148298.1	EST_HUMAN	cd69d09.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680593 3' similar to contains L1.L1 repetitive element ;
9813	22311	35293	4.45	1.0E-18	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11918	24295	31011	4.39	1.0E-18	AF003329.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
571	13202	25684	3.33	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
572	13202	25684	2.66	9.0E-19	AA281961.1	EST_HUMAN	MER19 repetitive element ;
7760	20333		5.93	9.0E-19	F06688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
8622	21161	34076	2.46	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8622	21161	34077	2.46	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11007	23521	36556	3.92	9.0E-19	AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
11678	13202	25684	28.32	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
1088	13691		1.38	8.0E-19	AW974902.1	EST_HUMAN	MER19 repetitive element ;
8090	20631	33544	1	8.0E-19	BE158936.1	EST_HUMAN	EST387007 MAGI resequences, MAGN Homo sapiens cDNA
2287	14861	27436	1.72	7.0E-19		NT	MR0-HT0404-210200-001-g08 HT0404 Homo sapiens cDNA
6584	19182	31982	1.91	7.0E-19	AF092090.1	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA
7341	19868	32732	0.95	7.0E-19	P28444	SWISSPROT	Rattus norvegicus cp151 mRNA, partial cds
9925	22421	35395	0.47	7.0E-19	AI344951.1	EST_HUMAN	BETA CRYSTALLIN A2
11823	25088		2.95	7.0E-19	AA705884.1	EST_HUMAN	tb01c08.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052302 3'
3847	16446		1.21	6.0E-19	AW852930.1	EST_HUMAN	260d01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
							PMO-CT0248-131069-001-g01 CT0248 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4582	17145	29592	1.39	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 8 (M50)
4582	17145	29593	1.39	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 8 (M50)
4919	17494		1.15	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
6019	18638	31378	5.29	5.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
8385	18969	31747	0.79	5.0E-19	AW663302.1	EST_HUMAN	hh77b08.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2668787 5'
10322	22816	35812	0.66	5.0E-19	AJ297689.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11412	23863	36924	7.61	5.0E-19	AW183725.1	EST_HUMAN	x87b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2684171 3' similar to contains element MSR1 repetitive element;
12544	24823		1.36	5.0E-19	U66060.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S6A3N2T, TCRBV13S9A2T, TCRBV6S9P, TCRBV5S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S6A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12Z
580	13210	25688	0.95	4.0E-19	AB007670.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2707	15284	27831	1.25	4.0E-19	BF697362.1	EST_HUMAN	602130910F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4287674 5'
5593	18223	30672	1.1	4.0E-19	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3919	16517	28982	1.58	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4373	16560	29405	0.9	3.0E-19	O43900	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4373	16980	29406	0.9	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4544	17128	29571	1.33	3.0E-19	AV708136.1	EST_HUMAN	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
5484	18118		0.8	3.0E-19	AF223467.1	NT	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
7418	18942		1.83	3.0E-19	11432214	NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
9380	20319	33220	1.2	3.0E-19	X69685.1	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA
12084	24347		16.44	3.0E-19	AF165520.1	NT	Musculus mRNA for TPCR33 protein
2595	15157	27725	7.09	2.0E-19	AL163201.2	NT	Homo sapiens pterbinol I protein (PBI) mRNA, complete cds
4542	17126		1.26	2.0E-19	AI311783.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
8272	20813	33735	8.35	2.0E-19	AA012854.1	EST_HUMAN	q091a02.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386 POLY(V) GENE
9823	23221	35308	0.81	2.0E-19	Q95155	SWISSPROT	ze34c09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
507	13140		1.85	1.0E-19	BE408611.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
							801304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2209	14785	27359	1.46	1.0E-19	H30795.1	EST_HUMAN	y078g07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element;
2743	15298		2.16	1.0E-19	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2873	15491		5.99	1.0E-19	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3448	16055	28531	1.37	1.0E-19	AA834987.1	EST_HUMAN	aj49b12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12
5322	17884		2.47	1.0E-19	AW117377.1	EST_HUMAN	xd88h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604739 3' similar to contains L1.b2 L1 L1 repetitive element;
6225	18834	31607	3.54	1.0E-19	U12186.1	NT	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
6356	25115		0.74	1.0E-19	AA595527.1	EST_HUMAN	nh22d03.s1 NCI_CGAP_Pri1 Homo sapiens cDNA clone IMAGE:953093 similar to contains L1.11 L1 repetitive element;
7624	20137	33015	0.86	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
7624	20137	33016	0.86	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
8387	20927	33847	1.78	1.0E-19	M84657.1	NT	Rabbit phosphorylase kinase beta subunit mRNA, complete cds
8678	21215		2.48	1.0E-19	T98920.1	EST_HUMAN	y072b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element;
10090	22585	35578	25.84	1.0E-19	AW812259.1	EST_HUMAN	RCO-ST0174-191099-031-b05 ST0174 Homo sapiens cDNA
10090	22584	35587	1.69	1.0E-19	N44631.1	EST_HUMAN	y031609.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:272972 5'
11353	23807		2.24	1.0E-19	AW023137.1	EST_HUMAN	df49h01.y1 Marten Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487000 5'
11504	24037	37106	1.64	1.0E-19	U09163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
6754	19347	32155	2.39	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6754	19347	32156	2.39	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
7527	20047	32817	1.4	8.0E-20	A1221371.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
7527	20047	32818	1.4	8.0E-20	A1221371.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3314	15924	28402	0.78	7.0E-20	BF328455.1	EST_HUMAN	PM4-AN0096-050900-003-a04 AN0096 Homo sapiens cDNA
7068	18087	30443	5.61	7.0E-20	AL138120.1	EST_HUMAN	DKFZp547D092_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D092 5'
8433	20973	33687	9.45	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCI_CGAP_Pri4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
8433	20973	33688	9.45	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCI_CGAP_Pri4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
11561	24008		8.21	7.0E-20	6912633	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
3611	16214	28694	4.64	8.0E-20	P39188	SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4359	16946	29388	4	8.0E-20	BE622434.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4700	17282		1.11	5.0E-20	AV725123.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HTC8TA01 5'
7189	19701	32548	1.33	5.0E-20	AF075301.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250
7886	20428	33336	4.79	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element ;
7886	20428	33337	4.79	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element ;
8047	20589	33498	0.79	5.0E-20	BE185980.1	EST_HUMAN	MIR3-110487-150200-113-g01 HT0487 Homo sapiens cDNA
8769	21308	34231	1.53	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
8769	21308	34232	1.53	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9366	20305		1.08	5.0E-20	O60809	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.1
5630	18454		0.92	4.0E-20	Q86880	SWISSPROT	HISTONE H2B C (H2B/C)
7866	20408		5.58	4.0E-20	A1874352.1	EST_HUMAN	QV3-DT0043-030200-080-c04 DT0043 Homo sapiens cDNA
10393	22887	35882	1.36	4.0E-20	AW937469.1	EST_HUMAN	QV3-DT0043-030200-080-c04 DT0043 Homo sapiens cDNA
2184	14760	27330	1.11	3.0E-20	U03388.1	NT	Human BXP21 gene
4288	16874	28323	1.49	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I14
4408	16993	29436	0.67	3.0E-20	AF230376.1	NT	Meriones unguliculatus prestin (Pres) mRNA, complete cds
4731	17312	29755	0.93	3.0E-20	AA037616.1	EST_HUMAN	zK36b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element ;
8665	21404		2.94	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
10223	22718	35708	0.82	3.0E-20	BF185264.1	EST_HUMAN	601843561F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4084343 5'
10543	23080		1.84	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11387	23839	36902	2.42	3.0E-20	A1284244.1	EST_HUMAN	q70d02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
11387	23839	36903	2.42	3.0E-20	A1284244.1	EST_HUMAN	q70d02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
11836	24202	31039	17.42	3.0E-20	BE888422.1	EST_HUMAN	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
863	13478		23.08	2.0E-20	AW303868.1	EST_HUMAN	x724e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
1150	13753	26262	2.92	2.0E-20	AA516335.1	EST_HUMAN	P97481 40S RIBOSOMAL PROTEIN S5 ;
							hg69h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
1150	13753	26263	2.92	2.0E-20	AA516335.1	EST_HUMAN	G1224066 ORF2: FUNCTION UNKNOWN ;
							hg69h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
							G1224066 ORF2: FUNCTION UNKNOWN ;

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2843	13478		16.26	2.0E-20	AW303868.1	EST_HUMAN	xr24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
5081	17654	30094	4.35	2.0E-20	Q28983	SWISSPROT	P97461 40S RIBOSOMAL PROTEIN S5 ;
5081	17654	30095	4.35	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5328	17889		1.43	2.0E-20	5174538	NT	ZONADHESIN PRECURSOR
8061	20603	33514	0.97	2.0E-20	AA309457.1	EST_HUMAN	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
9118	21654	34595	5.33	2.0E-20	D10083.1	NT	EST180328 Liver III Homo sapiens cDNA 5' end
9118	21654	34590	5.33	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
11622	24064	37128	1.76	2.0E-20	AA766755.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
11922	24064	37129	1.76	2.0E-20	AA766755.1	EST_HUMAN	MER4 repetitive element ;
12236	24809	30789	2.84	2.0E-20	H55371.1	EST_HUMAN	oa35b08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1306935 3' similar to contains MER4.b2
2058	15386	27211	3.02	1.0E-20	AA281981.1	EST_HUMAN	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
4533	17117	29563	1.18	1.0E-20	BF115158.1	EST_HUMAN	z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
6975	19551	32376	0.72	1.0E-20	AF049587.1	EST_HUMAN	MER19 repetitive element ;
8080	21626	34562	2.48	1.0E-20	11418491	NT	h84b08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1
11427	23678	36943	3.02	1.0E-20	AF223391.1	NT	repetitive element ;
11966	24286		6.39	1.0E-20	AA420453.1	EST_HUMAN	AF049587 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
11681	24098		3.8	9.0E-21	AW898189.1	EST_HUMAN	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
8746	21285		1.77	8.0E-21	AW674891.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11413	23864	36925	4.8	8.0E-21	AA809411.1	EST_HUMAN	nc60g08.r1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:745694 similar to contains L1.13 L1
11852	24212		5.02	8.0E-21	O21930	SWISSPROT	repetitive element ;
2113	14691	27258	1.61	7.0E-21	P15800	SWISSPROT	RC3-NN0068-090500-021-503 NN0068 Homo sapiens cDNA
2113	14691	27259	1.61	7.0E-21	P15800	SWISSPROT	bb30a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2884714 5' similar to SW:NIAM_HUMAN
3764	16365	28832	0.59	7.0E-21	AL163300.2	NT	O95189 NADH-UBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR ;
4341	16928		4.31	7.0E-21	AA046502.1	EST_HUMAN	o57106.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1338835 3'
6564	19162	31960	0.79	7.0E-21	AL183218.2	NT	ATP SYNTHASE A CHAIN (PROTEIN 6)
							LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
							LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
							Homo sapiens chromosome 21 segment HS21C100
							z667a08.r1 Spares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
							Homo sapiens chromosome 21 segment HS21C018

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8327	20868	33791	1.47	7.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
8810	21149	34084	10.47	7.0E-21	D14718.1	NT	Human chromosomal protein HMG1 related gene
10022	22517	35512	0.73	7.0E-21	AW856922.1	EST_HUMAN	RCO-CT0301-271189-031-F03 CT0301 Homo sapiens cDNA
10575	23110	36123	3.18	7.0E-21	AA723404.1	EST_HUMAN	zp73d03.s1 Soares_fetal_heart_NHH19W Homo sapiens cDNA clone IMAGE:398981 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); contains THR.3 OFR repetitive element;
11147	23655	36697	1.94	7.0E-21	7706668	NT	Homo sapiens PTD013 protein (PTD013), mRNA
4179	16770	29219	0.89	6.0E-21	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
9063	21600		0.58	6.0E-21	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA
980	13571	26087	0.82	5.0E-21	5902031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4453	17039	29482	3.12	5.0E-21	BE968839.1	EST_HUMAN	601849871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
4922	17497	29948	5.67	5.0E-21	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
6860	19594		0.83	5.0E-21	AW440864.1	EST_HUMAN	he05e10.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918154 3'
7086	19657	32496	1	5.0E-21	BE856505.1	EST_HUMAN	7f83d11.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303573 3' similar to contains OFR.t1 OFR repetitive element;
10466	22860	35970	0.79	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLT1 (GLI-1)
10466	22860	35971	0.79	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLT1 (GLI-1)
11766	24157		1.49	5.0E-21	AA393574.1	EST_HUMAN	z172c04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5'
1789	14359	26904	1.24	4.0E-21	AA970713.1	EST_HUMAN	co08e08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530 PMS3 MRNA; contains OFR.t1 OFR repetitive element;
6953	19530	32355	3.04	4.0E-21	AB019576.1	NT	Rattus norvegicus mRNA for rTLM, complete cds
9695	22194	35167	0.61	4.0E-21	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
1877	14463	27020	5.92	3.0E-21	AA218891.1	EST_HUMAN	zq15d06.s1 Stralagena fetal retina 937202 Homo sapiens cDNA clone IMAGE:629771 3'
2313	14885	27460	1.2	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3116	15730	28200	3.35	3.0E-21	AJ007973.1	NT	Homo sapiens LGMD2B gene
5691	18317	30818	0.97	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5691	18317	30817	0.97	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5913	18535		0.75	3.0E-21	AV661044.1	EST_HUMAN	AV661044 GLC Homo sapiens cDNA clone GLG0A10 3'
6326	18932		60.27	3.0E-21	BF184739.1	EST_HUMAN	501844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064945 5'

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7129	19469	32287	7.35	3.0E-21	BF361093.1	EST_HUMAN	IGC1-OT0083-100800-019-g08 OT0083 Homo sapiens cDNA
9609	22109	35071	0.98	3.0E-21	AW897760.1	EST_HUMAN	CM1-NN0063-280400-203-h08 NN0063 Homo sapiens cDNA
12359	25013	30617	2.75	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
167	12820		19.17	2.0E-21	BE163247.1	EST_HUMAN	QV3-HIT0458-170200-090-g12 HIT0458 Homo sapiens cDNA
970	13581	28083	0.71	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
970	13581	28094	0.71	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1256	13853		2	2.0E-21	BED64410.1	EST_HUMAN	RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA
2665	15223	27795	2.45	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2665	15223	27796	2.45	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5675	18302	30784	1.81	2.0E-21	AI624582.1	EST_HUMAN	ts30r03.x1 NCI_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854
5765	18391	31103	0.91	2.0E-21	AA027211.1	EST_HUMAN	HYPOTHETICAL 51.1 KD PROTEIN ;
5765	18391	31104	0.91	2.0E-21	AA027211.1	EST_HUMAN	z897a12.r1 Soares_fetal_hear NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8304	20845	33768	5.08	2.0E-21	BE141785.1	EST_HUMAN	QV0-HIT0103-091189-050-g11 HIT0103 Homo sapiens cDNA
8757	21296	34216	3.84	2.0E-21	AU136779.1	EST_HUMAN	AU136778 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'
10837	23454		2.2	2.0E-21	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
11199	23704	38754	2.24	2.0E-21	BE973829.1	EST_HUMAN	MER29 repetitive element ;
11199	23704	38755	2.24	2.0E-21	BE973829.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
12072	24351		10.78	2.0E-21	AF176815.1	NT	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
1298	13892	28415	1.54	1.0E-21	AA597657.1	EST_HUMAN	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
1448	14040		3.58	1.0E-21	AI601264.1	EST_HUMAN	n46c04.s1 NCI_CGAP_P44 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
5397	17955	30368	14.37	1.0E-21	P08548	SWISSPROT	MER29 repetitive element ;
6613	19210		2.59	1.0E-21	AL078752.1	EST_HUMAN	ar88d12.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
7243	19772	32829	4.66	1.0E-21	AI223104.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10477	22971		1.45	1.0E-21	5730038	NT	DKFZp434i0830_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434i0830 5'
12485	24616		2.46	1.0E-21	AF046133.1	NT	gg47e05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:M64241 QM
4500	17084	29534	2.78	9.0E-22	AI702438.1	EST_HUMAN	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
8540	21079	33998	1.2	9.0E-22	AL163201.2	NT	Homo sapiens chromosome Xp22 410-8
8540	21079	33999	1.2	9.0E-22	AL163201.2	NT	h294a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TR:Q15408 Q15408
10670	23202	36215	5.06	9.0E-22	AV761874.1	EST_HUMAN	NEUTRAL PROTEASE LARGE SUBUNIT ;
							Homo sapiens chromosome 21 segment HS21C001
							Homo sapiens chromosome 21 segment HS21C001
							AV761874 MDS Homo sapiens cDNA clone MDSGCG05 5'

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11553	24001	37073	3.44	9.0E-22	AU140358.1	EST_HUMAN	AU140358 PLAGE2 Homo sapiens cDNA clone PLAGE2000394 5'
984	13596		4.19	8.0E-22	BE144748.1	EST_HUMAN	CM0-HT0179-281099-078-h05 HT0179 Homo sapiens cDNA
7837	20379		3.26	8.0E-22	AA046502.1	EST_HUMAN	Z07a08.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
693	13316	25801	5.27	7.0E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
4370	16957	29399	2.55	7.0E-22	Q61838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
5180	17755	30184	1.12	7.0E-22	AB008881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
8624	21163		1.99	7.0E-22	AF151054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
8766	21305	34227	3.39	7.0E-22	M75990.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBFCF07
9520	22020	34977	1.83	7.0E-22	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8184	20725		2.67	6.0E-22	AW028123.1	EST_HUMAN	wx05g07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542812 3'
6640	19236	32038	2.82	5.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10221	22716	35707	7.63	5.0E-22	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12314	24506		2.92	5.0E-22	BF476511.1	EST_HUMAN	naa27b06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3255898 3' similar to contains Alu repetitive element;
3698	16299		0.83	4.0E-22	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
8049	20591	33498	0.53	4.0E-22	AV703223.1	EST_HUMAN	AV703223 ADB Homo sapiens cDNA clone ADBAUE12 5'
8352	25122		3.36	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10601	23135	36149	2.85	4.0E-22	BF218030.1	EST_HUMAN	601882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095434 5'
12492	24621		3.39	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
984	13606		0.99	3.0E-22	A469679.1	EST_HUMAN	tm14h10.x1 NCI_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gb:U19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1.11 L1 repetitive element ;
3735	16336		1.44	3.0E-22	D14718.1	NT	Human chromosomal protein HMGI related gene
4921	17496	29947	3.04	3.0E-22	A090125.1	EST_HUMAN	qb28c07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.12 MER12 repetitive element ;
8172	20713		1.07	3.0E-22	BE156613.1	EST_HUMAN	QV0-HT0368-090200-099-f12 HT0368 Homo sapiens cDNA
8177	20718	33633	2.55	3.0E-22	BE089841.1	EST_HUMAN	RC5-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
8301	20842	33762	1	3.0E-22	X60660.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
8301	20842	33763	1	3.0E-22	X60660.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
1896	14578		2.49	2.0E-22	N24942.1	EST_HUMAN	yc73d05.s1 Soares_melanocyte2NbHM Homo sapiens cDNA clone IMAGE:287369 3'
2564	15128	27697	1.61	2.0E-22	P24916	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
3467	18074	28547	5.3	2.0E-22	8394043	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4310	16896	29340	1.35	2.0E-22	AW817794.1	EST_HUMAN	PM1-S.T0262-281199-001-d12 S.T0262 Homo sapiens cDNA
6015	24753	31372	1.95	2.0E-22	W39458.1	EST_HUMAN	zc20f01.11 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:322873 5' similar to gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);

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6324	18930	31706	3.3	2.0E-22	BF082116.1	EST_HUMAN	RCO-TN0079-150900-025-h12 TN0079 Homo sapiens cDNA
9619	22119	35082	1.59	2.0E-22	A1276522.1	EST_HUMAN	q176h06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879299 3' similar to contains
9712	22210	35182	0.69	2.0E-22	AA715316.1	EST_HUMAN	MER29.i3 MER29 repetitive element;
9712	22210	35183	0.69	2.0E-22	AA715315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219269 3'
11595	24038	37107	2.33	2.0E-22	AW418660.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219269 3'
11644	24605	30886	2.57	2.0E-22	AL163280.2	NT	ha24f04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874655 3'
1921	14506	27083	1.59	1.0E-22	AW885517.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2620	15182	27748	1.88	1.0E-22	U50871.1	NT	PM4-SN0020-010400-009-h02 SN0020 Homo sapiens cDNA
3457	16064	28539	1.45	1.0E-22	D14547.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
7723	20231	33120	1.29	1.0E-22	BE084667.1	EST_HUMAN	Human DNA, SINE repetitive element
10446	22840	35950	0.94	1.0E-22	A1365435.1	EST_HUMAN	MRO-BT0859-220200-002-h07 BT0859 Homo sapiens cDNA
10446	22840	35951	0.94	1.0E-22	A1365435.1	EST_HUMAN	qz09b07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER29.b2
12540	24650		12.67	9.0E-23	AW802801.1	EST_HUMAN	MER29 repetitive element;
3829	18232	28707	0.64	8.0E-23	AF198349.1	NT	MER29 repetitive element;
3352	15980		2.37	7.0E-23	AV647246.1	EST_HUMAN	IL2-UM0076-070400-061-F11 UM0076 Homo sapiens cDNA
10918	23437	36458	4.4	7.0E-23	5031952	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3481	16087		1.63	6.0E-23	AF198333.1	NT	AV647248 GLC Homo sapiens cDNA clone GLCAW007 3'
4355	16942	29384	1.1	6.0E-23	AL163249.2	NT	Homo sapiens Naf56 (D. melanogaster)-like protein (NOT56L) mRNA
11790	24173	31026	3.44	6.0E-23	AF224669.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
11790	24173	31027	3.44	6.0E-23	AF224669.1	NT	Homo sapiens chromosome 21 segment HS21C049
11960	24300	30985	4.26	6.0E-23	AI209130.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
5635	18284	30736	5.78	5.0E-23	U82671.2	NT	(UBE2D3) genes, complete cds
6386	24763	31770	3.66	5.0E-23	AF179818.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
7463	24763	31770	3.02	5.0E-23	AF179818.1	NT	qz59e03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to
5375	17934	30348	0.92	3.0E-23	AW846839.1	EST_HUMAN	SW.MV10_MOUSE P23249 PROTEIN MOV.10.;
6569	19167	31983	1.01	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6569	19167	31984	1.01	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7780	20323	33228	4.27	3.0E-23	AA130165.1	EST_HUMAN	z35g09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503968 5' similar to contains MER29.12 MER29 repetitive element ;
9173	21760	34694	2.69	3.0E-23	Z70684.1	NT	Human endogenous retroviral element HC2
9173	21750	34695	2.69	3.0E-23	Z70684.1	NT	Human endogenous retroviral element HC2
10219	22714		1.23	3.0E-23	AW897927.1	EST_HUMAN	RC3-NN0066-270400-011-h01 NN0066 Homo sapiens cDNA
10989	23503						Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
694	13317	25802	1.54	3.0E-23	AF280107.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1182	15391		3.65	2.0E-23	AJ289880.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2821	15373	27942	4.01	2.0E-23	M55270.1	NT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2821	15373	27943	1.47	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3418	18026		1.47	2.0E-23	P22105	SWISSPROT	qs73f11.x1 NCJ CGAP_P228 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
3779	18379		1.36	2.0E-23	AI201459.1	EST_HUMAN	MR3-HT0487-150200-113-q01 HT0487 Homo sapiens cDNA
4048	16645	29112	3.93	2.0E-23	BE165980.1	EST_HUMAN	y16a02.r1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:205418 5'
4048	16645	29113	3.01	2.0E-23	H59931.1	EST_HUMAN	y16a02.r1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:205418 5'
7814	20357		3.01	2.0E-23	H59931.1	EST_HUMAN	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
8777	21316	34238	4.59	2.0E-23	AF280107.1	NT	Homo sapiens chromosome 21 segment HS21C103
11772	24161		1.05	2.0E-23	AL163303.2	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
12326	24512		3.5	2.0E-23	M32858.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
12454	25017		4.44	2.0E-23	AF009660.1	NT	AU133931 OVARC1 Homo sapiens cDNA clone OVARC1000948 5'
4627	17210	29660	1.35	2.0E-23	AU133931.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C052
4881	17456		1.72	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C010
6821	19411		5.35	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8297	20838	33759	4.93	1.0E-23	BE378471.1	EST_HUMAN	601238455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5' PTR5 repetitive element ;
578	13208		4.53	1.0E-23	AA448097.1	EST_HUMAN	zw82006.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:762898 5' similar to contains PTR5.12
4753	17334	29777	1.48	9.0E-24	AA663213.1	EST_HUMAN	ab75a08.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852758 3' similar to TR:E19822 E19822 CA PROTEIN. ;
4753	17334	29778	1.18	8.0E-24	P23269	SWISSPROT	OLFATORY RECEPTOR-LIKE PROTEIN I3
4753	17334	29778	1.18	8.0E-24	P23269	SWISSPROT	OLFATORY RECEPTOR-LIKE PROTEIN I3

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
6576	19174	31973	1.06	8.0E-24	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
3941	16539		1.23	7.0E-24	EST_HUMAN	QV0-DT0047-170200-122-a08 DT0047 Homo sapiens cDNA
5345	17906		18.11	7.0E-24	EST_HUMAN	DKFZp434A2311_r1 434 (synonym: h153) Homo sapiens cDNA clone DKFZp434A2311 5'
10519	23057		2.8	7.0E-24	EST_HUMAN	xv17f03.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element;
735	13355		2.28	6.0E-24	NT	Macaca fuscata mRNA for Testis-Specific Protein Y (TSPY), complete cds
871	13486	26001	12.95	6.0E-24	NT	Homo sapiens chromosome 21 segment HS21C049
4042	16840	29107	9.12	5.0E-24	NT	Homo sapiens 989 kb contig between AML1 and CBRI on chromosome 21q22, segment 3/3
7735	20243	33134	0.9	5.0E-24	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
6087	18703	31451	3.17	4.0E-24	EST_HUMAN	nm31h05.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW:POL_MLVRK P31795 POL POLYPROTEIN;
8615	21154	34088	1.37	4.0E-24	EST_HUMAN	RC3-ST0197-130100-014-008 ST0197 Homo sapiens cDNA
11059	23571	36608	1.65	4.0E-24	EST_HUMAN	601078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464488 5'
12165	24405	30980	4.77	4.0E-24	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
12428	24611	30889	1.37	4.0E-24	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
8362	20902		2.57	3.0E-24	EST_HUMAN	hh68c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967950 3' similar to contains MER29 b2
8414	20954		1.51	3.0E-24	EST_HUMAN	MER29 repetitive element;
9369	21809	34760	3.79	3.0E-24	NT	EST374149 IMAGE resequences, MAGG Homo sapiens cDNA
12247	24488	30959	2.85	3.0E-24	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C052
2384	14953	27525	3.07	2.0E-24	EST_HUMAN	601810449F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053398 5'
3867	16465		0.82	2.0E-24	EST_HUMAN	zp11f09.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609161 5'
7490	20013	32879	1.14	2.0E-24	NT	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
8675	21214	34135	2.59	2.0E-24	EST_HUMAN	Mus musculus rho/tec-interacting citron kinase (Crik) mRNA, complete cds
8712	21251		0.87	2.0E-24	EST_HUMAN	DKFZp781L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781L1712 5'
9769	22266	35250	0.92	2.0E-24	EST_HUMAN	y92b09.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains MER28 repetitive element;
9768	22266	35251	0.82	2.0E-24	EST_HUMAN	h77a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
12080	25082		13.88	2.0E-24	NT	h77a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
1734	14325	28667	3.18	1.0E-24	NT	Human O family dispersed repeat element
2697	15254		1.43	1.0E-24	EST_HUMAN	Homo sapiens CGI-127 protein (LOC51646), mRNA
3055	15671	28147	0.76	1.0E-24	NT	QV0-ST0294-100400-185-c10 ST0294 Homo sapiens cDNA
4357	16944		1.97	1.0E-24	NT	Mus musculus mRNA for HGT keratin, partial cds
						Homo sapiens PTEN (PTEN) gene, exon 2

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7551	20070	32948	4.08	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7713	20222	33109	0.8	1.0E-24	BE144526.1	EST_HUMAN	MRO-HT0166-271199-005-009 HT0166 Homo sapiens cDNA
7885	20427	33335	1.38	1.0E-24	AW601164.1	EST_HUMAN	CMQ-NN1010-130300-281-c07 NN1010 Homo sapiens cDNA
11545	23993	37064	1.58	8.0E-25	7706707	NT	Homo sapiens putative secreted protein (SIG11), mRNA
5443	17888		2.05	8.0E-25	6138972	NT	Homo sapiens adrenergic, beta, receptor kinase 2 (ADRBK2), mRNA
5136	17708	30140	2.99	7.0E-25	AA483944.1	EST_HUMAN	ne2e10.st NCL CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2
8160	20701	33616	5.07	7.0E-25	AA486646.1	EST_HUMAN	MER1 repetitive element;
11547	23895	37087	9.93	7.0E-25	AA583540.1	EST_HUMAN	ne06a09.st1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element;
7065	18094		4.4	6.0E-25	W87623.1	EST_HUMAN	nt25h06.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914843 similar to SW.R14A_YEAST
7708	20215	33103	10.77	6.0E-25	7305360	NT	P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA.;
11196	23701	36752	4.55	5.0E-25	AW979107.1	EST_HUMAN	zh65h07.r1 Sceres_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416989 5'
1496	14088	26628	2.75	4.0E-25	T98107.1	EST_HUMAN	Mus musculus otogelin (Otog), mRNA
3449	16058		3.2	4.0E-25	AW887871.1	EST_HUMAN	EST391217 MAGE resequences, MAGEP Homo sapiens cDNA
3974	16572	29042	1.42	4.0E-25	AF000368.1	NT	ye58h04.r1 Sceres_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:121783 5'
4407	16982		4.05	4.0E-25	BE170957.1	EST_HUMAN	PM3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
3362	15970	28447	3.73	3.0E-25	8923321	NT	Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
3362	15970	28448	3.73	3.0E-25	8923321	NT	QV3-HT0543-140400-149-g11 HT0543 Homo sapiens cDNA
5022	17598	30039	0.69	3.0E-25	P2622	SWISSPROT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
6728	19322	32127	0.84	3.0E-25	AA603590.1	EST_HUMAN	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
8279	20820	33739	3.84	3.0E-25	AL163210.2	NT	np27b02.st1 NCL CGAP_P22 Homo sapiens cDNA clone IMAGE:1117515 3' similar to gb:M61866 ZINC FINGER PROTEIN 85 (HUMAN);
10911	23430	36450	2.02	3.0E-25	AA579013.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
1392	13986	26513	9.82	2.0E-25	5032158	NT	nt30h10.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:915331 similar to contains L1.L1 L1 repetitive element;
2347	14918	27492	7.6	2.0E-25	BE688016.1	EST_HUMAN	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2858	15142	27711	3.84	2.0E-25	P17008	SWISSPROT	60T511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
4268	18854	29301	2.04	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4268	18854	29302	2.04	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
9680	22179	35154	1.9	2.0E-25	AL449573.1	EST_HUMAN	40S RIBOSOMAL PROTEIN S16
387	13033	25522	0.71	1.0E-25	AL040229.1	EST_HUMAN	AL449573 Homo sapiens Testis (Starides GS) Homo sapiens cDNA
1291	13886		1.67	1.0E-25	9635487	NT	DKFZp434H0313_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0313 5'
							Human endogenous retrovirus, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2478	15045	27613	1.13	1.0E-25	Q06055	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4984	17558	30001	3.08	1.0E-25	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-h08 HT0454 Homo sapiens cDNA
6683	19278		0.85	1.0E-25	AA189080.1	EST_HUMAN	zq45b06.s1 Stragene HNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632827 3' similar to contains Alu repetitive element;
6890	24775	32460	3.08	1.0E-25	AA582890.1	EST_HUMAN	nm54h11.s1 NCI_QGAP_Kid6 Homo sapiens cDNA clone IMAGE:1087749 3'
7855	20397	33303	4.27	1.0E-25	AA709079.1	EST_HUMAN	z88g04.s1 Soares_fetal_heart_NbHH18W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains PTR5.0 PTR5 repetitive element;
9465	21890	34848	0.68	1.0E-25	X60660.1	NT	R.rattus RYZG5 mRNA for a potential ligand-binding protein
9465	21890	34847	0.68	1.0E-25	X60660.1	NT	R.rattus RYZG5 mRNA for a potential ligand-binding protein
10849	23370	36389	3.71	1.0E-25	U93163.1	NT	Homo sapiens IMAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
11787	24171	36777	1.8	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
11787	24171	36778	1.8	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
2523	15087	27660	1.57	9.0E-28	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11645	24828		1.69	9.0E-28	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5872	18494		1.55	8.0E-28	D14547.1	NT	Human DNA, SINE repetitive element
1621	14214	28745	0.92	7.0E-28	AF003528.1	NT	Homo sapiens X-linked antihydrolytic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4052	16649	28117	1.18	7.0E-28	X80211.1	NT	H. sapiens DNA for endogenous retroviral like element
4239	16827	28276	2.04	7.0E-26	AW340153.1	EST_HUMAN	hd02e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808366 3'
5819	18443	31165	0.86	7.0E-28	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11520	23968		8.46	7.0E-26	AA115895.1	EST_HUMAN	zn30d08.r1 Stragene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gbM14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
12376	24544		3.49	7.0E-28	AW954559.1	EST_HUMAN	EST366629 MAGE resequences, MAGO Homo sapiens cDNA
2287	14841	27418	2.32	6.0E-26	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
3390	15988	28476	1.37	6.0E-28	AA206131.1	EST_HUMAN	zq52b04.r1 Stragene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645271 5'
10426	22820	35922	0.48	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10426	22820	35923	0.48	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11531	23979	37049	5.92	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1219	13819	26334	3.55	5.0E-28	A1708235.1	EST_HUMAN	es38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371 ;
1219	13819	26335	3.55	5.0E-28	A1708235.1	EST_HUMAN	es38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371 ;

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1591	14184		2.25	4.0E-26	AA328548.1	EST33446 Embryo, 12 week II Homo sapiens cDNA 5' end
9333	21847		3.53	4.0E-26	7657670	NT
10539	23076	36090	3.69	4.0E-26	BE266187.1	601191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535210 5'
1796	14386	28930	1.2	3.0E-26	D14547.1	NT
2046	14628	27197	1	3.0E-26	AL045855.2	Human DNA, SINE repetitive element
						DKFZb4341066_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp4341066 5'
2077	14657		2.22	3.0E-26	AA115895.1	zn30d08.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:U14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3846	16445	28906	1.48	3.0E-26	AA152464.1	G695374 THYROID RECEPTOR INTERACTOR ;
3846	16445	28907	1.48	3.0E-26	AA152464.1	z030f10.r1 Stratagene cdon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
6991	19489	32311	6.04	3.0E-26	BF245458.1	G695374 THYROID RECEPTOR INTERACTOR ;
10804	23138		1.97	3.0E-26	AF038405.1	601188486F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'
11442	23892	36957	2.58	3.0E-26	AW876651.1	Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds
11442	23892	36958	2.58	3.0E-26	AW876651.1	QV2-PT0012-040400-124-e05 P.T0012 Homo sapiens cDNA
						QV2-PT0012-040400-124-e05 P.T0012 Homo sapiens cDNA
11472	23922	36992	13.09	3.0E-26	AA583173.1	m37d05.s1 NCL_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.t1 OFR repetitive element ;
12566	24685		2.21	3.0E-26	AW073434.1	xa57b09.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2570873 3' similar to contains MER30.11
12661	24732	30857	1.46	3.0E-26	AF165520.1	MER30 repetitive element ;
710	13331	26818	5.38	2.0E-26	AL163282.2	Homo sapiens phorbolins I protein (PBI) mRNA, complete cds
1909	14494		2.42	2.0E-26	AL038099.2	Homo sapiens chromosome 21 segment HS21C082
3288	15880	28363	4.94	2.0E-26	X86694.1	DKFZp566L171_s1 566 (synonym: hfd2) Homo sapiens cDNA clone DKFZp566L171 3'
10633	23165		3.35	2.0E-26	D87675.1	M.musculus mRNA for astrocytic phosphoprotein, PEA-15
						Homo sapiens DNA for amyloid precursor protein, complete cds
11096	23607	36647	5.24	2.0E-26	AI801412.1	tc89a01.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu
11296	23748		2.17	2.0E-26	AF055066.1	repetitive element; contains element MER20 MER20 repetitive element ;
11894	24237		1.85	2.0E-26	AB037859.1	Homo sapiens MHC class 1 region
12101	25005	30612	3.03	2.0E-26	BE170371.1	Homo sapiens mRNA for KIAA1438 protein, partial cds
142	12807	25295	13.71	1.0E-26	BE170371.1	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2091	14871	27241	1.5	1.0E-26	AL039363.2	QV4-HT0538-020300-123-a02 HT0538 Homo sapiens cDNA
2598	15160	27728	1.48	1.0E-26	BE814995.1	DKFZp434H1910_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H1910 5'
2710	15287		6.31	1.0E-26	AF261085.1	MR2-BN0114-240500-030-g07 BN0114 Homo sapiens cDNA
						Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds
6927	19588		2.52	1.0E-26	BE165980.1	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10772	23266		2.98	1.0E-26	AL038487.1	EST_HUMAN	DKFZp566C2146_r1 566 (synonym: hfk2) Homo sapiens cDNA clone DKFZp566C2146 5'
12151	25084		2.78	1.0E-26	H5093.1	EST_HUMAN	CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
12625	24703		1.27	1.0E-26	AW408742.1	EST_HUMAN	U1-HF-BM0-adv-4-10-0.U1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063210 5'
7584	20099		1.17	9.0E-27	BF371227.1	EST_HUMAN	RC6-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA
9227	21949		4	9.0E-27	U93163.1	NT	Homo sapiens IMAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
11648	24080		6.15	9.0E-27	BF445558.1	EST_HUMAN	naa03c07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3253844 3' similar to contains OFR.11
11	12890	25148	3.07	8.0E-27	A1831462.1	EST_HUMAN	W49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2
583	13213		3.36	8.0E-27	AL163227.2	NT	THR repetitive element 1
1461	14053	26585	28.2	8.0E-27	AW162737.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
1461	14053	26588	28.2	8.0E-27	AW162737.1	EST_HUMAN	eu87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558
2212	14787	27382	1.48	8.0E-27	AW864776.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN); eu87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558
3219	15831	28310	1.89	8.0E-27	P12236	SWISSPROT	TUBULIN ALPHA-1 CHAIN (HUMAN); PM2-SN0018-220300-002-a07 SN0018 Homo sapiens cDNA
3396	16004	28485	0.59	8.0E-27	AF181897.1	NT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
5873	18495	31221	1.14	8.0E-27	AV792214.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
7054	18073		2.9	8.0E-27	BE26560.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HTFBC808 5'
7111	19451	32287	2.49	8.0E-27	N84970.1	EST_HUMAN	MR4-BT0398-250800-204-d06 BT0398 Homo sapiens cDNA
9136	21671	34613	1.35	8.0E-27	AW857579.1	EST_HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to
9136	21671	34614	1.35	8.0E-27	AW857579.1	EST_HUMAN	REPETITIVE ELEMENT L1
712	13333		1.39	7.0E-27	Z70684.1	NT	CM1-CT0315-091289-063-d07 CT0315 Homo sapiens cDNA
5252	17815		2.68	7.0E-27	AW629172.1	EST_HUMAN	CM1-CT0315-091289-063-d07 CT0315 Homo sapiens cDNA
8791	21330		0.77	7.0E-27	D86984.1	NT	CM1-CT0315-091289-063-d07 CT0315 Homo sapiens cDNA
10628	23160		4.39	7.0E-27	AJ271735.1	NT	Human endogenous retroviral element HC2
12288	24495		3.27	7.0E-27	AV723365.1	EST_HUMAN	h151h12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875879 3' similar to TR:O76040
10605	23139	36151	11.92	6.0E-27	M26697.1	NT	O76040 ORF2: FUNCTION UNKNOWN. ; Human mRNA for KIAA0231 gene, partial cds
11621	24063	37127	2.33	6.0E-27	U93163.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2 AV723366 HTB Homo sapiens cDNA clone HTBAHE02 5' Human nuclear protein (B23) mRNA, complete cds Homo sapiens IMAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7752	20260		0.79	5.0E-27	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10136	22631	35619	2.86	5.0E-27	BF666814.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
10136	22631	35620	2.86	5.0E-27	BF666814.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
2423	14991	27564	4.86	4.0E-27	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
6842	19432	32247	1.37	4.0E-27	9910569	NT	Mus musculus sperm tail associated protein (Stap), mRNA
7880	20422		1.14	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
7925	20467		1.22	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8659	22156	35130	0.8	4.0E-27	AW880859.1	EST_HUMAN	QV0-OT0033-070300-152-b10 OT0033 Homo sapiens cDNA
11473	23923	36993	2.38	4.0E-27	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2085	14666	27237	6.19	3.0E-27	X60658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4358	16945	26387	1.56	3.0E-27	BE071924.1	EST_HUMAN	PMO-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA
5549	16181	30596	6.22	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
9229	21951	34900	3.67	3.0E-27	BF035327.1	EST_HUMAN	60145853F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
45	12724	25185	29.89	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1940	14524		12.18	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
3143	15757		12.54	2.0E-27	AW629172.1	EST_HUMAN	h151h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:076040
3281	15873	28353	1.74	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3281	15873	28354	1.74	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6779	19370	32185	0.68	2.0E-27	H02655.1	EST_HUMAN	y36e01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150840 5' similar to
8034	20576	33481	1.24	2.0E-27	A1866347.1	EST_HUMAN	SP-HMGC_MOUSE Q02591 HOMEBOX PROTEIN ;
9183	21710		2.25	2.0E-27	AA551527.1	EST_HUMAN	w28g07.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426268 3'
9707	22205	35178	1	2.0E-27	X60658.1	NT	nh08h05.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.t3 L1
9948	22443	35421	1.03	2.0E-27	M78590.1	EST_HUMAN	R. rattus RYA3 mRNA for a potential ligand-binding protein
9948	22443	35422	1.03	2.0E-27	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
10834	23355	36370	3.38	2.0E-27	AU121685.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
11360	14524		15.88	2.0E-27	AA565345.1	EST_HUMAN	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000746 5'
461	13095		1.17	1.0E-27	AL163246.2	NT	nk01b10.s1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
							ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
							Homo sapiens chromosome 21 segment HS21C046

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1034	13644	28157	1.25	1.0E-27	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4155	16747		1.02	1.0E-27	BE350127.1	EST_HUMAN	h09q01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER29.b3 MER29 repetitive element ;
6865	19261	32085	6.88	1.0E-27	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
6952	19529	32353	1.86	1.0E-27	F30158.1	EST_HUMAN	HSPD20481 HM3 Homo sapiens cDNA clone s4000095C10
6952	19529	32354	1.86	1.0E-27	F30158.1	EST_HUMAN	HSPD20481 HM3 Homo sapiens cDNA clone s4000095C10
8546	21085	34008	0.7	1.0E-27	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8916	21454		1.89	1.0E-27	BE079780.1	EST_HUMAN	RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
9638	22138	35104	2.68	1.0E-27	DB7449.1	NT	Human mRNA for KIAA0260 gene, partial cds
11551	23999	37071	3.65	1.0E-27	AF111093.1	NT	Bos taurus latrophilin 3 splice variant bbah mRNA, complete cds
148	12810		2.02	9.0E-28	BE348399.1	EST_HUMAN	hw17c11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
333	12885	25472	2.19	9.0E-28	AU126260.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR, [3] TR:Q07280 TR:Q07313 ;
11732	24137		4.71	9.0E-28	BF377859.1	EST_HUMAN	AU126260 NT2RP1 Homo sapiens cDNA clone NT2RP1000443 5'
12066	24923		4.41	8.0E-28	AW157571.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
1223	13823	26338	16.9	7.0E-28	AU142750.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to TR:O60302 O60302 KIAA0555 PROTEIN ; contains element MER22 repetitive element ;
11066	23578	36616	3.08	7.0E-28	11417866	NT	AU142750 Y79AA1 Homo sapiens cDNA clone Y79AA1000824 5'
11688	24104		2.37	7.0E-28	AV735348.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
8850	21389		1.04	8.0E-28	AF016052.1	NT	AV735348 CB Homo sapiens cDNA clone CBFACA12 5'
12346	24527		12.5	6.0E-28	AA504562.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
340	12992		2.28	5.0E-28	A1921003.1	EST_HUMAN	aa60e03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu repetitive element; contains element PTR5 repetitive element ;
4081	16877	29137	1.79	5.0E-28	R79762.1	EST_HUMAN	wo18c07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1 THR repetitive element ;
2654	15213	27786	1.12	4.0E-28	AW195066.1	EST_HUMAN	y89f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146443 5'
3005	15821	28098	0.78	4.0E-28	4505316	NT	xt33c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695504 3' similar to SW:GG95_HUMAN
3142	15756	28223	3.13	4.0E-28	BE409100.1	EST_HUMAN	Q08379 GOLGIN-95. ;
7368	19894	32757	1.79	4.0E-28	A188941.1	EST_HUMAN	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA 601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'
10745	23289		4.9	4.0E-28	AF029308.1	NT	qf66f10.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
							Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10885	23406		25.24	4.0E-28	AB038241.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
10904	19894	32757	3.33	4.0E-28	AI198941.1	EST_HUMAN	qf66f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb.M195503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN):
12116	24375		1.71	4.0E-28	AW854244.1	EST_HUMAN	RC3-CT0254-240400-210-112 CT0254 Homo sapiens cDNA
12657	24728		72.51	4.0E-28	AW157571.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to TR:O60302 O60302 KIAA0555 PROTEIN; contains element MER22 repetitive element;
1328	13920		1.95	3.0E-28	AF155382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
8761	21300	34221	3.77	3.0E-28	BF354030.1	EST_HUMAN	MR3-HT0713-280500-013-09 HT0713 Homo sapiens cDNA
10815	23336	36349	2.08	3.0E-28	U53588.1	NT	Homo sapiens MHC class 1 region
12147	24390		2.53	3.0E-28	AI831991.1	EST_HUMAN	wj98f07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element;
12284	24488		1.77	3.0E-28	BE082801.1	EST_HUMAN	RC2-BT0842-210200-013-03 BT0842 Homo sapiens cDNA
82	12768	26261	8.71	2.0E-28	BE062167.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
1207	13807	26320	9.63	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
2517	15081	27654	2.47	2.0E-28	AI348634.1	EST_HUMAN	gc35b06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element;
3407	16016	28495	0.64	2.0E-28	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
6449	19050	31836	1.2	2.0E-28	BF224402.1	EST_HUMAN	h76c03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element;
6472	19073		5.22	2.0E-28	BF212905.1	EST_HUMAN	601814198F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
7988	20530	33437	0.77	2.0E-28	AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
9505	22005		11	2.0E-28	AW972305.1	EST_HUMAN	EST384394 MAGE resequences, MAGI, Homo sapiens cDNA
11481	23931	37002	1.81	2.0E-28	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12127	24383		1.74	2.0E-28	H06376.1	EST_HUMAN	y79c09.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:44300 5'
1526	14118	26655	3.52	1.0E-28	D38044.1	NT	Human gene for Ahr-receptor, exon 7-9
2261	14835	27413	1.64	1.0E-28	BF333236.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
2708	15265	27832	1.38	1.0E-28	AF000995.1	NT	Homo sapiens ubiquitous TPR motif, Y isoform (UTY) mRNA, alternative transcript 2, complete cds
4688	17250		0.86	1.0E-28	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
7801	20344		7.69	1.0E-28	11429885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC63091), mRNA
7861	20503		3.2	1.0E-28	8922793	NT	Homo sapiens hypothetical protein FLJ10988 (FLJ10988), mRNA
9202	21719	34683	4.72	1.0E-28	AA308744.1	EST_HUMAN	EST178615 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9760	22288	35272	9.67	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
9760	22288	35273	9.67	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
11693	24108		10.45	1.0E-28	AA054182.1	EST_HUMAN	zf51c01.r1 Soares retina N2b4-HR Homo sapiens cDNA clone IMAGE:380448 5'
12484	24811		1.56	1.0E-28	AL163247.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
12596	25034	30502	3.5	9.0E-28	AW663987.1	EST_HUMAN	h176g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978266 3'
12245	24456		5.36	8.0E-28	Q00130	SWISSPROT	HYPOTHETICAL GENE 50 PROTEIN
1646	14238	26773	1.04	7.0E-28	AW968447.1	EST_HUMAN	EST1378521 MAGE resequences, MAGI Homo sapiens cDNA
3607	19211		0.91	7.0E-28	BE254708.1	EST_HUMAN	601114990F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355367 5'
12644	24718		13.85	7.0E-28	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
621	13248	25722	7.35	6.0E-28	A1936748.1	EST_HUMAN	wp69b01.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
12002	24307		9.28	8.0E-28	BE940436.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN, contains LTR7.b1 LTR7 repetitive element ;
5138	17710		1.02	5.0E-28	AL163203.2	NT	RC3-UT0062-210800-021-c05 UT0062 Homo sapiens cDNA
8666	21205		7.83	5.0E-28	AW887541.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
12276	24480		1.32	5.0E-28	BE612449.1	EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
3269	15881		2.92	4.0E-28	A1752367.1	EST_HUMAN	601451827F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855726 5'
8160	18773		6.52	4.0E-28	BE164830.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
8025	20587	33469	0.92	4.0E-28	A1678101.1	EST_HUMAN	QV1-HT0471-280300-121-a05 HT0471 Homo sapiens cDNA
8025	20587	33470	0.92	4.0E-28	A1678101.1	EST_HUMAN	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
8680	21219	34139	6.03	4.0E-28	J04988.1	NT	MER29.12 MER29 repetitive element ;
4506	17080	29538	1.58	3.0E-28	AB042297.1	NT	Human 90 kD heat shock protein gene, complete cds
4839	17417	29870	1.28	3.0E-28	BF333236.1	EST_HUMAN	Homo sapiens PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds
6088	18704	31452	0.98	3.0E-28	BE314018.1	EST_HUMAN	QV1-BT0821-120800-360-b03 BT0821 Homo sapiens cDNA
8668	21207	34124	2.6	3.0E-28	D38044.1	NT	601152857F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508527 5'
9224	21740	34883	1.93	3.0E-28	AW303317.1	EST_HUMAN	Human gene for Ah-receptor, exon 7-9
9450	21976		2.01	3.0E-28	AL163246.2	NT	xv17703.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu
9869	22366		0.76	3.0E-28	BE350127.1	EST_HUMAN	repetitive element; contains MER19.12 MER19 repetitive element ;
11148	23656	36898	1.88	3.0E-28	AA403053.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
							h109g01.x1 NCL CGAP_KidT3 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
							MER29 repetitive element ;
							z162b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728889 5' similar to TR:G1335769
							G1335769 GAG-POL POLYPROTEIN. ;

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11891	24234		2.61	3.0E-29	D63882.1	NT	Human HsLIM15 mRNA for HsLIM15, complete cds
12553	25044		1.95	3.0E-29	D63882.1	NT	Human HsLIM15 mRNA for HsLIM15, complete cds
518	13150	25632	1.07	2.0E-29	AF084889.1	NT	Homo sapiens envelope protein RIC-6 (env) gene, complete cds
518	13150	25633	1.07	2.0E-29	AF084889.1	NT	Homo sapiens envelope protein RIC-6 (env) gene, complete cds
1580	14173	26703	7.26	2.0E-29	A1963604.1	EST_HUMAN	wr65d10.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
1580	14173	26704	7.26	2.0E-29	A1963604.1	EST_HUMAN	wr65d10.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
4366	16953	28393	2.01	2.0E-29	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5991	18611	31346	0.86	2.0E-29	A1082459.1	EST_HUMAN	os71e04.x1 NCL CGAP_GC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1.12 L1 repetitive element ;
6327	18933	31708	1.45	2.0E-29	A1806418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element ;
7560	18933	31708	1.2	2.0E-29	A1806418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element ;
7917	20459	33366	1.15	2.0E-29	BE807157.1	EST_HUMAN	601442206F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846848 5'
8514	21053	33975	0.55	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
8514	21053	33976	0.55	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
9427	21936	34684	3.74	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9427	21936	34685	3.74	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10138	22633	35622	3.15	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10138	22633	35623	3.15	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11350	23805		2.03	2.0E-29	11425108	NT	Homo sapiens splicing factor similar to dhsJ (SPF31), mRNA
11390	23842		2.46	2.0E-29	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
11635	24075		1.93	2.0E-29	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8727	21266	34186	7.44	1.0E-29	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
10503	22997	36006	0.76	1.0E-29	X60658.1	NT	Rattus RYA3 mRNA for a potential ligand-binding protein
6696	19292	32086	3.08	9.0E-30	AA761215.1	EST_HUMAN	n220c07.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1 MER4 repetitive element ;
11773	24162		2.08	9.0E-30	11422745	NT	Homo sapiens zinc/iron regulated transporter-like (ZIRT), mRNA
6461	19062		9.33	8.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8214	20755	33669	2.65	8.0E-30	AA363873.1	EST_HUMAN	EST197317 Thymus 1 Homo sapiens cDNA 5' end similar to EST containing O family repeat
8617	21156	34069	4.94	8.0E-30	A1557072.1	EST_HUMAN	PT2.1_13_B11.r.tumor2 Homo sapiens cDNA 3'
1562	14154		0.91	7.0E-30	BE091133.1	EST_HUMAN	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA

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7779	20291	33190	1.28	7.0E-30	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'
1810	14400	26945	1.35	6.0E-30	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3224	15836	28314	2.38	6.0E-30	BE008026.1	EST_HUMAN	QVO-BN0147-280400-214-f12 BN0147 Homo sapiens cDNA
4872	15838	28314	1.1	6.0E-30	BE008026.1	EST_HUMAN	QVO-BN0147-280400-214-f12 BN0147 Homo sapiens cDNA
10432	22826	35832	0.72	6.0E-30	AF177227.1	NT	Homo sapiens CTCL tumor antigen se20-10 mRNA, partial cds
12615	18024		1.6	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4085	16681	29141	39.51	5.0E-30	AI399992.1	EST_HUMAN	igb2g03.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element
5448	24850		4.03	5.0E-30	U87931.1	NT	Human aconitase hydratase (ACO2) gene, exon 7
10767	23281		3.31	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11034	23548	36583	6.29	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11034	23548	36584	6.29	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2188	14784	27333	1.32	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
2188	14784	27334	1.32	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
8936	21375	34289	3.16	4.0E-30	AW812488.1	EST_HUMAN	CM1-ST0181-091199-035-f08 ST0181 Homo sapiens cDNA
1191	13792		3.43	3.0E-30	AI385551.1	EST_HUMAN	qq9c05.x1 Soares_tetral_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29.b2 MER29 repetitive element
3821	18421	28883	0.87	3.0E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
7893	20435		0.47	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8423	20863		0.5	3.0E-30	AF078778.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10330	22824	35820	1.69	3.0E-30	BE350127.1	EST_HUMAN	h09g01.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element
10460	22954	35864	0.53	3.0E-30	AB032869.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
10460	22954	35965	0.53	3.0E-30	AB032869.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
11084	23596	36832	1.78	3.0E-30	P34056	SWISSPROT	TRANSCRIPTION FACTOR AP-2
703	13324	25811	1.3	2.0E-30	AW857315.1	EST_HUMAN	CM0-CT0307-310100-158-h03 CT0307 Homo sapiens cDNA
1123	13726		2.35	2.0E-30	F08988.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
1527	14119	28658	7.23	2.0E-30	BE175877.1	EST_HUMAN	RCS-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2740	15285	27862	9.08	2.0E-30	BE765232.1	EST_HUMAN	IL2-NT0101-280700-118-E04 NT0101 Homo sapiens cDNA
2844	15560	28034	6.74	2.0E-30	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3857	16455	28919	2.18	2.0E-30	AW206881.1	EST_HUMAN	UI-H-BH-af0-c-12-0-UJ.st NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4892	17467	28922	2.07	2.0E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4892	17467	28923	2.07	2.0E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
6855	19443	32259	0.92	2.0E-30	BF306337.1	EST_HUMAN	601893208F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138993 5'

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8412	20952	33871	0.81	2.0E-30	AA019103.1	EST_HUMAN	ze58c10.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363186 5'
8474	21014	33830	5.63	2.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-570C01 5'
8570	21109	34027	3.55	2.0E-30	BE670617.1	EST_HUMAN	7e37c12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8570	21109	34028	3.55	2.0E-30	BE670617.1	EST_HUMAN	7e37c12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
9908	22405	35380	3.21	2.0E-30	AW971568.1	EST_HUMAN	EST383657 MAGL Homo sapiens cDNA
9994	22489	35477	6.11	2.0E-30	AW470791.1	EST_HUMAN	ha33d06.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873499 3' similar to contains THR.b3 THR repetitive element ;
308	12863	25452	12.31	1.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-570C01 5'
563	13194	25673	3.84	1.0E-30	AW468897.1	EST_HUMAN	hd30b04.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.13 MER1 MER1 repetitive element ;
745	13365	25859	2.7	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2253	14827	27403	3.59	1.0E-30	AA664377.1	EST_HUMAN	ac77b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'
2502	15066	27640	1.64	1.0E-30	BF347728.1	EST_HUMAN	602022560.F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157991 5'
3035	15651	28129	1.36	1.0E-30	5803091	NT	Homo sapiens methionine aminopeptidase; eIF-2-associated p57 (VINPEP), mRNA
3090	15705	28177	1.06	1.0E-30	AA315045.1	EST_HUMAN	EST188868 HCC cell line (metastasis to liver in mouse) Homo sapiens cDNA 5' end
7708	20217	33105	16.59	1.0E-30	BF183230.1	EST_HUMAN	601809932.F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5'
12268	25029		1.48	1.0E-30	AA289211.1	EST_HUMAN	EST11698 Uterus Homo sapiens cDNA 5' end
12411	24949		8.63	1.0E-30	H55593.1	EST_HUMAN	CHR220332 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
3829	16429	28890	0.72	9.0E-31	T73025.1	EST_HUMAN	yc65e06.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
3829	16429	28891	0.72	9.0E-31	T73025.1	EST_HUMAN	yc65e06.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
8266	20807	33725	1.03	9.0E-31	R18214.1	EST_HUMAN	yc90b08.r1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS- RELATED PROTEIN RAB-2 (HUMAN);
8266	20807	33726	1.03	9.0E-31	R18214.1	EST_HUMAN	yc90b08.r1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS- RELATED PROTEIN RAB-2 (HUMAN);
8559	21098		1.84	9.0E-31	Z88283.1	EST_HUMAN	HSC05F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05f03 3'
8561	21100	34020	0.52	8.0E-31	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
12840	24715	30897	1.89	9.0E-31	G755441	NT	Mus musculus syndecan 4 (Sdc4), mRNA
1115	13718	26230	6.84	8.0E-31	8923389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2457	15024		4.22	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
11801	24910		2.71	8.0E-31	AF012385.1	EST_HUMAN	AF012385 Human testis (C. De Smet) Homo sapiens cDNA clone TDP3.12b

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740	13360		2.5	7.0E-31	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2692	15249	27818	2.37	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2692	15249	27819	2.37	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8340	20881	33800	0.82	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
8340	20881	33801	0.82	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
9190	21707		1.62	7.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3638310 5'
12243	24455	30958	1.53	7.0E-31	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3742	10343		2.28	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8094	20635		6.98	6.0E-31	AF055066.1	NT	Homo sapiens MHC class 1 region
8273	20814	33738	0.78	6.0E-31	BE350127.1	EST_HUMAN	ht09g01.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
10617	23149	36161	1.69	6.0E-31	AU119105.1	EST_HUMAN	MER29 repetitive element
11835	24199	31038	3.25	6.0E-31	AW372868.1	EST_HUMAN	AU119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'
11984	24888		2	6.0E-31	BE894488.1	EST_HUMAN	RC5-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA
206	12887	25352	3.89	5.0E-31	M60894.1	NT	601433087F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3918524 5'
206	12887	25353	3.89	5.0E-31	M60894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
8382	20922		0.75	5.0E-31	BF056540.1	EST_HUMAN	Homo sapiens type I DNA topoisomerase gene, exon 8
822	13249		2.67	4.0E-31	AJ271735.1	NT	7k08f04.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR.Q13537 Q13537
1854	14442		2.42	4.0E-31	AL163280.2	NT	SIMILAR TO POGO ELEMENT, contains L1.11 L1 repetitive element
2815	15367		1.02	4.0E-31	5730038	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
10427	22921	35924	0.65	4.0E-31	AF084464.1	NT	Homo sapiens chromosome 21 segment HS21C080
12006	24309		1.65	4.0E-31	AJ230125.1	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
12399	24559		1.51	4.0E-31	AB080881.1	NT	Rattus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds
7377	19903	32767	7.09	3.0E-31	4826853	NT	Homo sapiens GGT1 gene, exon 1
7505	20027	32891	1.62	3.0E-31	11420328	NT	Homo sapiens gene for activin receptor type IIB, complete cds
8102	20643		2.18	3.0E-31	AL163206.2	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH) (NDUFB8) mRNA
9500	22000	34957	14.98	3.0E-31	D14523.1	NT	Homo sapiens chromosome 21 segment HS21C006
10488	22982	35990	0.64	3.0E-31	AA421242.1	EST_HUMAN	Horse mRNA for ferritin L-chain, complete cds
10510	23048	36060	2.78	3.0E-31	P11174	SWISSPROT	z006d04.f1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:731047 5'
11032	23546		6.94	3.0E-31	BF035327.1	EST_HUMAN	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
1961	14545	27102	1.52	2.0E-31	AW838171.1	EST_HUMAN	601458531F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3862086 5'

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2255	14829	27405	1.16	2.0E-31	AI933388.1	EST_HUMAN	ig44g05.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
2378	14948	27622	2.08	2.0E-31	AL119245.1	EST_HUMAN	DKFZp761G1513_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1513 5'
2485	15050	27621	3.48	2.0E-31	AA458824.1	EST_HUMAN	aa8811.s1 Stratiene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR 12 THR repetitive element ;
5479	18113	30522	0.81	2.0E-31	AW444496.1	EST_HUMAN	UI-H-B10-akb-f-09-O-UI.s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2733833 3'
5888	18511	31237	2.97	2.0E-31	BE350127.1	EST_HUMAN	h09g01.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
9008	21543		2.32	2.0E-31	AA877784.1	EST_HUMAN	m0604.s1 NCI CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
9134	21669	34611	3.85	2.0E-31	7681535	NT	Homo sapiens B9 protein (B9), mRNA
9820	22318	35301	1.04	2.0E-31	AV710948.1	EST_HUMAN	AV710948.Cu Homo sapiens cDNA clone CUAALB07 5'
9820	22318	35302	1.04	2.0E-31	AV710948.1	EST_HUMAN	AV710948.Cu Homo sapiens cDNA clone CUAALB07 5'
9987	22482	35467	1.73	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
9987	22482	35468	1.73	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
11934	24288		3.08	2.0E-31	AF148512.1	NT	Homo sapiens hexokinase II gene, promoter region
12078	25106		2.43	2.0E-31	AI114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
18	12897	25154	8.8	1.0E-31	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
1703	14298	26831	3.28	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1703	14298	26832	3.28	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1703	14298	26833	3.28	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4742	17323	28763	1.19	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547B235 5'
4742	17323	28764	1.19	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547B235 5'
6496	18130	30538	3.47	1.0E-31	AW391679.1	EST_HUMAN	MR3-ST0220-151299-028-a08_1 ST0220 Homo sapiens cDNA
6282	18990	31658	1.84	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite ccb1 repeat region
7332	19859	32722	0.84	1.0E-31	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
7772	20281	33178	0.68	1.0E-31	BE972818.1	EST_HUMAN	601652052F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935293 5'
10135	22630	35618	0.67	1.0E-31	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
10796	23319	36328	2.94	1.0E-31	AI086434.1	EST_HUMAN	q121h03.x1 NCI CGAP_Brm25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16595 Q16595 FRATAXIN ;
6749	19342	32149	2.29	9.0E-32	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
7591	20106		1.07	9.0E-32	11430822	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2122	14700	27270	3.49	8.0E-32	AI058770.1	EST_HUMAN	oz15a09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
5673	18300	30781	0.9	8.0E-32	AW897214.1	EST_HUMAN	RC2-BN0048-200300-015-a04 BN0048 Homo sapiens cDNA
4985	17559	30002	3.69	7.0E-32	P52591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)
11809	24247		3.42	7.0E-32	X17283.1	NT	Human chromosome 22 Immunoglobulin V(K) gene, part, with 5' breakpoint between orphion and neighbouring non-amplified region
2759	15314	27880	0.91	6.0E-32	AI478104.1	EST_HUMAN	tm34a10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2159994 3' similar to contains MER29.13
7402	18927		1.37	6.0E-32	BE888016.1	EST_HUMAN	MER29 repetitive element;
12350	25088		1.51	6.0E-32	AA884653.1	EST_HUMAN	ch37c03.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:3913087 5'
1072	13677	26187	75.63	5.0E-32	AF116627.1	NT	repetitive element;
966	13577		1.53	4.0E-32	AL163246.2	NT	Homo sapiens PRO1181 mRNA, complete cds
7599	20112	32987	3.11	4.0E-32	11432574	NT	Homo sapiens chromosome 21 segment HS21C046
7599	20112	32988	3.11	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
8300	20841		0.77	4.0E-32	BE064410.1	EST_HUMAN	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
481	13114	25604	2.79	3.0E-32	Y17293.1	NT	RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA
1502	14094	28633	8.08	3.0E-32	AV731500.1	EST_HUMAN	Homo sapiens FLI-1 gene, partial
2833	15549	28025	0.73	3.0E-32	5174574	NT	AV731500 HTF Homo sapiens cDNA clone HTFAK007 5'
2933	15549	28026	0.73	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
9315	21829	34780	16.81	3.0E-32	AV758634.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
9315	21829	34781	16.81	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBFBH12 5'
10805	23328	36339	7.7	3.0E-32	AA777621.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBFBH12 5'
11093	23605		1.63	3.0E-32	BF035327.1	EST_HUMAN	z95a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR13 THR repetitive element;
11937	24270		6.37	3.0E-32	BE278086.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
12325	15549	28025	6.26	3.0E-32	5174574	NT	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
12325	15549	28026	6.26	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
12491	24620		5.38	3.0E-32	BE278086.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
5011	17584	30027	1.01	2.0E-32	BE286613.1	EST_HUMAN	601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528159 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6400	19003	31781	0.9	2.0E-32	M35418.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6605	19202	32007	5.69	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
6805	19202	32008	5.69	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
8220	20781	33876	2.06	2.0E-32	AA114294.1	EST_HUMAN	zn66c08.17 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
8220	20781	33877	2.06	2.0E-32	AA114294.1	EST_HUMAN	zn66c08.17 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
12810	24694	30859	1.41	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBF8IA08 5'
12810	24694	30860	1.41	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBF8IA08 5'
7115	19455	32271	6.86	1.0E-32	11439789	NT	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
8532	21071	33991	4.86	1.0E-32	AA720574.1	EST_HUMAN	hw21g02.s1 NCL_CGAP_G080 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element;
3527	16132		5.7	9.0E-33	BE327112.1	EST_HUMAN	hw07c05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539 WW DOMAIN BINDING PROTEIN 11.;
6552	19150		4.1	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8723	21262	34182	2.52	9.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCL_CGAP_Brm87 Homo sapiens cDNA clone IMAGE:4156670 5'
10877	23209		6.39	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
65	12744	25219	2.71	7.0E-33	5031738	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
65	12744	25220	2.71	7.0E-33	5031738	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2206	14782	27355	1.92	7.0E-33	AI590115.1	EST_HUMAN	bt2b09.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.11 OFR repetitive element;
2875	15233		6.8	7.0E-33	AV730058.1	EST_HUMAN	AV730058 HTF Homo sapiens cDNA clone HTFAVE06 5'
3279	15890		15.76	7.0E-33	AW971307.1	EST_HUMAN	EST333396 MAGE resequences, MAGL Homo sapiens cDNA
8876	21415		1.08	7.0E-33	X54890.1	NT	Human hLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphate) (EC 3.1.3.48)
10708	23236	36249	4.73	7.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCL_CGAP_Brm87 Homo sapiens cDNA clone IMAGE:4156670 5'
11127	23635	36678	2.53	7.0E-33	AW971568.1	EST_HUMAN	EST333657 MAGE resequences, MAGL Homo sapiens cDNA
11815	24253	31009	7.43	7.0E-33	AA801416.1	EST_HUMAN	no18h01.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.11 L1 repetitive element;
3800	16400		0.79	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6217	18827	31699	1.11	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
6217	18827	31600	1.11	6.0E-33	F30631.1	EST_HUMAN	HSPD21201:HM3 Homo sapiens cDNA clone s4000107H06
8515	21054	33977	7.9	6.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
8636	21175	34084	4.14	6.0E-33	11429188	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
9923	22419	35393	1.73	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9823	22419	35394	1.73	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1814	14404		1.48	5.0E-33	BF373515.1	EST_HUMAN	QV1-FT0169-100700-271-a02 FT0169 Homo sapiens cDNA
1925	14510		1.2	5.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA
1943	14527	27082	1.32	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1943	14527	27083	1.32	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
4132	18724	28178	0.8	5.0E-33	AB014599.1	NT	Homo sapiens mRNA for KIAA0699 protein, partial cds
10147	22642	35632	0.76	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
10147	22642	35633	0.76	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
11720	24129		1.43	5.0E-33	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1167	13769		1.82	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2170	14747	27318	1.67	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2464	15031		2.24	4.0E-33	AA626621.1	EST_HUMAN	ab51b11.r1 Straglene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element ;
2582	15145	27713	1.92	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4581	17184	29607	1.39	4.0E-33	AW293349.1	EST_HUMAN	UI-H-B12-ah1-c03-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5599	18228	30877	21.96	4.0E-33	AA053053.1	EST_HUMAN	z171e08.r1 Straglene colon (#937204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb:X12671.mat HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6526	18128	31919	0.76	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6526	19128	31920	0.76	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1128	13731		5.55	3.0E-33	BE350127.1	EST_HUMAN	h108g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
1129	13731		3.84	3.0E-33	BE350127.1	EST_HUMAN	h108g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
2493	15468		1.01	3.0E-33	AV647851.1	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone GLC8CF09 3'
10336	22830	35824	1.19	3.0E-33	AA861510.1	EST_HUMAN	ak32b12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407647 3' similar to TR:Q13579 Q13579 MARINER TRANSPOSASE. ;
19	12698		0.82	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element ;
109	12698		2.24	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element ;
1415	14008	26536	2.48	2.0E-33	AA010242.1	EST_HUMAN	z108e08.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:430214 5'
1415	14008	26537	2.48	2.0E-33	AA010242.1	EST_HUMAN	z108e08.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:430214 5'
4510	17094		4.41	2.0E-33	BE159039.1	EST_HUMAN	MRO-HT0405-160300-202-008 HT0405 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5122	17694	30131	12.23	2.0E-33	AA626883.1	EST_HUMAN	ab51g11.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:944388 5' similar to gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5255	17818	30242	1.93	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5255	17818	30243	1.93	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
6555	19153	31949	1.5	2.0E-33	A1277492.1	EST_HUMAN	q186d01.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1880161 3'
9029	21568		2.63	2.0E-33	A1052256.1	EST_HUMAN	cc21d03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675973 3' similar to gb:M29536 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
10497	22991	36000	0.65	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
10497	22991	36001	0.65	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
10982	23496	36525	1.8	2.0E-33	AA453647.1	EST_HUMAN	zx48f05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795489 3' similar to TR:G1263081 G1263081 MARINER TRANSPOSASE.;
9	12688		1.08	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7437	19981	32827	1.21	1.0E-33	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
9834	25128		0.62	1.0E-33	U60922.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11202	23707	36759	2.63	1.0E-33	AW998818.1	EST_HUMAN	QV3-BN0047-230200-102-b03 BN0047 Homo sapiens cDNA
11515	23863	37033	5.83	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12214	24437		1.8	1.0E-33	A1927191.1	EST_HUMAN	wo88c06.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2462410 3'
12403	12688		2.81	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12434	24575	30913	2.55	1.0E-33	AV727809.1	EST_HUMAN	AV727809 HTC Homo sapiens cDNA clone HTCCNC12 5'
12628	24706		4.56	9.0E-34	A1271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1494	14086	26826	2.3	7.0E-34	T70845.1	EST_HUMAN	yd15e05.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
9911	14086	26826	0.66	7.0E-34	T70845.1	EST_HUMAN	yd15e05.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
11989	24289		1.75	7.0E-34	H12866.1	EST_HUMAN	yt14c10.r1 Soares_placenta_NB21P Homo sapiens cDNA clone IMAGE:148722 5'
496	13128	25616	1.61	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
496	13128	25617	1.61	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
11787	24177	31028	1.92	6.0E-34	U03886.1	NT	Mus musculus DAB/2J hair-specific (hacl-1) gene
1923	14508		2.5	5.0E-34	7708500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
5218	17783	30201	5.85	6.0E-34	U30883.1	NT	Human splicing factor SRp65-1 (SRp-65) mRNA, complete cds
8800	21339	34268	1.18	5.0E-34	AF078778.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10534	23071	36084	2.26	5.0E-34	AB037856.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
11133	23641		1.9	6.0E-34	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2041	14823	27182	3.42	4.0E-34	A1804687.1	EST_HUMAN	h94c06.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2249194 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2745	15300	27866	1.06	4.0E-34	8922807	NT	Homo sapiens hypothetical protein FLJ10989 (FLJ10989), mRNA
8968	21506	34427	1.35	4.0E-34	BF209778.1	EST_HUMAN	601874950F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102213 5'
6379	18983	31763	1.13	3.0E-34	M37277.1	NT	Human Ig germline H-chain D-region genes, partial cds
11031	23545		5.04	3.0E-34	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
8881	21419	34343	1.87	2.0E-34	AI878101.1	EST_HUMAN	w435g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element ;
8881	21419	34344	1.87	2.0E-34	AI878101.1	EST_HUMAN	w435g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element ;
1552	14144	26678	7.44	1.0E-34	P12236	SWISSPROT	ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3736	16337	28802	1.24	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4145	16737	29190	0.62	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4145	16737	29191	0.62	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4578	17161		8.22	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0506-240400-016-h08 BT0506 Homo sapiens cDNA
6287	18895	31664	2.69	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888999 5'
6287	18895	31665	2.69	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888999 5'
9813	22113	35076	17.45	1.0E-34	AL036635.1	EST_HUMAN	DKFZp564A1563_1 564 (synonym: hfr2) Homo sapiens cDNA clone DKFZp564A1563 5'
11077	23589	36627	1.94	1.0E-34	11439598	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12178	25037		3.1	1.0E-34	AA807097.1	EST_HUMAN	cc31c11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb:X68203
12423	24508		4.82	1.0E-34	AL163210.2	NT	TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);
3707	16308	28776	1.45	9.0E-35	AW663302.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
243	12802		10.67	8.0E-35	6031180	NT	h77806.y1 NCI_CGAP_GUT Homo sapiens cDNA clone IMAGE:2968787 5'
1772	14362	26907	2.03	8.0E-35	BF589937.1	EST_HUMAN	Homo sapiens prohibitin (PHB) mRNA
1772	14362	26908	2.03	8.0E-35	BF589937.1	EST_HUMAN	naa33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
4991	17565	30010	3.45	8.0E-35	BF183195.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA. ;
10570	23105	38120	1.8	8.0E-35	BE378480.1	EST_HUMAN	naa33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
11907	24245		2.98	8.0E-35	BF569292.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA. ;
6610	19207	32015	2	7.0E-35	11425417	NT	601809588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
1458	14050	26582	1.08	6.0E-35	AA757115.1	EST_HUMAN	601236468F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'
2010	14592	27152	1.29	6.0E-35	6005975	NT	602184624T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300660 3'
							Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
							ah53h03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1309397 3'
							Homo sapiens zinc finger protein 208 (ZNF208), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4127	16719	29174	0.67	6.0E-35	AW297191.1	EST_HUMAN	UHH-BW0-aid-409-0-U1.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731433 3'
7838	20380	33285	3.41	6.0E-35	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
8643	21182	34101	0.49	6.0E-35	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
8643	21182	34102	0.49	6.0E-35	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
9584	22084	35048	0.7	6.0E-35	AB002364.1	NT	Human mRNA for KIAA0366 gene, partial cds
9817	22315	35296	2.42	6.0E-35	AB037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
152	12815	25303	37.67	5.0E-35	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
1747	14337	26883	1.26	5.0E-35	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
3043	15659	28139	1.39	5.0E-35	6812639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
4499	17083	29533	1.81	5.0E-35	AF023268.1	NT	Homo sapiens cdk2 kinase (CLK2), propin1, cote1, glucocerebrosidase (GBA), and metadn genes, complete cds, melanin pseudogene and glucocerebrosidase pseudogene, and thrombospondin3 (THBS3) gene, partial cds
8125	20666		3.51	5.0E-35	BE860962.1	EST_HUMAN	601431984F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
8151	20692	33608	2.29	5.0E-35	AI208765.1	EST_HUMAN	qg38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN_Q92539 HYPOTHETICAL PROTEIN KIAA0249.;
8151	20692	33607	2.29	5.0E-35	AI208765.1	EST_HUMAN	qg38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN_Q92539 HYPOTHETICAL PROTEIN KIAA0249.;
11056	23586		3.53	5.0E-35	AA001786.1	EST_HUMAN	zh84f12.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
1481	14074	26613	13.95	4.0E-35	BE257807.1	EST_HUMAN	601109719F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350405 5'
1855	14443	26999	4.12	4.0E-35	H91193.1	EST_HUMAN	yu8a07.r1 Soares_fetal_liver_spleen_INFLS_Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element ;
4927	17502		0.58	4.0E-35	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7260	19788		2.06	4.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
8455	20995	33913	6.68	4.0E-35	AL046596.1	EST_HUMAN	DKFZp434L148_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L148 5'
1623	14216	26748	31.49	3.0E-35	BE268182.1	EST_HUMAN	601125560F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
2369	14940		2.22	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
5543	18175	30589	22.73	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2. ;
5543	18175	30590	22.73	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2. ;
9409	21918		1.72	3.0E-35	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10078	22573	35568	0.8	3.0E-35	AW003083.1	EST_HUMAN	wr03a05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2480432 3' similar to SW:POL1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
113	15407	25269	1.18	2.0E-35	N88965.1	EST_HUMAN	A971F Heart Homo sapiens cDNA clone A971
1230	13829	26344	1.13	2.0E-35	T11909.1	EST_HUMAN	Homo sapiens mRNA for Gab2, complete cds
2259	14833	27411	4.88	2.0E-35	AB018413.1	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3353	15981	28437	0.79	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3353	15981	28438	0.79	2.0E-35	6912459	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
3613	16218		0.85	2.0E-35	AB020702.1	NT	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
3981	16579	28049	0.86	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
3981	16579	29050	0.86	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
4777	17358		2.99	2.0E-35	H49239.1	EST_HUMAN	Yq19a12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:274079 5'
5770	18398	31110	1.48	2.0E-35	BF332417.1	EST_HUMAN	QV0-BT0701-210400-199-b04 BT0701 Homo sapiens cDNA
10675	23207	36219	4.14	2.0E-35	X59417.1	NT	H. sapiens PROS-27 mRNA
11683	15981	28437	1.34	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
11683	15981	28438	1.34	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12405	24563		42.99	2.0E-35	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
12525	15407	25269	1.4	2.0E-35	N88965.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
50	12730	25194	5.95	1.0E-35	AA631949.1	EST_HUMAN	frnc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
50	12730	25195	5.95	1.0E-35	AA631949.1	EST_HUMAN	frnc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
782	13401	25903	55.23	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0102-131099-008-d12 ST0102 Homo sapiens cDNA
782	13401	25904	55.23	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0102-131099-008-d12 ST0102 Homo sapiens cDNA
942	13555		1.15	1.0E-35	T87947.1	EST_HUMAN	y493a01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP:A44282 A44282 RETROVIRUS-RELATED POL POLYPROTEIN - HUMAN ;
2579	15141	27710	1.98	1.0E-35	7705994	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
2795	15348	27917	1.36	1.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
2795	15348	27918	1.36	1.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
3177	15790	28262	1.03	1.0E-35	6006030	NT	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3189	15811	28284	1.52	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCE06 3'
3189	15811	28285	1.52	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCE06 3'
4513	17097	29543	5.19	1.0E-35	7656305	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
4513	17097	29544	5.19	1.0E-35	7656305	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
5701	18327	30831	1.31	1.0E-35	11526238	NT	Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA
7069	18088	30444	0.73	1.0E-35	AW808665.1	EST_HUMAN	MR1-ST0111-111189-011-d07 ST0111 Homo sapiens cDNA
7069	18088	30445	0.73	1.0E-35	AW808665.1	EST_HUMAN	MR1-ST0111-111189-011-d07 ST0111 Homo sapiens cDNA
7496	20019	32883	0.8	1.0E-35	AB033105.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
7637	20149	33033	0.98	1.0E-35	11418002	NT	Homo sapiens KIAA0645 gene product (KIAA0645), mRNA
9461	24794	34941	3.33	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
9461	24794	34942	3.33	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
10470	22884	35974	0.57	1.0E-35	BF588584.1	EST_HUMAN	nc00606 x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341
10470	22884	35975	0.57	1.0E-35	BF588584.1	EST_HUMAN	nc00606 x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341
11601	24044		4.48	1.0E-35	A1525119.1	EST_HUMAN	prommer7.D01.r bvtumor Homo sapiens cDNA 5'
11695	24996		1.3	1.0E-35	11418274	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
12287	24489		1.87	1.0E-35	BE792832.1	EST_HUMAN	601584833F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939985 5'
9156	21691	34635	0.51	8.0E-36	AA348480.1	EST_HUMAN	EST54938 Hippocampus II Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus 9, 5' LTR
10060	22555		2.13	8.0E-36	7706259	NT	Homo sapiens CGI-09 protein (LOC51605), mRNA
2957	15573	28050	1.15	7.0E-36	AW857579.1	EST_HUMAN	CM1-CT0315-091299-083-d07 CT0315 Homo sapiens cDNA
3152	15766		5.38	7.0E-36	4557498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
7650	20162	33049	6.73	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) mRNA
7650	20162	33050	6.73	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
12070	24350	30965	5.15	7.0E-36	AF052051.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
2048	14630	27169	2.5	6.0E-36		NT	Homo sapiens glutathione transferase A4 gene, exon 1
2461	15028		5.35	6.0E-36	AB035346.1	NT	Homo sapiens ninjurin 2 (NINJ2), mRNA
3701	18302	28770	0.98	6.0E-36	BF515101.1	EST_HUMAN	Homo sapiens TGL6 gene, exon 12
5534	18168	30580	9.75	6.0E-36	AI435169.1	EST_HUMAN	U1-H-BW1-antv-c-12-0-JL1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
7163	19695	32541	3.97	6.0E-36	AW780143.1	EST_HUMAN	th93b08.x1 Soares NSF_F8_9W_OT_PA_P S1 Homo sapiens cDNA clone IMAGE:2126185 3' similar to gb:M11949 PANCRAEATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
8586	21125	34045	2.54	6.0E-36	AF208161.1	NT	nc00802.x1 NCL CGAP_C014 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMA2_HUMAN P52292 IMPORTIN ALPHA-2 SUBUNIT ;
						NT	Homo sapiens syncytin precursor, mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10125	22620		0.54	6.0E-36	C19827.1	EST_HUMAN	C16927 Clontech human eorta polyA+ mRNA (#5572) Homo sapiens cDNA clone GEN-535C11 5'
11422	23873	36936	2.62	6.0E-36	AJ380498.1	EST_HUMAN	195c09.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER9 b2
143	12808	25286	12.3	5.0E-36	AJ271735.1	NT	MER9 repetitive element ;
2779	15332	27801	15.02	5.0E-36	BE388438.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
3672	16273	28739	1.07	5.0E-36	AL163209.2	NT	601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
4803	17478	28935	1.8	5.0E-36	5729729	NT	Homo sapiens chromosome 21 segment HS21C009
4903	17478	28936	1.8	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
11661	12808	25286	4.05	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
11963	24285	31024	2.88	5.0E-36	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1287	13864	26381	2.14	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1491	14083	26624	1.88	4.0E-36	P10268	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
1687	14279	26813	1.35	4.0E-36	BE362574.1	EST_HUMAN	ENDONUCLEASE]
2264	14838		1.7	4.0E-36	AW247772.1	EST_HUMAN	601285574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386 5'
3397	16005	28486	0.83	4.0E-36	BE389289.1	EST_HUMAN	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3397	16005	28487	0.83	4.0E-36	BE389289.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
4866	17442	28893	0.57	4.0E-36	AL163204.2	NT	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
5310	17872	30294	0.58	4.0E-36	AA905361.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
5892	18515		0.94	4.0E-36	R64023.1	EST_HUMAN	ok05b11.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1506908 3' similar to
6205	18815	31586	2.19	4.0E-36	11497041	NT	SW:D3HI_RAT P28266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
7649	20181	33048	1.77	4.0E-36	M33320.1	NT	Y19705.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139713 5'
8490	21029	33947	1.15	4.0E-36	D87675.1	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
8490	21029	33948	1.15	4.0E-36	D87675.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
10867	23386	38403	2.38	4.0E-36	AA400370.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
11981	24292		1.46	4.0E-36	11420516	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
12026	24872		6.32	4.0E-36	AV753628.1	EST_HUMAN	zu69c10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743250 5'
725	13345	25837	2.82	3.0E-36	AF098810.1	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
1545	14137	26671	1.01	3.0E-36	AF110239.1	NT	AV753629 TP Homo sapiens cDNA clone TP6ABH01 5'
1545	14137	26672	1.01	3.0E-36	AF110239.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
2338	14909	27481	0.88	3.0E-36	7662401	NT	Homo sapiens calcineurin/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
							Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
							Homo sapiens KIAA0952 protein (KIAA0952), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4600	17184	28631	7.36	3.0E-36	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
10985	23499	36529	2.06	3.0E-36	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
3204	15816	28292	3.78	2.0E-36	BE259287.1	EST_HUMAN	601106343F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3342708 5'
5094	17667	30106	9.22	2.0E-36	AW880376.1	EST_HUMAN	QV0-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA
5977	18304	30788	2.55	2.0E-36	AF287747.1	NT	Mus musculus p47-phox gene, complete cds
6012	18532	31367	4.22	2.0E-36	T08756.1	EST_HUMAN	EST06648 Infant Brain, Bonto Soares Homo sapiens cDNA clone HIBBJ28 5' end
6680	19286	32089	12.01	2.0E-36	T69629.1	EST_HUMAN	yc44a07.r1 Stralagene liver (#937224) Homo sapiens cDNA clone IMAGE:83508 5'
9310	21824	34772	0.96	2.0E-36	BF512794.1	EST_HUMAN	UH-BW1-amu-e-11-Q.U1.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'
9468	21867	34817	0.6	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
9488	21867	34818	0.6	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
918	13531	28049	2.35	1.0E-36	BE409310.1	EST_HUMAN	601300038F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2180	14768	27337	0.81	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
2190	14768	27338	0.91	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
2243	14818	27392	1.34	1.0E-36	BF673761.1	EST_HUMAN	602136493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272866 5'
2538	15102		1.75	1.0E-36	AW276898.1	EST_HUMAN	xs57a05.x1 NCL_CGAP_Ov39 Homo sapiens cDNA clone IMAGE:2744434 3' similar to WP:C13F10.7
3388	15997		1.23	1.0E-36	AF156962.1	NT	CE08148 ; Homo sapiens human endogenous retrovirus W, provC6-19 protease (pro) gene, partial cds
5904	18526	31252	0.86	1.0E-36	AL044446.1	EST_HUMAN	DKFZp434G022.r1 434 (synonym: hless3) Homo sapiens cDNA clone DKFZp434G022 5'
6059	18576	31418	0.97	1.0E-36	4827064	NT	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA
6330	18936		3.97	1.0E-36	AB67714.1	EST_HUMAN	wb37c12.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu repetitive element
6524	19124	31916	1.13	1.0E-36	R25012.1	EST_HUMAN	y936g10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6524	19124	31917	1.13	1.0E-36	R25012.1	EST_HUMAN	y936g10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6783	19374	32190	0.7	1.0E-36	AL120542.1	EST_HUMAN	DKFZp761A229.r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A229 5'
7901	20443	33347	3.18	1.0E-36	AA148034.1	EST_HUMAN	zo51a12.r1 Stralagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
7901	20443	33348	3.18	1.0E-36	AA148034.1	EST_HUMAN	zo51a12.r1 Stralagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
7997	20539	33441	1.22	1.0E-36	AA420487.1	EST_HUMAN	nc60a08.r1 NCL_CGAP_P71 Homo sapiens cDNA clone IMAGE:745670
7997	20539	33442	1.22	1.0E-36	AA420487.1	EST_HUMAN	nc60a08.r1 NCL_CGAP_P71 Homo sapiens cDNA clone IMAGE:745670
8120	20661	33570	0.73	1.0E-36	AU141688	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
8120	20661	33571	0.73	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
8959	21497	34420	2.89	1.0E-36	AW103658.1	EST_HUMAN	xs82b07.x1 NCL_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614357 3'
10023	22518	35513	3.89	1.0E-36	BF364169.1	EST_HUMAN	QV3-NN1023-010600-199-h01 NN1023 Homo sapiens cDNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10231	22726	35717	0.71	1.0E-36	AW855868.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA
10231	22726	35718	0.71	1.0E-36	AW855868.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA
10826	23347	36363	3.55	1.0E-36	AW897636.1	EST_HUMAN	CM3-NN0061-140400-147-h12 NN0061 Homo sapiens cDNA
11258	23788	36844	4.94	1.0E-36	AW504143.1	EST_HUMAN	UI-HF-BNO-aie-c-03-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA IMAGE:3079277 5'
11848	24208		6.11	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12316	24507		6.19	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
12592	24683		3.59	1.0E-36	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7415	19940	32804	1.94	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
7415	19940	32805	1.94	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
12113	24374		1.63	9.0E-37	W22618.1	EST_HUMAN	73D4 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
3398	16006	28488	1.01	8.0E-37	4757979	NT	Homo sapiens chimerin (chimerin) 2 (CHN2) mRNA
5458	18091		1.58	8.0E-37	BE698077.1	EST_HUMAN	CM0-UT0003-050800-503-d09 UT0003 Homo sapiens cDNA
5994	18614	31348	4.02	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
5994	18614	31348	4.02	8.0E-37	BE350127.1	EST_HUMAN	MER29 repetitive element;
5994	18614	31349	4.02	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
6037	18656	31368	6.7	8.0E-37	AW840840.1	EST_HUMAN	MER29 repetitive element;
7825	20387	33275	6.31	8.0E-37	X87344.1	NT	RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA
1328	13922		2.3	7.0E-37	AL042800.1	EST_HUMAN	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
1780	14370	26914	1.55	7.0E-37	AF111167.2	NT	DKFZp434E0422_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0422 5'
1780	14370	26915	1.55	7.0E-37	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
10637	23169	36180	7.76	7.0E-37	AI817700.1	EST_HUMAN	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
10774	23298	36303	3.74	7.0E-37	AI536702.1	EST_HUMAN	wk25b11.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:127850 5'
5304	17866		2.5	6.0E-37	RI10039.1	EST_HUMAN	PTR5 repetitive element;
8377	20917	33837	0.54	6.0E-37	AF169888.1	NT	tm87g03.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165140 3' similar to contains L1.b3 L1 repetitive element;
12455	24588		3.85	6.0E-37	AF202723.1	NT	yf25a02.r1 Scars fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127850 5'
6243	18852	31622	4.92	5.0E-37	AA307123.1	EST_HUMAN	Homo sapiens protocadherin alpha 10 alternate isoform (PCDH-alpha10) mRNA, complete cds
6243	18852	31623	4.92	5.0E-37	AA307123.1	EST_HUMAN	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
8891	21230	34150	0.85	5.0E-37	AV750211.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
							EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
							AV750211 NPC Homo sapiens cDNA clone NPCBGH09 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10800	23323		4.94	5.0E-37	7657117	NT	Homo sapiens glycine C-acetyltransferase (2-aminino-3-ketobutyrate-CoA ligase) (GCAT), mRNA
11843	24205		5.21	5.0E-37	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
2468	15035	27602	1.7	4.0E-37	AA702794.1	EST_HUMAN	280b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
9278	21804	34755	0.68	4.0E-37	AA843806.1	EST_HUMAN	ak09c02.s1 Soares_parathyroid_tumor_1NHFA Homo sapiens cDNA clone IMAGE:1405442 3'
10912	23431	38451	1.74	4.0E-37	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
10912	23431	38452	1.74	4.0E-37	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2061	14641	27215	2.58	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2418
2061	14641	27216	2.58	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2418
2992	15608		3.5	3.0E-37	AW981150.1	EST_HUMAN	EST1373222 MAGE resequences, MAGF Homo sapiens cDNA
6126	17698		0.79	3.0E-37	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
7557	20075	32951	0.79	3.0E-37	A1749952.1	EST_HUMAN	at04c05.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2373896 3' similar to TR:Q13537
404	13079	25571	0.9	2.0E-37	D89780.1	NT	Q13537 SIMILAR TO POGO ELEMENT. ;
404	13079	25572	0.9	2.0E-37	D89780.1	NT	Homo sapiens mRNA for AML1, complete cds
1119	13722	26234	2.1	2.0E-37	AU131202.1	EST_HUMAN	Homo sapiens mRNA for AML1, complete cds
1119	13722	26235	2.1	2.0E-37	AU131202.1	EST_HUMAN	Homo sapiens mRNA for AML1, complete cds
2006	14588	27148	1.45	2.0E-37	AL163247.2	NT	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002186 5'
3962	16560	28029	6.99	2.0E-37	4503210	NT	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002186 5'
4330	16917	28360	0.59	2.0E-37	4826885	NT	Homo sapiens chromosome 21 segment HS21C047
6765	19358	32167	3.94	2.0E-37	AA346720.1	EST_HUMAN	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
7938	20480	33390	0.53	2.0E-37	BE537764.1	EST_HUMAN	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
7938	20480	33391	0.53	2.0E-37	BE537764.1	EST_HUMAN	EST52931 Fetal heart II Homo sapiens cDNA 5' end
7981	20523	33429	2.75	2.0E-37	BF204032.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
11434	23884	36951	19.39	2.0E-37	AF176013.1	NT	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
12633	24710		5.1	2.0E-37	11417872	NT	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111406 5'
2135	14713	27286	2.49	1.0E-37	AL163281.2	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
3231	15843		0.98	1.0E-37	AW862082.1	EST_HUMAN	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
4243	18831	28282	0.96	1.0E-37	BE872385.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
5075	17648	30089	3.67	1.0E-37	BF31719.1	EST_HUMAN	RC3-CT0347-210400-016-h03 CT0347 Homo sapiens cDNA
6155	18768		0.8	1.0E-37	7305360	NT	601448619F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852652 5'
8156	20697	33610	0.84	1.0E-37	BE546032.1	EST_HUMAN	QVO-FN0180-280700-318-e10 FN0180 Homo sapiens cDNA
8670	21208	34127	3.03	1.0E-37	AA171408.1	EST_HUMAN	Mus musculus otogelin (Otog), mRNA
							601072419F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308 5'
							zp21b02.r1 Stralagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610059 5' similar to
							contains L1.12 L1 repetitive element ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10577	23112	36125	5.51	1.0E-37	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
12187	24409		3.8	1.0E-37	BE771814.1	EST_HUMAN	CM3-FT0096-140700-243-407 FT0096 Homo sapiens cDNA
5950	18571	31303	1.71	9.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC58788), mRNA
1264	13881	28378	2.05	8.0E-38	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
2543	15107	27680	1.49	8.0E-38	BF346221.1	EST_HUMAN	602018401F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4153992 5'
12231	13881	26378	1.62	8.0E-38	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
4307	16893	29336	0.63	7.0E-38	H19092.1	EST_HUMAN	yn5107.r1 Soares adult brain N2bSHB55Y Homo sapiens cDNA clone IMAGE:171973 5'
3078	15693	28167	2.75	6.0E-38	BF033033.1	EST_HUMAN	601455722F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859348 5'
5776	18401	31118	1.34	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5776	18401	31117	1.34	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
11698	24110		10.47	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12201	24427	30952	14.11	6.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12614	24837	30787	1.7	6.0E-38	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
756	13375	25870	1.28	5.0E-38	AW971819.1	EST_HUMAN	EST383608 MAGE resequences, MAGL Homo sapiens cDNA
2495	15059	27633	1.94	5.0E-38	AJ237740.1	NT	Homo sapiens RIBLIR gene (partial), exon 8
7096	19887	32508	2.15	5.0E-38	BE871810.1	EST_HUMAN	601450148F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854074 5'
124	12793	25277	3.63	4.0E-38	Z25466.1	NT	B taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
124	12793	25278	3.63	4.0E-38	Z25466.1	NT	B taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
1199	13800	26312	1.06	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2148	14725		2.39	3.0E-38	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3759	16360		1.37	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnal-like) (HIRIP4), mRNA
3922	16520	28987	2.12	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3922	16520	28988	2.12	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4721	17302		0.66	3.0E-38	BE278301.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
6850	24772	32254	7.24	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7588	20103	32978	6.83	3.0E-38	BF373664.1	EST_HUMAN	CM3-FT0181-140700-241-407 FT0181 Homo sapiens cDNA
8584	21123	34043	2.01	3.0E-38	H85494.1	EST_HUMAN	y68b04.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775 5'
8584	21123	34044	2.01	3.0E-38	H85494.1	EST_HUMAN	y68b04.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775 5'
9882	22379		1.7	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11198	23703		1.54	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12461	13800	26312	1.44	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
54	12734	25202	1.84	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1422	14015	26544	2.23	2.0E-38	5902097	NT	Homo sapiens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1888	14280	28814	1.99	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1888	14280	28815	1.99	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
4881	17283	28714	2.98	2.0E-38	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
5293	17855	30280	0.63	2.0E-38	BE286224.1	EST_HUMAN	601177386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532580 5'
5293	17855	30281	0.63	2.0E-38	BE286224.1	EST_HUMAN	601177386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532580 5'
5327	17837	30284	0.63	2.0E-38	AA437181.1	EST_HUMAN	zw61d09.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:758129 5' similar to TR:G817957
7704	20213	33102	1.57	2.0E-38	AV721103.1	EST_HUMAN	G817957 GLYCINE RECEPTOR SUBUNIT ALPHA 4 ;
8420	20960	BE165980.1	5.5	2.0E-38	BE165980.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'
8826	21365	34289	0.51	2.0E-38	F09450.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
8885	21433	34356	1.37	2.0E-38	AF069755.1	NT	HSC18F031 normalized infant brain cDNA Homo sapiens cDNA clone c-18f03
9148	21683		0.89	2.0E-38	BE222256.1	EST_HUMAN	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
10345	22839	35835	1.98	2.0E-38	D63479.2	NT	hu09g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:Q02710 Q02710
							GAG POLYPEPTIDE ;
							Homo sapiens mRNA for KIAA0145 protein, partial cds
11114	23824	36665	3.38	2.0E-38	AA595480.1	EST_HUMAN	nc34g03.s1 NCI_CGAP_Pr23 Homo sapiens cDNA clone IMAGE:1102612 3' similar to TR:E212316
11114	23824	36666	3.38	2.0E-38	AA595480.1	EST_HUMAN	E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE ;
11363	23815	36876	6.15	2.0E-38	BE172790.1	EST_HUMAN	nc34g03.s1 NCI_CGAP_Pr23 Homo sapiens cDNA clone IMAGE:1102612 3' similar to TR:E212316
							E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE ;
							QV2-HT0698-080800-283-a05 HT0698 Homo sapiens cDNA
11498	23945	37014	3.87	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
11498	23945	37015	3.97	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
11753	24149		7.01	2.0E-38	AV726988.1	EST_HUMAN	AV726988 HTC Homo sapiens cDNA clone HTCAHX07 5'
11755	24150		1.68	2.0E-38	AB012723.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
12050	24334		3.19	2.0E-38	M55830.1	NT	Human topoisomerase I pseudogene 2
12060	24343	31000	5.31	2.0E-38	H5564.1	EST_HUMAN	CHR220580 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
12128	24384		2.87	2.0E-38	S74906.1	NT	E1 beta-pyruvate dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]
12824	24702		1.55	2.0E-38	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1132	13735		2.17	1.0E-38	AA401570.1	EST_HUMAN	zw62b02.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element MER19 repetitive element ;
2042	14624	27183	1.7	1.0E-38	4885288	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2065	14845	27219	1.46	1.0E-38	7661969	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2539	15103	27676	1.71	1.0E-38	AF270831.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
2645	15204	27777	14.26	1.0E-38	4758371	NT	Homo sapiens fibrinogen-like 1 (FGL1), mRNA
4235	16823	29274	1.03	1.0E-38	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4411	16996	29439	0.81	1.0E-38	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4416	17001	29444	1.52	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4416	17001	29445	1.52	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4702	17284	29729	1.18	1.0E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
5289	17851		29.49	1.0E-38	N46880.1	EST_HUMAN	Y58a01.r1 Soares_multiple_sclerosis_2NBHSP Homo sapiens cDNA clone IMAGE:277704 5' similar to SW/CA1H_MOUSE P39061 COLLAGEN ALPHA 1(XVIII) CHAIN PRECURSOR. ;
6178	18788	31556	4.28	1.0E-38	7305360	NT	Mus musculus dlogelin (Olog), mRNA
6178	18788	31557	4.28	1.0E-38	7305360	NT	Mus musculus dlogelin (Olog), mRNA
7435	19969	32824	3	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
9080	21616	34551	0.97	1.0E-38	11422250	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
9331	21845	34795	6.34	1.0E-38	BE350127.1	EST_HUMAN	nt09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3145256 3' similar to contains MER29.b3 MER29 repetitive element ;
11485	23915	36883	1.91	1.0E-38	7662109	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
11906	24808		2.57	1.0E-38	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
58	12738	25209	8.81	8.0E-39	4502312	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1438	14031	26559	1.49	8.0E-39	4758228	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
1869	14455		0.88	8.0E-39	AI823404.1	EST_HUMAN	wh53f10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890 POL. PROTEIN ;
2141	14719	27280	3.68	7.0E-39	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10688	23218	36230	2.32	6.0E-39	BF331828.1	EST_HUMAN	QV1-BT0631-Q40900-357-f02 BT0631 Homo sapiens cDNA
11639	24078	37138	1.54	6.0E-39	11526372	NT	Homo sapiens hyaluronan-mediated motility receptor (RHAMM) (HMMR), mRNA
12532	24645		2.82	6.0E-39	BE670394.1	EST_HUMAN	7c34c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R151.6 CE00828 ;
1045	13653	26165	1.85	5.0E-39	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3014	15630	28108	7.14	5.0E-39	AI750154.1	EST_HUMAN	at36b04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;contains LTR7.1 LTR7 repetitive element ;
12219	24441		2.69	5.0E-39	11420289	NT	Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
576	13203	25686	35.11	4.0E-39	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
3631	19234	28709	0.75	4.0E-39	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5995	18615	31350	0.73	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
5995	18615	31351	0.73	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
8020	20562	33463	0.95	4.0E-39	AA682948.1	EST_HUMAN	ae92g04.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains
9252	21778	34728	0.82	4.0E-39	D84116.1	NT	OFB.b1 OFR repetitive element ;
9252	21778	34729	0.82	4.0E-39	D84116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12337	24452		4.45	4.0E-39	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12363	24536		5.52	4.0E-39	BE836452.1	EST_HUMAN	Q10-FN0063-260600-278-c08 FN0063 Homo sapiens cDNA
51	12731	25196	16.82	3.0E-39	AA631949.1	EST_HUMAN	Imf16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
51	12731	25197	16.82	3.0E-39	AA631949.1	EST_HUMAN	Imf16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
51	12731	25198	16.82	3.0E-39	AA631949.1	EST_HUMAN	Imf16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
11744	24143	36764	6.46	3.0E-39	A1084557.1	EST_HUMAN	ox63a10.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1660988 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
11744	24143	36765	6.46	3.0E-39	A1084557.1	EST_HUMAN	ox63a10.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1660988 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
11791	24174		8.63	3.0E-39	H37903.1	EST_HUMAN	yp51c06.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190954 3'
930	13543		9.84	2.0E-39	BE409203.1	EST_HUMAN	601301807F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
945	13558		15.07	2.0E-39	A1525119.1	EST_HUMAN	promina-7.D01.7 bvtumor Homo sapiens cDNA 5'
1069	13674		3.85	2.0E-39	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
1577	14170		41.87	2.0E-39	AW372318.1	EST_HUMAN	PMO-BT0340-211289-003-d02 BT0340 Homo sapiens cDNA
2018	14598	27162	2.5	2.0E-39	AA720574.1	EST_HUMAN	hw21g02.s1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
2657	15216	27788	1.56	2.0E-39	AL163248.2	NT	THR repetitive element ;
4492	17077	28527	1.7	2.0E-39	BF370207.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
5682	18309	30804	3.89	2.0E-39	AA508880.1	EST_HUMAN	RC4-FN0037-280700-011-a10 FN0037 Homo sapiens cDNA
7405	19930	32794	1.95	2.0E-39	AA080867.1	EST_HUMAN	ng86f03.s1 NCI_CGAP_P16 Homo sapiens cDNA clone IMAGE:941693
8252	20793	33710	0.55	2.0E-39	AF078778.1	NT	zn06f02.r1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546651 5'
9415	21924		0.56	2.0E-39	AA984531.1	EST_HUMAN	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9544	22044		0.54	2.0E-39	A1686660.1	EST_HUMAN	am88c11.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1630196 3'
11309	23802	36863	3.11	2.0E-39	D86964.1	NT	tu35e03.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2253052 3'
1560	14152	26884	2.33	1.0E-39	AJ006345.1	NT	Human mRNA for KIAA0209 gene, partial cds
1560	14152	26885	2.33	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1578	14171	28700	9.78	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4719	17300	29745	0.87	1.0E-39	AW286073.1	EST_HUMAN	UI-H-BWO-aliu-h-06-0-UI.s1 NCJ CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2730850 3'
4764	17345	29793	4.98	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGE resequences, MAGB Homo sapiens cDNA
4764	17345	29784	4.98	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGE resequences, MAGB Homo sapiens cDNA
4812	17390	29841	10.18	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
5561	18192	30638	0.86	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5561	18192	30639	0.86	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5812	18436	31157	1.13	1.0E-39	T80876.1	EST_HUMAN	yd28g06.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:109402 5' similar to contains Alu repetitive element; contains LTR1 repetitive element;
5845	18469	31184	5.75	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
5845	18469	31195	5.75	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
6914	19573		1.87	1.0E-39	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7400	19925	32790	2.28	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8499	21038	33959	0.85	1.0E-39	O46530	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNASE K6)
12181	24401		4.3	1.0E-39	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
581	13211	25889	2.07	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1278	13873	26392	20.54	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1278	13873	26393	20.54	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1488	14080	26630	1.54	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3853	18451	28914	0.68	9.0E-40	4503764	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
4045	18004	29108	3.57	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
3077	15992	28166	1	8.0E-40	AA078185.1	EST_HUMAN	7H15A04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H15A04
3996	16594		1.74	8.0E-40	BC398541.1	EST_HUMAN	601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619166 5'
7702	20211	33098	2.01	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
7702	20211	33099	2.01	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
10776	23300	36308	2.48	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2753	15308	27873	5.43	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2753	15308	27874	5.43	6.0E-40	AA381275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
6094	18710		2.11	6.0E-40	BE504766.1	EST_HUMAN	h240g01.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3210480 3'
6296	18904		1.42	6.0E-40	7691999	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
7016	18513	32334	4.18	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7015	18513	32335	4.18	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
9887	22384	35360	8.69	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
9887	22384	35361	8.69	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
1919	14504	27061	1.42	4.0E-40	AI686005.1	EST_HUMAN	h91b01.x1 NCL_CGAP_Pz28 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN ;
2155	14732		1.38	4.0E-40	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4478	17063	29513	9.28	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
7827	20369	33277	0.59	4.0E-40	AU127831.1	EST_HUMAN	AU127831 NT2RP2 Homo sapiens cDNA clone NT2RP2002172 5'
7933	20475	33384	4.44	4.0E-40	AA742809.1	EST_HUMAN	h24e10.1 NCL_CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
8985	21523	34451	3.91	4.0E-40	BE009416.1	EST_HUMAN	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
8985	21523	34452	3.91	4.0E-40	BE009416.1	EST_HUMAN	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
10595	23129	36143	3.06	4.0E-40	AW841585.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4212	16801	28250	0.89	3.0E-40	AI925949.1	EST_HUMAN	h1207.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
6750	18343	32150	7.27	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semapherin) 5A (SEMA5A), mRNA
8321	20862	33787	3.69	3.0E-40	5454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
8899	21437	34360	1.28	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8138	21673	34615	1.58	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10541	23078	36092	1.79	3.0E-40	D86964.1	NT	Human mRNA for KIAA0209 gene, partial cds
10903	23423	36442	2.21	3.0E-40	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
11145	23653	36895	13.89	3.0E-40	6005813	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
11445	23895	36960	1.58	3.0E-40	AW118789.1	EST_HUMAN	xd96h02.x1 Soares NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2605491 3' similar to TR:Q15804 Q15804 SIMILAR TO ENV OF TYPE A AND TYPE B RETROVIRUSES AND TO CLASS II HERVS ;
347	12888		4.35	2.0E-40	AI223036.1	EST_HUMAN	qg52h08.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
827	13444		22.71	2.0E-40	AW303868.1	EST_HUMAN	h24e10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97481 40S RIBOSOMAL PROTEIN S5 ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1865	14451		1.38	2.0E-40	AV731801.1	EST_HUMAN	AV731801 HTF Homo sapiens cDNA clone HTFAZE05 5'
1878	14581	27119	1.39	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1878	14561	27120	1.39	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2116	14694	27282	0.95	2.0E-40	AI988562.1	EST_HUMAN	wt80a11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91929 Q91929 ZINC FINGER PROTEIN ;
2214	14789	27363	1.88	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
2714	15271		1.25	2.0E-40	BE275932.1	EST_HUMAN	601121587F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
3180	15774	28242	4.32	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
5027	17601	30046	1.84	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5027	17601	30047	1.84	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5378	17838	30351	3.28	2.0E-40	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
916	13529		1.05	1.0E-40	AA225989.1	EST_HUMAN	nc09a09.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007608
3337	15947		1.47	1.0E-40	4507142	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
4716	17297	29742	4.95	1.0E-40	4508012	NT	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
8403	19008	31786	0.69	1.0E-40	W92708.1	EST_HUMAN	zh78f11.s1 Soares fetal liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
8403	19008	31787	0.69	1.0E-40	W92708.1	EST_HUMAN	zh78f11.s1 Soares fetal liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7145	19678	32518	2.12	1.0E-40	AA573201.1	EST_HUMAN	h42704.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:985167 3'
7145	19678	32519	2.12	1.0E-40	AA573201.1	EST_HUMAN	h42704.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:985167 3'
7283	19811	32667	0.83	1.0E-40	P26808	SWISSPROT	POLYPROTEIN[CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; RIBONUCLEASE H]
10787	23320	36330	4.13	1.0E-40	AU149345.1	EST_HUMAN	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
11615	24057		1.72	1.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12182	24956		7.52	1.0E-40	BF334112.1	EST_HUMAN	MIR2-CT0222-211099-002-e10 CT0222 Homo sapiens cDNA
3878	16474	28938	0.65	8.0E-41	W01598.1	EST_HUMAN	za38a02.r1 Soares fetal liver spleen_1NFLS Homo sapiens cDNA clone IMAGE:294802 5'
7862	20404	33311	1.68	8.0E-41	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
861	15427	25990	1.58	7.0E-41	AI934364.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
861	15427	25991	1.58	7.0E-41	AI934364.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
5411	17888	30377	0.95	7.0E-41	11431114	NT	Homo sapiens hypothetical protein (FLJ10936), mRNA
5469	18103	30422	0.84	7.0E-41	11645770	NT	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA
6159	18772	31535	3.44	7.0E-41	11419208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6494	19095	31879	0.8	7.0E-41	11433010	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
7067	18086	30442	0.95	7.0E-41	U72335.1	NT	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIS1) gene, exons 3 and 4

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11311	23804	36864	1.98	7.0E-41	4758445	NT	Homo sapiens guanine nucleotide binding protein 10 (GNG10) mRNA
12631	24952		8.97	7.0E-41	11417972	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PEST1), mRNA
302	12957	25447	1.42	6.0E-41	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
2157	14734	27307	2.33	6.0E-41	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
7912	20454	33380	1.58	6.0E-41	BF513783.1	EST_HUMAN	UIH-BW1-amp-b-03-Q-U1.s1 NCI_CGAP_Sub57 Homo sapiens cDNA clone IMAGE:3070421 3'
12611	24873		1.61	6.0E-41	AW873637.1	EST_HUMAN	nc64f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3042183 3' similar to contains MER32.b3 MER32 repetitive element;
1838	14426	26977	2.16	5.0E-41	T62628.1	EST_HUMAN	yc03e10.s1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:79626 3'
4184	18774		1.01	5.0E-41	4885636	NT	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
6667	19263		1.97	5.0E-41	BE067042.1	EST_HUMAN	PM4-BT0341-251189-002-F11 BT0341 Homo sapiens cDNA
414	13048		1.58	4.0E-41	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
1137	13740	26249	1.12	4.0E-41	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
1455	14047	26577	9.23	4.0E-41	AI027117.1	EST_HUMAN	ow45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR5 repetitive element;
1455	14047	26578	9.23	4.0E-41	AI027117.1	EST_HUMAN	ow45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR5 repetitive element;
1469	14061	26598	1.67	4.0E-41	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
1677	14269	26802	8.43	4.0E-41	AI500408.1	EST_HUMAN	bm98c04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element;
2913	15530	28001	3.73	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3
2913	15530	28002	3.73	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3
4225	18813	29260	2.27	4.0E-41	X92685.1	NT	H. sapiens DNase I hypersensitive site (HSS-3) enhancer element
6632	19228		1.36	4.0E-41	AV758295.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMFBHC06 5'
9610	22110	35072	6.75	4.0E-41	BF304683.1	EST_HUMAN	60188096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
11522	23970		9.87	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Cu Homo sapiens cDNA clone CUAACC07 5'
12375	24841		2.28	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
12570	24689	30875	4.65	4.0E-41	BE887118.1	EST_HUMAN	601508315F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910059 5'
983	13595	26109	1.64	3.0E-41	AB030176.1	NT	Homo sapiens PAO-H19 mRNA for peptidylarginine deiminase type II, complete cds
4428	17014	29458	2.7	3.0E-41	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5273	17834		1.03	3.0E-41	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
5683	18310	30805	9.55	3.0E-41	X87689.1	NT	H. sapiens mRNA for putative p64 CLCP protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6518	19118	31609	1.73	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
7761	20269	33167	0.7	3.0E-41	R52785.1	EST_HUMAN	y75d08.r1 Soares breast 2NbhBst Homo sapiens cDNA clone IMAGE:154575 5'
11575	24021	37050	1.78	3.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11703	24116		1.84	3.0E-41	AA609768.1	EST_HUMAN	af77f10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1031947 3'
1864	14200	26734	15.09	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
2001	14583	27142	1.76	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week I Homo sapiens cDNA 5' end
2260	14834	27412	1.13	2.0E-41	D89862.1	NT	Human mRNA for KIAA0207 gene, complete cds
2308	14880	27456	3.79	2.0E-41	X89631.1	NT	G.gorilla DNA for ZNF80 gene homolog
2855	14200	26734	10.67	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
4728	17309	29753	2.07	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4728	17309	29754	2.07	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
7666	20178	33065	6.67	2.0E-41	AF038404.1	NT	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds
8013	20555	33458	1.36	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8013	20555	33459	1.36	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8040	20592	33489	1.59	2.0E-41	AA328265.1	EST_HUMAN	EST31723 Embryo, 12 week I Homo sapiens cDNA 5' end
8905	21443	34366	1.61	2.0E-41	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
9338	21852	34800	0.74	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9338	21852	34801	0.74	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11359	23813	36873	3.76	2.0E-41	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3240	15852	28333	1.11	1.0E-41	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3849803 5'
3240	15852	28334	1.11	1.0E-41	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3849803 5'
4666	17248	29701	11.21	1.0E-41	6678468	NT	Mus musculus tubulin alpha 6 (Tuba6), mRNA
9339	21853	34802	1.82	1.0E-41	AI217868.1	EST_HUMAN	q775c10.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755858 3'
11039	23553	36588	2.41	1.0E-41	AW847812.1	EST_HUMAN	IL3-CT0213-190200-040-F09 CT0213 Homo sapiens cDNA
11842	24204		2.37	1.0E-41	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8457	20997		1.34	9.0E-42	BE178191.1	EST_HUMAN	RCO-HT0613-210300-032-g01 HT0613 Homo sapiens cDNA
9101	21637	34575	2.43	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9101	21637	34576	2.43	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
489	13121	25607	7.59	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
11881	24959		53.38	8.0E-42	AA493896.1	EST_HUMAN	nh07c02.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304
11900	24830		2.62	8.0E-42	AW089062.1	EST_HUMAN	367BP EXPRESSED SEQUENCE TAG MRNA ;
987	13578		2.5	7.0E-42	AL163285.2	NT	xc97a04.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2592174 3' similar to contains OFR.12 OFR repetitive element ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8408	20948		0.62	7.0E-42	R10963.1	EST_HUMAN	y38g04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129174 5'
9168	21745	34688	1.99	7.0E-42	AI204358.1	EST_HUMAN	qf59g12.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1754278 3'
11052	23565	36600	1.59	7.0E-42	AA569592.1	EST_HUMAN	nf23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
11052	23565	36601	1.59	7.0E-42	AA569592.1	EST_HUMAN	nf23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
1898	14481	27039	4.44	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1898	14481	27040	4.44	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
							xp29f08.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L1.11 L1 repetitive element
2328	14899		3.36	6.0E-42	AW238656.1	EST_HUMAN	Homo sapiens mRNA for KIAA1067 protein, partial cds
5659	18286	30764	1.46	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
5893	18286	30764	1.5	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
141	12808		6.21	5.0E-42	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region: segment 112
463	13097	25588	1.39	5.0E-42	BE217813.1	EST_HUMAN	h31e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
512	13145		4.36	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
513	13148		2.72	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
							Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6788	19379	32194	1.23	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6788	19379	32195	1.23	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6893	19827	32464	2.58	5.0E-42	11417957	NT	Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
							Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
7253	19781	32637	1.64	5.0E-42	AF071569.1	NT	cds
8713	21252	34174	2.85	5.0E-42	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
10495	22889	35997	0.6	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
10495	22889	35998	0.6	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
10977	23398	36415	1.92	5.0E-42	8923162	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
783	13402	25905	7.93	4.0E-42	AF055066.1	NT	Homo sapiens MHC class I region
783	13402	25906	7.93	4.0E-42	AF055066.1	NT	Homo sapiens MHC class I region
1104	13708	26217	2.39	4.0E-42	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4272	16858	29307	1.46	4.0E-42	X59417.1	NT	H. sapiens PROS-27 mRNA
4335	16922	29364	5.27	4.0E-42	4506498	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
4683	17265	29715	13.42	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
5353	17913	30328	0.94	4.0E-42	7681635	NT	Homo sapiens DKFZP564O2082 protein (DKFZP564O2082), mRNA
10378	22872	35865	0.46	4.0E-42	AW371201.1	EST_HUMAN	CMO-BT0282-171299-127-503 BT0282 Homo sapiens cDNA
10528	23065	36076	1.76	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10528	23065	36077	1.76	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-0400-018-h11 ST0278 Homo sapiens cDNA
11290	23742	36799	3.45	4.0E-42	BF05327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1530	14122	26661	4.49	2.0E-42	BF376834.1	EST_HUMAN	RC0-TN0078-110900-024-q07 TN0078 Homo sapiens cDNA
2436	15003	27575	0.92	2.0E-42	AV690218.1	EST_HUMAN	AV690218 GKC Homo sapiens cDNA clone GKCCBB08 5'
2458	15023		2.69	2.0E-42	AW898344.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2469	15038	27603	2.41	2.0E-42	AW250059.1	EST_HUMAN	2819293.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819293 3'
5931	18553	31278	13.21	2.0E-42	AW955388.1	EST_HUMAN	EST367438 MAGC resequences, MAGC Homo sapiens cDNA
5931	18553	31280	13.21	2.0E-42	AW955388.1	EST_HUMAN	EST367438 MAGC resequences, MAGC Homo sapiens cDNA
6949	19439	32253	0.84	2.0E-42	AI052586.1	EST_HUMAN	ow63405.x1 Soares_fetal_liver_TNFLS_S1 Homo sapiens cDNA clone IMAGE:1653417 3'
9755	22253	35235	1.1	2.0E-42	BE538919.1	EST_HUMAN	601061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'
9987	22462	35445	0.53	2.0E-42	P81849	SWISSPROT	RIBONUCLEASE K3 (RNASE K3)
9987	22462	35446	0.53	2.0E-42	P81849	SWISSPROT	RIBONUCLEASE K3 (RNASE K3)
11585	24030	37100	1.55	2.0E-42	AI163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
763	19381	25980	1.52	1.0E-42	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
1080	13685	26197	0.84	1.0E-42	AW295809.1	EST_HUMAN	UH-HB1-afh-e04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1140	13743	26252	2.08	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1140	13743	26253	2.08	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1285	15437	26404	10.72	1.0E-42	AF067186.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1285	15437	26405	10.72	1.0E-42	AF067186.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1738	14328	26872	1.86	1.0E-42	11423219	NT	Homo sapiens rec (LOC51201), mRNA
2581	15144	27712	5.25	1.0E-42	5174458	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2991	15607	28087	6.58	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3770	16371	28836	2.85	1.0E-42	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3862	18460	28924	0.83	1.0E-42	5031670	NT	Homo sapiens Golgi vesicular membrane trafficking protein p18 (BET1) mRNA
3999	16597	29069	1.07	1.0E-42	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4331	16918	28361	1.92	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4997	17279	29725	0.86	1.0E-42	AW813617.1	EST_HUMAN	RC3-ST0197-161099-012-a03 ST0197 Homo sapiens cDNA
4956	17434	29885	2.65	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4856	17434	29886	2.65	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4893	17468	29924	6.23	1.0E-42	4508798	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
5274	17835	30260	1.49	1.0E-42	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5274	17835	30261	1.48	1.0E-42	4501812	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
9998	22493	35482	3.35	9.0E-43	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
10916	23435	38455	3.57	9.0E-43	AA435719.1	EST_HUMAN	z79a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728532 3'
680	13304	25786	22.52	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
680	13304	25787	22.52	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
729	13349	25841	7.38	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297). mRNA
729	13349	25842	7.38	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297). mRNA
729	13349	25843	7.38	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297). mRNA
5877	18499	31225	0.82	8.0E-43	H13952.1	EST_HUMAN	y08a11.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148172 5'
3703	16304	28772	7.6	7.0E-43	AW248442.1	EST_HUMAN	2822251.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'
5414	17971	30381	1.1	7.0E-43	AA989045.1	EST_HUMAN	α88a07.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602900 3' similar to contains LTR8.b3 LTR8 repetitive element;
5414	17971	30382	1.1	7.0E-43	AA989045.1	EST_HUMAN	α88a07.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602800 3' similar to contains LTR8.b3 LTR8 repetitive element;
8704	21243		3.4	7.0E-43	A1938748.1	EST_HUMAN	wp69b01.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN; contains LTR7.b1 LTR7 repetitive element;
1388	13982		9.98	6.0E-43	AA491890.1	EST_HUMAN	ne72a06.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909803 similar to gb:L05095 60S
2628	15180		2.44	6.0E-43	AV708201.1	EST_HUMAN	RIBOSOMAL PROTEIN L30 (HUMAN);
6453	10054	31839	2.54	6.0E-43	9955973	NT	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA
6988	19486	32308	2.15	6.0E-43	AW468897.1	EST_HUMAN	h33b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810991 3' similar to contains MER1.k3 MER1 repetitive element;
9765	22263	35246	2.2	6.0E-43	AA195154.1	EST_HUMAN	z735e06.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665410 5' similar to TR:G529841 G529841 DB1, COMPLETE CDS; contains element PTR7 repetitive element;
10980	23494		6.53	6.0E-43	AL119158.1	EST_HUMAN	DKFZp761L1712.r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'
149	12812		1.7	5.0E-43	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
528	13160	25841	3.37	5.0E-43	AA382780.1	EST_HUMAN	EST196033 Testis 1 Homo sapiens cDNA 5' end
2872	15490	27961	1.18	5.0E-43	AV732578.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANC06 5'
6447	19481	32302	1.23	5.0E-43	A1613509.1	EST_HUMAN	tw22e07.x1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260452 3'
6983	19481	32302	0.77	5.0E-43	A1613509.1	EST_HUMAN	tw22e07.x1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260452 3'
8812	21351		0.49	5.0E-43	H7427.1	EST_HUMAN	y449g12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:229510 5'
9286	21886	34831	3.67	5.0E-43	AA485288.1	EST_HUMAN	aa33d08.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10287	22791	35781	2.17	5.0E-43	AI733244.1	EST_HUMAN	cc52c10.x5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P90591 P90591 PV14 GENE.
10332	22826	35821	2.14	5.0E-43	AL049110.1	EST_HUMAN	DKFZP434D0119_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZP434D0119
10844	23176	38188	5.05	5.0E-43	AW863007.1	EST_HUMAN	MR2-SN0007-290400-004-c02 SN0007 Homo sapiens cDNA
10850	23371	38390	4.1	5.0E-43	W28011.1	EST_HUMAN	5584 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
11332	23030	36039	1.71	5.0E-43	X15804.1	NT	Human mRNA for alpha-actinin
1008	15390	28133	5.38	4.0E-43	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5464	18099	30417	0.98	4.0E-43	AI056338.1	EST_HUMAN	oy47h03.x1 NCI_CGAP_Brm23 Homo sapiens cDNA clone IMAGE:1669013 3'
6507	18107	31882	0.82	4.0E-43	6986009	NT	Homo sapiens glycyl-tRNA synthetase (GARS), mRNA
7184	18716		2.22	4.0E-43	11416793	NT	Homo sapiens protocadherin beta 6 (PCDH6), mRNA
8118	20859	33568	4.54	4.0E-43	AI244341.1	EST_HUMAN	q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
8118	20859	33569	4.54	4.0E-43	AI244341.1	EST_HUMAN	q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
10217	22712	35704	1.33	4.0E-43	6005967	NT	Homo sapiens zinc finger protein 161 (ZNF161), mRNA
11184	23689	38736	1.68	4.0E-43	T77380.1	EST_HUMAN	yd72h10.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:113827 5'
11819	24189		4.47	4.0E-43	R20950.1	EST_HUMAN	y908b05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element.
1255	13852		3.54	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1733	14324	28868	1.8	3.0E-43	X97869.1	NT	H. sapiens gene encoding Le autantigen
2178	14753	27323	1.15	3.0E-43	AJ278230.1	NT	Homo sapiens mRNA for partial phospholipase D1, splice variant PLD1a/b2
3630	16233	28708	1.25	3.0E-43	S69002.1	NT	AML1-EVI-1=AML1-EVI-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]
4378	16985	29411	0.9	3.0E-43	AA548154.1	EST_HUMAN	nk55d08.s1 NCI_CGAP_P77 Homo sapiens cDNA clone IMAGE:1017419
6498	19099	31883	2.08	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
6498	19099	31884	2.08	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
6827	19417	32233	3.71	3.0E-43	U65487.1	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
8104	20645		8.03	3.0E-43	AA458824.1	EST_HUMAN	aa88f11.s1 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR.12 THR repetitive element.
8754	21293	34213	1.59	3.0E-43	7661721	NT	Homo sapiens hypochelical protein (HSA011916), mRNA
9778	22278	35281	0.77	3.0E-43	11420217	NT	Homo sapiens similar to ornithine carbamoyltransferase (H. sapiens) (LOC63648), mRNA
11572	24018	37089	2.6	3.0E-43	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
198	12856		9.15	2.0E-43	A180784.1	EST_HUMAN	gd61c09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains PTR7.13 PTR7 PTR7 repetitive element;
6601	19198	32003	0.95	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element;
6601	19198	32004	0.95	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element;
7320	19847	32707	1.12	2.0E-43	AW207390.1	EST_HUMAN	U1-H-B11-af-e-09-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3'
8250	20791		9.58	2.0E-43	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
11079	23591		3.66	2.0E-43	T03007.1	EST_HUMAN	FB1G5 Fetal brain, Stragene Homo sapiens cDNA clone FB1G5 3' end similar to LINE-1
1690	14282	26817	2.54	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1690	14282	26818	2.54	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1743	14333	26879	1.63	1.0E-43	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2750	15305	27669	4.08	1.0E-43	BF348283.1	EST_HUMAN	602022313F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157666 5'
6723	19317	32120	9.22	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
6723	19317	32121	9.22	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
7046	19068	30456	1.8	1.0E-43	R19751.1	EST_HUMAN	y940e01.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34732 5' similar to SP:BD38 MOUSE P28658 BRAIN PROTEIN DN38;
7873	20415	33323	1.04	1.0E-43	AF175265.1	NT	Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds
8010	20552		2.79	1.0E-43	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
8771	21310	34233	26.95	1.0E-43	AW963676.1	EST_HUMAN	EST375749 IMAGE resequences, MAGH Homo sapiens cDNA
10191	22686	35679	0.65	1.0E-43	AW953229.1	EST_HUMAN	EST365239 IMAGE resequences, MAGB Homo sapiens cDNA
10843	23364	36380	8.02	1.0E-43	A1984961.1	EST_HUMAN	wr87h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494705 3'
11244	23774	36831	3.74	1.0E-43	11424378	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
11757	24152		1.95	1.0E-43	AL137964.1	EST_HUMAN	DKFZp761D1015_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761D1015 5'
12054	24337	30998	3.9	1.0E-43	A1675416.1	EST_HUMAN	w598b04.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2313775 3'
12286	24488	30942	4.3	9.0E-44	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
923	13536	26054	5.83	8.0E-44	A1222985.1	EST_HUMAN	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
923	13536	26055	5.83	8.0E-44	A1222985.1	EST_HUMAN	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
6424	17981	30388	0.69	8.0E-44	A1381520.1	EST_HUMAN	ta76c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2092622 3' similar to TR:P93107 P93107 PF20;
8476	21015	33931	2.74	8.0E-44	X94354.1	NT	H. sapiens DNA for Core cGMP-PDE gene
11043	23557	36593	3.86	8.0E-44	Y10498.2	NT	Homo sapiens mRNA for thymidine kinase, partial
11536	23984	37058	1.86	8.0E-44	L29139.1	NT	Homo sapiens myosin mRNA, partial cds
12008	24310	30992	2.76	8.0E-44	11527389	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12419	24859	30703	2.39	8.0E-44	11418099	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
687	13311		0.83	7.0E-44	R06035.1	EST_HUMAN	y089601.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124920 5'
2276	14850	27428	1.12	7.0E-44	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2693	15609	28088	2.84	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
2993	15609	28089	2.84	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3928	16527	28994	2.76	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4326	16912	29354	0.96	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4326	16912	29355	0.96	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
8126	20667	33376	6.38	7.0E-44	AU159839.1	EST_HUMAN	AU159839 Y79AA1 Homo sapiens cDNA clone Y79AA1000496 3'
6252	18861	31633	0.77	6.0E-44	Z20948.1	EST_HUMAN	HSAAADEYU P, Human fetal Brain Whole tissue Homo sapiens cDNA
11611	24054	37118	2.92	6.0E-44	AW954050.1	EST_HUMAN	EST1366120 IMAGE resequences, MAGC Homo sapiens cDNA
325	12979		3.12	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
354	13003		1.75	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
7829	20371	33278	3.5	5.0E-44	AI568523.1	EST_HUMAN	h40d02.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.t1 OFR OFR repetitive element ;
9306	21906		1.85	5.0E-44	AU124571.1	EST_HUMAN	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
3461	16068	28541	2.18	4.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
5158	17727		1.16	4.0E-44	AI435225.1	EST_HUMAN	h11402.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
8215	20758	33670	0.76	4.0E-44	L21948.1	NT	Human fibrillin (FBN1) locus polymorphism
8811	21350		0.54	4.0E-44	BE176618.1	EST_HUMAN	RC3-H170585-010400-073-008 H170585 Homo sapiens cDNA
11117	23626	36668	7.04	4.0E-44	U90878.1	NT	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds
1821	14410		1.09	3.0E-44	6912477	NT	Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNA6), mRNA
3132	15746	28215	5.8	3.0E-44	AA169851.1	EST_HUMAN	zp18b05.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609777 5'
3959	16557	29028	2.94	3.0E-44	AA337234.1	EST_HUMAN	EST42289 Endometrial tumor Homo sapiens cDNA 5' end similar to similar to alpha-1-antitrypsinase F
5404	17982	30373	2.57	3.0E-44	BF691080.1	EST_HUMAN	602247109F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332195 5'
9438	21984	34913	0.56	3.0E-44	AF050273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
1087	13692	26201	2.13	2.0E-44	4826885	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1087	13692	26202	2.13	2.0E-44	4826885	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1249	13846	26363	2.99	2.0E-44	5903200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1249	13846	26364	2.99	2.0E-44	5903200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1355	13949	26475	4.41	2.0E-44	AF133588.1	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1412	14005	26533	1.38	2.0E-44	BE465325.1	EST_HUMAN	hwt14g06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182838 3' similar to SW:OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2186	14772	27346	1.71	2.0E-44	AF070651.1	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
2841	15200		2.07	2.0E-44	5901933	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
3517	16122	28602	1.34	2.0E-44	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4669	17251	28703	1.86	2.0E-44	AW964379.1	EST_HUMAN	PM4-SN0016-120500-003-404 SN0016 Homo sapiens cDNA
5441	17898	30401	1.08	2.0E-44	4506378	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
6245	18854	31625	1.71	2.0E-44	11449901	NT	Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA
6941	18049	30471	1.05	2.0E-44	AF038988.1	NT	Homo sapiens general transcription factor 2-1 (GTF2) mRNA, alternatively spliced product, complete cds
7444	19668	32835	4.03	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
7444	19668	32836	4.03	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8367	20907	33825	0.85	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA
8367	20907	33826	0.85	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA
8554	21093	34013	1.47	2.0E-44	BE389058.1	EST_HUMAN	801286914F NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613586 5'
11657	24084		1.8	2.0E-44	BE244902.1	EST_HUMAN	TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2795
12608	24692		63.7	2.0E-44	11526283	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
56	12736	25205	5.03	1.0E-44	7657334	NT	Homo sapiens Mischapen/NIK-related kinase (MINK), mRNA
56	12736	25208	5.03	1.0E-44	7657334	NT	Homo sapiens Mischapen/NIK-related kinase (MINK), mRNA
606	13234	25708	2.28	1.0E-44	AW653132.1	EST_HUMAN	RC1-CT0249-030300-028-h12 CT0249 Homo sapiens cDNA
1239	13837		1.03	1.0E-44	AW984803.1	EST_HUMAN	RC1-BN0039-110300-012-501 BN0039 Homo sapiens cDNA
1618	14211		4.77	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2266	14840	27416	3.03	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.13 THR repetitive element;
2266	14840	27417	3.03	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.13 THR repetitive element;
2321	15463	27468	1.21	1.0E-44	AA398099.1	EST_HUMAN	z88g11.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:729476 5'
2788	15341	27911	1.54	1.0E-44	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α_2
3788	16388		4.07	1.0E-44	AA455869.1	EST_HUMAN	aa01c09.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'
8209	20750	33663	1.33	1.0E-44	AW967073.1	EST_HUMAN	EST379147 IMAGE resequences, MAGJ Homo sapiens cDNA
8209	20750	33664	1.33	1.0E-44	AW967073.1	EST_HUMAN	EST379147 IMAGE resequences, MAGJ Homo sapiens cDNA
8560	21119	34040	0.94	1.0E-44	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8956	21494	34417	0.68	1.0E-44	AI337183.1	EST_HUMAN	qx88g07.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2009628 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10892	23413		11.29	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DCB Homo sapiens cDNA clone DCBBYE03 5'
11404	23855	36921	5.07	1.0E-44	10092664	NT	Homo sapiens Sushi domain (SCR repeat) containing (BK65A6.2), mRNA
11460	23910	36976	3.83	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
11460	23910	36977	3.83	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
4678	17260	28711	1.31	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10379), mRNA
4678	17260	28712	1.31	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10379), mRNA
8757	19350	32158	1.34	9.0E-45	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
2565	15129	27698	6.45	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5241	17805	30226	7.14	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
8051	20593	33501	0.84	8.0E-45	AA377985.1	EST_HUMAN	EST190893 Synovial sarcoma Homo sapiens cDNA 5' end
2984	15600		0.99	7.0E-45	AL160131.1	NT	Novel human gene mapping to chromosome 22
4050	16647		6.39	6.0E-45	AW157570.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782809 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
12385	25063		2	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
925	13538		1.34	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2045	14627	27198	12.03	5.0E-45	BF333627.1	EST_HUMAN	GM4-CN0044-180200-515-101 CN0044 Homo sapiens cDNA
3246	15858	28341	2.25	5.0E-45	AI523768.1	EST_HUMAN	ig94f07.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2118453 3' similar to SW:PAX1_MOUSE
5703	18329	30832	8.34	5.0E-45	AA397781.1	EST_HUMAN	z172d03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element TAR1 repetitive element ;
6170	18782	31548	1.1	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6170	18782	31549	1.1	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6215	18825	31596	1.15	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6215	18825	31597	1.15	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6336	18942	31720	1.82	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6336	18942	31721	1.82	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8216	20759	33873	0.51	5.0E-45	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
8971	21509	34431	1.79	5.0E-45	4759223	NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA
11542	23990	37062	2.52	5.0E-45	8923668	NT	Homo sapiens golgin-like protein (GLP), mRNA
1183	13784	26284	11.57	4.0E-45	X95926.1	NT	H. sapiens ART4 gene
2330	14901	27472	21.18	4.0E-45	BE265622.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
4605	17188	28635	0.68	4.0E-45	4759249	NT	Homo sapiens TRAF family member-associated NFkB activator (TANK) mRNA
8886	21424		0.86	4.0E-45	AA226220.1	EST_HUMAN	nc26e07.s1 NCI CGAP_Prl Homo sapiens cDNA clone IMAGE:1009284 similar to contains element L1 repetitive element ;

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11629	24071		2.17	4.0E-45	BE044076.1	EST_HUMAN	h036h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
11673	25008	30813	1.66	4.0E-45	11435947	NT	MER29 repetitive element
12278	24482		2.14	4.0E-45	BF676077.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
4161	15982		1.32	3.0E-45	T71480.1	EST_HUMAN	602084052F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248253 5'
6383	18987	31767	1.28	3.0E-45	6753651	NT	y035f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
6383	18987	31768	1.29	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahtc11), mRNA
8388	20928		1.29	3.0E-45	AV723976.1	EST_HUMAN	Mus musculus dynein, axon, heavy chain 11 (Dnahtc11), mRNA
8726	21265	34185	3.78	3.0E-45	4758451	NT	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
10209	22704	35698	11.34	3.0E-45	AL163227.2	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA
10209	22704	35697	11.34	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
2547	15111		4.13	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
3067	15682	28154	0.99	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
6644	19240	32043	5.46	2.0E-45	L01665.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
7605	20118	32894	1.35	2.0E-45	BE782184.1	EST_HUMAN	601467783F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870838 5'
8354	20894	33615	0.75	2.0E-45	AW834834.1	EST_HUMAN	RCO-LT0001-150200-032-d11 LT0001 Homo sapiens cDNA
10682	24798	38225	28.86	2.0E-45	BE934350.1	EST_HUMAN	MRO-HT0923-190800-201-a02 HT0923 Homo sapiens cDNA
11055	23567	36603	5.39	2.0E-45	AA468770.1	EST_HUMAN	aa87f12.r1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838319 5' similar to
11378	23830	36892	2.33	2.0E-45	AW270280.1	EST_HUMAN	TR:G1144569 G1144569 R-SLY1..
11378	23830	36893	2.33	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
12548	24653		2.42	2.0E-45	11418157	NT	xp72a03.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
129	13067		2.71	1.0E-45	BE389855.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
434	13067		3.24	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
498	13130	25619	1.61	1.0E-45	4506412	NT	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
1216	13816	26331	1.54	1.0E-45	7657280	NT	Homo sapiens RAPIA, member of RAS oncogene family (RAPIA), mRNA
3137	15751	28219	10.2	1.0E-45	U32169.1	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3539	16144	28627	0.88	1.0E-45	8659558	NT	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds
3632	16235	28710	0.68	1.0E-45	AB046811.1	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
4575	17158	29602	5.67	1.0E-45	BE396633.1	EST_HUMAN	Homo sapiens mRNA for KIAA1591 protein, partial cds
5335	17896	30311	11.79	1.0E-45	7706128	NT	601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619803 5'
7974	20516	33422	0.71	1.0E-45	11422236	NT	Homo sapiens oxysterol 7alpha-hydroxylase (CYP39A1), mRNA
7974	20516	33423	0.71	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8543	21082	34003	0.88	1.0E-45	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9049	21586	34517	4.07	1.0E-45	BE897843.1	EST_HUMAN	601511226F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912535 5'
9441	21967	34916	0.96	1.0E-45	AB002287.1	NT	Human mRNA for KIAA0289 gene, partial cds
11875	24225	31045	4.89	1.0E-45	11418098	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
12063	24346		9.84	1.0E-45	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12068	24349		10.36	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12513	24632	30885	3.46	1.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
8170	20711	33628	1.87	9.0E-46	9910283	NT	Mus musculus keratin complex 2, gene 8g (Krl2-8g), mRNA
8589	21108		6.51	9.0E-46	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10374	22868	35861	10.22	9.0E-46	AW246964.1	EST_HUMAN	2822449.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'
2486	15051	27622	9.69	8.0E-46	AI433261.1	EST_HUMAN	I332708.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_ma2
2486	15051	27623	9.69	8.0E-46	AI433261.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
7698	20540		6.07	8.0E-46	BE167244.1	EST_HUMAN	RC3-H10506-280200-012-C12 HT0506 Homo sapiens cDNA
11513	23961		2.67	8.0E-46	11418728	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
2280	14854	27432	1.07	7.0E-46	U46007.1	NT	Rattus norvegicus espin mRNA, complete cds
4880	17262		6.36	7.0E-46	BE386185.1	EST_HUMAN	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
4929	17504		0.96	7.0E-46	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
6193	18803	31572	3.72	7.0E-46	8922708	NT	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
6620	19217	32022	1.29	7.0E-46	BF105845.1	EST_HUMAN	601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042736 5'
12203	24428		1.6	7.0E-46	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2783	15336	27908	3.13	6.0E-46	AI884381.1	EST_HUMAN	wm31f08.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.t2
2783	15336	27907	3.13	6.0E-46	AI884381.1	EST_HUMAN	MER19 repetitive element;
6278	18886	31655	9.32	6.0E-46	AI635448.1	EST_HUMAN	wm31f08.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.t2
7269	19797	32653	0.83	6.0E-46	AW513244.1	EST_HUMAN	Is58h10.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363
11268	23006		2.81	6.0E-46	BE784971.1	EST_HUMAN	SA GENE.
218	12879		5.85	5.0E-46	AL163210.2	NT	xc42e04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2706654 3' similar to gb:U08089 DNAJ
3581	18185	28667	1.37	5.0E-46	BE677194.1	EST_HUMAN	PROTEIN HOMOLOG 2 (HUMAN);
3581	18185	28668	1.37	5.0E-46	BE677194.1	EST_HUMAN	601478409F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880995 5'
							Homo sapiens chromosome 21 segment HS21C010
							7881g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
							7881g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6833	19423	32239	1.83	5.0E-46	BF590442.1	EST_HUMAN	naa3807.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3268757 3' similar to TR:O75202
7021	19555	32380	3.81	5.0E-46	BF347229.1	EST_HUMAN	O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC ;
7152	19684	32526	0.74	5.0E-46	AW58253.1	EST_HUMAN	602021164F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670 5'
9533	22033	34992	0.46	5.0E-46	AA398381.1	EST_HUMAN	QV4-ST0212-120100-075-f09 ST0212 Homo sapiens cDNA
669	13283		1.73	4.0E-46	AA601143.1	EST_HUMAN	z62c08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726926 3'
							nc54e09.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ma1
							FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1741	14331	26875	3.96	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1
							LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element ;
1741	14331	26876	3.96	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1
2767	15321	27687	3.11	4.0E-46	M18048.1	NT	LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element ;
5628	18257	30727	2.09	4.0E-46	M36652.1	NT	Human endogenous retrovirus RTVL-H2
5628	18257	30728	2.09	4.0E-46	M36652.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
12332	24516	30921	1.86	4.0E-46	AB002059.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
4482	17067	29517	0.81	3.0E-46	4506376	NT	Homo sapiens DNA for Human P2XM, complete cds
							Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4889	17464	29918	0.88	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
4889	17464	29919	0.88	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
8684	21223	34143	7.65	3.0E-46	A1831462.1	EST_HUMAN	w149c04.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2
8935	21473	34392	0.56	3.0E-46	L08850.1	NT	THR repetitive element ;
8935	21473	34393	0.56	3.0E-46	L08850.1	NT	Human AD amyloid mRNA, complete cds
11446	23696	36961	3.14	3.0E-46	D31755.1	NT	Human AD amyloid mRNA, complete cds
870	13485	26000	8.24	2.0E-46	AA469846.1	EST_HUMAN	Human mRNA for KIAA0061 gene, partial cds
1608	14201		1.41	2.0E-46	AA678246.1	EST_HUMAN	ne06a09.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR
1683	14275	26808	2.17	2.0E-46	U78027.1	NT	repetitive element ;
							z127a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431996 3'
							Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein
							(L44L) and FTP3 (FTP3) genes, complete cds
							z159e02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726850 5' similar to SW:RSP1_MOUSE
5110	17682	30119	1.2	2.0E-46	AA399286.1	EST_HUMAN	Q01730 RSP-1 PROTEIN. ;

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7497	20020	32884	6.85	2.0E-46	9910569	NT	Mus musculus sperm tail associated protein (Stap), mRNA
8014	20556		1.81	2.0E-46	BE869151.1	EST_HUMAN	601445137F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849297 5'
11125	23633		1.56	2.0E-46	7657233	NT	Homo sapiens small acidic protein (IMAGE145052), mRNA
11802	24863		1.74	2.0E-46	BF028854.1	EST_HUMAN	601765225F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3997326 5'
12094	24361		1.43	2.0E-46	AA001786.1	EST_HUMAN	zh84f12.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
12408	24846	30800	5.26	2.0E-46	AW277214.1	EST_HUMAN	xq78h03.x1 NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3'
1276	13871	26391	5.79	1.0E-46	4502894	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2320	14892	27467	4.58	1.0E-46	AW978516.1	EST_HUMAN	EST300625 MAGE resequences, MAGP Homo sapiens cDNA
2443	15010	27582	2.81	1.0E-46	H97330.1	EST_HUMAN	EST486095 WATMT1 Homo sapiens cDNA clone 486095
3286	15897	28375	22.33	1.0E-46	AA631812.1	EST_HUMAN	np78b02.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H. sapiens MT-1 mRNA (HUMAN);
4999	17572		3.21	1.0E-46	AB023197.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
5876	18500	31228	11.77	1.0E-46	BF194707.1	EST_HUMAN	7a92b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
6131	24757	31500	4.79	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6131	24757	31501	4.78	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6725	19319	32124	0.72	1.0E-46	BF196247.1	EST_HUMAN	7m48e07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567852 3' similar to contains element MER22 repetitive element;
10742	18500	31228	4.43	1.0E-46	BF194707.1	EST_HUMAN	7a92b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
11831	24196	31035	1.97	1.0E-46	BF531102.1	EST_HUMAN	602072284F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215398 5'
11831	24198	31036	1.97	1.0E-46	BF531102.1	EST_HUMAN	602072284F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215398 5'
12626	24704		1.39	1.0E-46	AV715377	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
798	13415		3.52	9.0E-47	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
5065	17638	30081	2.39	9.0E-47	AW770928.1	EST_HUMAN	hi93e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:O75703 O75703 HYPOTHETICAL 12.4 KD PROTEIN.;
6514	18114	31903	0.78	9.0E-47	11425439	NT	Homo sapiens zinc finger protein ZNF286 (ZNF286), mRNA
12355	24951	30827	3.64	9.0E-47	11417868	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1844	14432	26985	16.42	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
1844	14432	26986	16.42	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2742	15297	27864	1.1	8.0E-47	5453955	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
3058	15674	28150	2.05	8.0E-47	AJ228043.1	NT	Homo sapiens 950 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3686	16287	28756	0.8	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
3686	16287	28757	0.8	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
12436	24845		1.55	7.0E-47	AV683284.1	EST_HUMAN	AV683284 GKC Homo sapiens cDNA clone GKCASH11 5'

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8200	21717	34681	6.33	6.0E-47	AI095189.1	EST_HUMAN	tz98h02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296659 3'
9628	22128	35091	0.69	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
9628	22128	35092	0.69	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
6691	19287	32090	5.97	5.0E-47	11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
10674	23206		4.92	5.0E-47	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stragelene (cat#936206) Homo sapiens cDNA clone HFBCF07
1445	14037	26567	3.92	4.0E-47	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
6920	19579	32408	0.94	4.0E-47	BE938896.1	EST_HUMAN	MR4-TN0108-280800-201-404 TN0108 Homo sapiens cDNA
8417	20957	33874	2.47	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8417	20957	33875	2.47	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8553	21092	34012	0.57	4.0E-47	AW993777.1	EST_HUMAN	RC3-EN0034-220300-015-05 BN0034 Homo sapiens cDNA
11494	23943		6.19	4.0E-47	AW515509.1	EST_HUMAN	xx66b07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE
570	13201	25682	3.11	3.0E-47	BE907634.1	EST_HUMAN	Q84252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1];
570	13201	25683	3.11	3.0E-47	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
851	13467	25978	5.09	3.0E-47	N57483.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
981	13593	26108	9.88	3.0E-47	AL163284.2	NT	yy64b04.s1 Soares_multiple_sclerosis_2nbHMSF Homo sapiens cDNA clone IMAGE:277327 3'
3343	15953	28428	0.77	3.0E-47	4504116	NT	Homo sapiens chromosome 21 segment HS21C084
4038	18336		5.04	3.0E-47	U83181.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
6163	18776	31538	4.81	3.0E-47	AW408800.1	EST_HUMAN	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
6163	18778	31539	4.81	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BM0-adv-d-07-Q-UJ.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3083205 5'
6880	19278		1.71	3.0E-47	AI222413.1	EST_HUMAN	UI-HF-BM0-adv-d-07-Q-UJ.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3083205 5'
7416	18941	32806	0.75	3.0E-47	AI819755.1	EST_HUMAN	qh04a07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3'
7418	18941	32807	0.75	3.0E-47	AI819755.1	EST_HUMAN	wi11h08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
8767	21306	34228	0.56	3.0E-47	AW963766.1	EST_HUMAN	wj11h08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
8767	21306	34229	0.56	3.0E-47	AW963766.1	EST_HUMAN	EST375869 MAGI3 resequences, MAGH Homo sapiens cDNA
159	12822	25310	1.38	2.0E-47	4505318	NT	EST375869 MAGI3 resequences, MAGH Homo sapiens cDNA
1003	13614	26127	2.14	2.0E-47	AL163208.2	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
1003	13614	26128	2.14	2.0E-47	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
1613	14206	26762	1.1	2.0E-47	AI699279.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
1637	14229	26762	1.07	2.0E-47	7662109	NT	wq96b02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2478851 3'
1717	14309	26848	3.75	2.0E-47	AA524514.1	EST_HUMAN	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
4439	17025	29465	1.88	2.0E-47	4504866	NT	ng43h12.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:937607 3'
4473	17059	29508	1.91	2.0E-47	AA569592.1	EST_HUMAN	Homo sapiens ring finger protein (C3HC4 type) 8 (RNFB), mRNA
4473	17059	29507	1.91	2.0E-47	AA569592.1	EST_HUMAN	nt23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4473	17059	29507	1.91	2.0E-47	AA569592.1	EST_HUMAN	nt23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4604	17187	28634	2.94	2.0E-47	5174648	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
4935	17510	28957	1.28	2.0E-47	AW965166.1	EST_HUMAN	EST377239 MAGe resequences, MAGI Homo sapiens cDNA
5956	18578	31312	0.93	2.0E-47	AF073921.1	NT	Homo sapiens regulator of G-protein signaling 6 variant form (RGS6) mRNA, complete cds
6130	18745	31498	1.46	2.0E-47	BE778475.1	EST_HUMAN	601483932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
6130	18745	31499	1.46	2.0E-47	BE778475.1	EST_HUMAN	601483932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
7888	24788		1.25	2.0E-47	L09731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
7905	20447	33353	1.74	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
7905	20447	33354	1.74	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8652	21181	34109	1.77	2.0E-47	AF071771.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
9410	21819	34867	1.33	2.0E-47	11526138	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
11663	24894	30608	2.82	2.0E-47	R42423.1	EST_HUMAN	yf92e08.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:29866 3' similar to contains OFR repetitive element:
1451	14043	26371	6.05	1.0E-47	AI833429.1	EST_HUMAN	q99h03.x1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1931189 3'
3894	16493	28953	0.93	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3894	16493	28954	0.93	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
5235	17799	30218	2.44	1.0E-47	AW813906.1	EST_HUMAN	RC3-ST0197-130400-017-h02 ST0197 Homo sapiens cDNA
7109	19449	32265	5.59	1.0E-47	AI880886.1	EST_HUMAN	at19a06.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22895
8802	21341		7.68	1.0E-47	AW664648.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
10258	22753	35741	2.08	1.0E-47	L30115.1	NT	hi84e11.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878972 3' similar to gb:M26326
1654	14246	28779	2.38	9.0E-48	AF223391.1	NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
3612	16215	28695	0.78	9.0E-48	BF355947.1	EST_HUMAN	Papio hamedhyas alcohol dehydrogenase class I (ADH) gene, 5' region
5960	18482	31206	0.83	9.0E-48	BE888196.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5960	18482	31206	0.83	9.0E-48	BE888196.1	EST_HUMAN	CM2-MT0100-310700-290-705 MT0100 Homo sapiens cDNA
6373	18977	31755	0.69	9.0E-48	AU123240.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
10965	23509	36542	3.37	9.0E-48	BE393813.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
1293	13888		2.34	8.0E-48	4501900	NT	AU123240 NT2RM1 Homo sapiens cDNA clone NT2RM1000978 5'
1294	13888		1.76	8.0E-48	4501900	NT	601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5'
3169	15783	28254	3.3	8.0E-48	AW768477.1	EST_HUMAN	Homo sapiens aminocyclase 1 (ACY1), mRNA
3169	15783	28255	3.3	8.0E-48	AW768477.1	EST_HUMAN	Homo sapiens aminocyclase 1 (ACY1), mRNA
							hk61b03.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
							BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
							hk61b03.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
							BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4005	16603	28077	0.6	8.0E-48	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
516	13149		2.03	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
517	13149		20.88	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1544	14138	26670	1.08	7.0E-48	6912719	NT	Homo sapiens tousel-like kinase 1 (TLK1), mRNA
1679	14271	26804	3.49	7.0E-48	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6872	19268	32072	21.95	7.0E-48	11416831	NT	Homo sapiens histidyl-RNA synthetase (HARS), mRNA
3658	16261	28733	1.19	6.0E-48	AI761111.1	EST_HUMAN	wf69h03.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:23988613 3'
6208	18818	31589	0.98	8.0E-48	AB008955.1	NT	Homo sapiens mRNA for AIE-75, complete cds
6881	19815	32450	0.87	8.0E-48	11420995	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX), mRNA
9051	21588	34520	2.17	6.0E-48	AF028816.1	NT	Homo sapiens putative oncogene protein mRNA, partial cds
9460	21986	34940	1.72	8.0E-48	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
9608	22106	35069	3.5	6.0E-48	AA189080.1	EST_HUMAN	zq45b06.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element.
2293	14887	27442	1.43	5.0E-48	4827059	NT	Homo sapiens xylokinase (H. influenzae) homolog (XYLB) mRNA
2300	14873	27449	1.15	5.0E-48	4827059	NT	Homo sapiens xylokinase (H. influenzae) homolog (XYLB) mRNA
3350	18002	28435	1.64	5.0E-48	4826891	NT	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
5418	17975	30383	1.13	5.0E-48	AF219838.1	NT	Homo sapiens diacylglycerol kinase iota (DGKI) gene, exon 32
8511	21050	33972	6.94	5.0E-48	BE084410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
10836	23367	36373	4.24	4.0E-48	AI620420.1	EST_HUMAN	h47a02.x1 NCI CGAP_P28 Homo sapiens cDNA clone IMAGE:2254154 3'
1428	14021	28549	1.75	3.0E-48	AV690964.1	EST_HUMAN	AV690964 GKC Homo sapiens cDNA clone GKCDRE12 5'
2019	14601	27165	9.63	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2019	14601	27168	9.63	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3465	16072	28545	0.98	3.0E-48	AF172453.1	NT	Homo sapiens opiod growth factor receptor mRNA, complete cds
3693	16294	28764	0.78	3.0E-48	AW664531.1	EST_HUMAN	h14b12.x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972265 3' similar to SW:DCRB_HUMAN
4332	18919		0.97	3.0E-48	AA009541.1	EST_HUMAN	P56555 DOWN SYNDROME CRITICAL REGION PROTEIN B. ;
6053	18671	31410	2.98	3.0E-48	BE084571.1	EST_HUMAN	z04g03.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429844 5'
7087	19658	32497	1.01	3.0E-48	AF087913.1	NT	MR4-BT0657-060400-201-e10 BT0657 Homo sapiens cDNA
8330	20871		3.02	3.0E-48	AA659930.1	EST_HUMAN	Human endogenous retrovirus HERV-P-T47D
10753	23277	38260	6.32	3.0E-48	BF514170.1	EST_HUMAN	n03f05.s1 NCI CGAP_P22 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains PTR5.b1
5	12685	25142	2.18	2.0E-48	AA485007.1	EST_HUMAN	PTR5 repetitive element ;
49	12729	25193	2.12	2.0E-48	AA631940.1	EST_HUMAN	UIH-BW1-anti-a-10-0-U1.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267 3'
							zx80c03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810052 5'
							fmc7 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-26

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4629	17212	28663	0.93	2.0E-48	BE246085.1	EST_HUMAN	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP3842
5095	17688	30107	1.8	2.0E-48	T03176.1	EST_HUMAN	FB2E2 Fetal brain, Stratagene Homo sapiens cDNA clone FB2E2 3'end
5095	17688	30108	1.8	2.0E-48	T03176.1	EST_HUMAN	FB2E2 Fetal brain, Stratagene Homo sapiens cDNA clone FB2E2 3'end
7528	20048	32919	4.15	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7528	20048	32920	4.15	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7539	20059	32933	3.51	2.0E-48	11498238	NT	Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA
8298	20837	33758	1.53	2.0E-48	AV743451.1	EST_HUMAN	AV743451 CB Homo sapiens cDNA clone CBCCGG10 5'
11828	12685	25142	4.4	2.0E-48	AA465007.1	EST_HUMAN	z880c03.r1 Soares ovary tumor NHOt Homo sapiens cDNA clone IMAGE:810052 5'
60	12739	25210	3.22	1.0E-48	7706534	NT	Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA
906	13520	26038	5.3	1.0E-48	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1114	13718	26228	2.58	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1114	13718	26229	2.58	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1339	13934	26455	4.33	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 6 (RBM6) mRNA
1962	14546	27103	19.18	1.0E-48	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3535	16140	28622	0.81	1.0E-48	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5312	17874	30296	1.37	1.0E-48	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
6431	19034	31618	1.14	1.0E-48	AI889077.1	EST_HUMAN	Id17c01.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14588 SIMILARITY TO U73941 ;
6431	19034	31819	1.14	1.0E-48	AI889077.1	EST_HUMAN	Id17c01.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14588 SIMILARITY TO U73941 ;
6625	19222	31819	1.14	1.0E-48	AI889077.1	EST_HUMAN	Id17c01.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14588 SIMILARITY TO U73941 ;
7303	19631	32690	0.94	1.0E-48	Y18000.1	NT	Homo sapiens NF2 gene
7303	19631	32690	2.58	1.0E-48	4755137	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
8765	21304	34225	0.52	1.0E-48	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8765	21304	34226	0.52	1.0E-48	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9140	21675	34818	0.84	1.0E-48	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
9192	21709	34653	6	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
9485	21942	34889	0.73	1.0E-48	BE169410.1	EST_HUMAN	QV3-HT0513-060400-147-401 HT0513 Homo sapiens cDNA
9502	22002	34959	3.86	1.0E-48	BF304683.1	EST_HUMAN	601888096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
10272	22767	35754	3.54	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
10272	22767	35755	3.54	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
11789	24937		1.62	1.0E-48	W26765.1	EST_HUMAN	15d6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2052	14633	27204	0.96	8.0E-49	AB028497.1	NT	Mus musculus MysPDZ mRNA for myosin containing PDZ domain, complete cds
6204	18814	31584	3.44	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
6204	18814	31585	3.44	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
8236	20777	33688	3.22	8.0E-49	U23850.1	NT	Human Inositol 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
9900	22397	35372	1.23	8.0E-49	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
10738	23261	36276	1.6	8.0E-49	AI623722.1	EST_HUMAN	ts38d12.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230871 3' similar to contains Alu repetitive element; contains element PTR5 repetitive element;
145	13052	25542	2.62	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
145	13052	25543	2.62	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
417	13052	25542	2.38	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
417	13052	25543	2.38	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
418	13052	25542	2.59	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
418	13052	25543	2.59	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1263	13860	26377	3.49	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5851	18278	30755	1.97	7.0E-49	AI807191.1	EST_HUMAN	wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923
5861	18288	30768	1.11	7.0E-49	AL120937.1	EST_HUMAN	O54923 RSEC15;
5973	18278	30755	1.14	7.0E-49	AI807191.1	EST_HUMAN	DKFZp782C033_s1 762 (synonym: hme12) Homo sapiens cDNA clone DKFZp782C033 3'
211	12672	25358	57.13	6.0E-49	AW731740.1	EST_HUMAN	wf25h04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900504 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
4163	16782	28231	0.59	6.0E-49	AL162091.1	EST_HUMAN	DKFZp761A138_s1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A138 3'
6571	19169	31966	0.89	6.0E-49	AI140742.1	EST_HUMAN	AI140742 PLACE4 Homo sapiens cDNA clone PLACE4000148 5'
11159	23686	36711	3.66	6.0E-49	AW452218.1	EST_HUMAN	UI-H-B19-alo-a-05-0-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068048 3'
11514	23982	37031	3.9	6.0E-49	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
11514	23982	37032	3.9	6.0E-49	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
12166	24925		7.5	6.0E-49	AA707587.1	EST_HUMAN	z29c08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451694 3'
741	13361	25854	8.61	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
741	13361	25855	6.61	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1830	14419	26968	3.16	5.0E-49	AA172121.1	EST_HUMAN	z29c07.r1 Stratiagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610960 5' similar to TR:G233226 G233226 RTVL-H PROTEIN; contains LTR7.13 LTR7 LTR7 repetitive element;
2778	15331	27900	4.95	5.0E-49	U17714.1	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3311	15922	28398	6.09	5.0E-49	11436355	NT	Homo sapiens similar to ribosomal protein S27 (metalloproteinin 1) (H. sapiens) (LOC63362). mRNA
551	13182	25659	26.48	4.0E-49	AW189533.1	EST_HUMAN	X08801.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2675593 3' similar to WP:B0350.2B CE06703 ;
7316	19843	32704	0.79	4.0E-49	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
7316	19843	32705	0.79	4.0E-49	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
8798	21337	34263	0.46	4.0E-49	11425374	NT	Homo sapiens copine III (CPNE3), mRNA
8798	21337	34264	0.46	4.0E-49	11425374	NT	Homo sapiens copine III (CPNE3), mRNA
12021	25055		4.9	4.0E-49	AA210798.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 1 (GSTT1) and glutathione S-transferase theta 2 (GSTT2) genes, complete cds
12110	24371		3.14	4.0E-49	AF240786.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
586	13216	25683	1.08	3.0E-49	X58968.1	NT	z831c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.3 L1 repetitive element ;
2674	15232		1.43	3.0E-49	AA016131.1	EST_HUMAN	Human type IV collagen (COL4A6) gene, exon 40
5120	17692	30130	2.33	3.0E-49	U46999.1	NT	EST25612 WATM1 Homo sapiens cDNA clone 25e12
7448	19872	32839	9.89	3.0E-49	H39479.1	EST_HUMAN	EST42572 Endometrial tumor Homo sapiens cDNA 5' end
11181	23687	36734	1.98	3.0E-49	AA337581.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
689	13313		1.57	2.0E-49	BE165980.1	EST_HUMAN	y23d08.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:262571 5'
3259	15871	28351	1.3	2.0E-49	N28446.1	EST_HUMAN	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
3627	16230	28706	0.67	2.0E-49	AF026564.1	NT	alphaB9d02.x1 Soares senescent fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1682403 3' similar to gb:M31470 RAS-LIKE PROTEIN TC10 (HUMAN); contains Alu repetitive element; contains element MER22 repetitive element ;
4918	17493	28845	0.67	2.0E-49	AI167357.1	EST_HUMAN	U1-H-B14-aps-d-02-Q.U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3088538 3'
4932	17507	28954	0.61	2.0E-49	BF511846.1	EST_HUMAN	AV717838 DCB Homo sapiens cDNA clone DCBALB01 5'
6834	19424	32240	1.13	2.0E-49	AV177938.1	EST_HUMAN	EST702558 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBY50
8043	20585		1.71	2.0E-49	MB6033.1	EST_HUMAN	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
12121	24929		1.81	2.0E-49	AF163864.1	NT	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
932	13545		8.12	1.0E-49	BF035327.1	EST_HUMAN	Homo sapiens keratin 18 (KRT18) mRNA
1800	14192	26723	14.26	1.0E-49	4557887	NT	601115769F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356273 5'
1837	14425	26978	4.07	1.0E-49	BE255216.1	EST_HUMAN	601820053F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052052 5'
5562	18193	30640	8.31	1.0E-49	BF131007.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6228	18837	31610	0.95	1.0E-49	H18291.1	EST_HUMAN	yr48h04.r1 Soares adult brain N255H85Y Homo sapiens cDNA clone IMAGE:171703 5' similar to SP:GBG1_HUMAN Q08447 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T) GAMMA-1 SUBUNIT ;
6234	18843	31615	0.94	1.0E-49	AW064840.1	EST_HUMAN	EST376713 MAGE resequences, MAGH Homo sapiens cDNA
7275	19803	32661	3.31	1.0E-49	BE398110.1	EST_HUMAN	601280330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7275	19803	32862	3.31	1.0E-49	BE398110.1	EST_HUMAN	601280330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7342	19869	32733	2.3	1.0E-49	N25884.1	EST_HUMAN	yw78g12.s1 Soares_placenta_8tc9weeks_2N8HP8tc9w Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
7342	19869	32734	2.3	1.0E-49	N25884.1	EST_HUMAN	yw78g12.s1 Soares_placenta_8tc9weeks_2N8HP8tc9w Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
8023	20565	33467	1.23	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
8023	20565	33468	1.23	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
8609	21148		0.93	1.0E-49	9994184	NT	Homo sapiens RNA binding motif protein 7 (LOC51120), mRNA
8923	21481	34378	1.28	1.0E-49	BE409340.1	EST_HUMAN	601300992F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3633398 5'
10033	22528	35523	1.26	1.0E-49	AL043129.2	EST_HUMAN	DKFZp434D2423_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2423 5'
10927	23445	36466	2.28	1.0E-49	AV751477.1	EST_HUMAN	AV751477 NPD Homo sapiens cDNA clone NPDAWE04 5'
11190	23695	36744	3.48	1.0E-49	11427368	NT	Homo sapiens brafelid A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
11653	24081		1.39	1.0E-49	BE159343.1	EST_HUMAN	MRO-HT0407-010200-008-102 HT0407 Homo sapiens cDNA
12015	24314		2.48	1.0E-49	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6538	25117		0.88	9.0E-50	BE295758.1	EST_HUMAN	601176250F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531588 5'
181	12843	25327	2.91	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
748	13368	25862	1.7	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
748	13368	25863	1.7	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
1070	13675		6.61	8.0E-50	AF000573.1	NT	Homo sapiens homogenitase 1, 2-dioxygenase gene, complete cds
1800	14390	26935	2.81	8.0E-50	4501890	NT	Homo sapiens actinin, alpha 1 (ACTN1), mRNA
2522	15086	27658	1	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51874), mRNA
2522	15086	27659	1	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51874), mRNA
2723	15278	27845	0.98	8.0E-50	4826658	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
4182	16772	29221	0.99	8.0E-50	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
647	13270	25748	0.97	7.0E-50	BE088591.1	EST_HUMAN	QV0-BT0703-280400-211-e08 BT0703 Homo sapiens cDNA
6880	19814	32448	0.94	7.0E-50	BF091922.1	EST_HUMAN	RC8-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
6880	19814	32449	0.94	7.0E-50	BF091922.1	EST_HUMAN	RC8-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
7346	19872	32738	1.25	7.0E-50	AA627822.1	EST_HUMAN	mq58e12.s1 NCL_CGAP_C08 Homo sapiens cDNA clone IMAGE:1148206 3' similar to gb:X69391 60S RIBOSOMAL PROTEIN L6 (HUMAN);
10636	23168	36179	22.7	7.0E-50	AI872137.1	EST_HUMAN	wm55g11.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4435	17021		0.62	6.0E-50	BE794381.1	EST_HUMAN	601589565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
8155	20898		6.9	6.0E-50	BE044076.1	EST_HUMAN	h036h04.x1 NCL_CGAP_UH Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29 b3
10694	23224	36237	5.53	6.0E-50	AA312079.1	EST_HUMAN	MER29 repetitive element ;
10694	23224	36238	5.53	6.0E-50	AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
1829	14418	26968	0.88	5.0E-50	BF332938.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
1829	14418	26967	0.88	5.0E-50	BF332938.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
							CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
9022	21559		4.65	5.0E-50	AA557683.1	EST_HUMAN	nl45h10.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5 repetitive element ;
							zf62b01.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769
11619	24061	37125	1.57	5.0E-50	AA403053.1	EST_HUMAN	G1335769 GAG-POL POLYPOLYPROTEIN. ;
950	13562		1.74	4.0E-50	AA601143.1	EST_HUMAN	nc54609.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_rna1
7285	19813	32669	1.04	4.0E-50	BE087536.1	EST_HUMAN	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1982	14565		2.4	3.0E-50	MT8048.1	NT	QV1-BT0681-280300-127-f12 BT0681 Homo sapiens cDNA
3338	15848	28424	0.78	3.0E-50	AA748142.1	EST_HUMAN	Human endogenous retrovirus RTVL-H2
							cd03008.s1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322627 3'
3815	18415	28879	0.93	3.0E-50	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5
							Cardiomyopathy associated gene 5
6862	19568	32427	1.45	3.0E-50	11421514	NT	Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC83232), mRNA
							Homo sapiens FVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
7640	20152	33036	4.41	3.0E-50	AF233436.2	NT	Homo sapiens FVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
7640	20152	33037	4.41	3.0E-50	AF233436.2	NT	Homo sapiens FVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
8518	21057	33980	0.73	3.0E-50	6601599	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
9732	22230	35207	1.32	3.0E-50	AB048818.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
9741	22239	35220	0.86	3.0E-50	11418514	NT	Homo sapiens t-complex 10 (a murine top homolog) (TCP10), mRNA
10412	22906	35903	0.67	3.0E-50	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
10981	23495	36524	1.76	3.0E-50	11438955	NT	Homo sapiens Gtb2-associated binder 2 (KIAA0571), mRNA
11339	23037	36046	5.96	3.0E-50	AJ245621.1	NT	Homo sapiens CTL2 gene
810	13427		9.29	2.0E-50	AF055088.1	NT	Homo sapiens MHC class 1 region
1118	13721	26233	4.82	2.0E-50	4557752	NT	Homo sapiens midline 1 (Optiz/BBB syndrome) (MID1) mRNA
1492	14084	26625	3.58	2.0E-50	AF138303.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
3328	15936	28412	0.61	2.0E-50	AF11186.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4347	16934	29375	0.6	2.0E-50	D88424.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
8258	20789	33716	1.24	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefol factor, complete cds
8258	20789	33717	1.24	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefol factor, complete cds
8393	20933	33854	9.32	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
8393	20933	33855	9.32	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
9789	22287	35281	2.89	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
9789	22297	35282	2.89	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
11512	23860		2.09	2.0E-50	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
487	13120	25606	1.58	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2403	14971		6.87	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
10085	22590	35583	0.77	1.0E-50	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
6136	18750	31507	0.89	9.0E-51	AW511225.1	EST_HUMAN	h444a02.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:O95636
6372	18976	31754	0.69	9.0E-51	AA744837.1	EST_HUMAN	O95636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II. ;
8608	21145	34060	0.7	9.0E-51	A1791154.1	EST_HUMAN	ny67h03.s1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1283381 3'
9248	21774	34725	1.16	9.0E-51	AA043738.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841886 3' similar to
							SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
							z451c09.r1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486352 5'
9420	21929	34875	0.52	9.0E-51	A1791154.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841886 3' similar to
							SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
9420	21929	34876	0.52	9.0E-51	A1791154.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841886 3' similar to
4532	17116	29581	2.81	8.0E-51	4503932	NT	SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
4532	17116	29582	2.81	8.0E-51	4503932	NT	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
							Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
4667	17249	29702	13.1	8.0E-51	AA810842.1	EST_HUMAN	np98a09.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:X12671_mat
5319	17881	30300	1.68	8.0E-51	AF092132.1	NT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
7648	20160	33047	2.08	8.0E-51	11439587	NT	Homo sapiens PAK2 mRNA, complete cds
9385	21808		0.89	8.0E-51	AU138590.1	EST_HUMAN	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
							AU138590 PLACET1 Homo sapiens cDNA clone PLACE1008887 5'
3051	15667	28145	0.72	7.0E-51	AW274720.1	EST_HUMAN	xn34a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340
3321	15931	28408	1.51	7.0E-51	AW869219.1	EST_HUMAN	Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
							QV4-NT0028-200400-180-405 NT0028 Homo sapiens cDNA
3408	16017	28496	0.76	7.0E-51	AW274720.1	EST_HUMAN	xn34a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340
4247	16835	29286	2.14	7.0E-51	AL079628.1	EST_HUMAN	Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
							DKFZp434B2228_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2228 5'

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4247	16835	29287	2.14	7.0E-51	AL079628.1	EST_HUMAN	DKFZp434B2229_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2229 5'
4443	17029	29469	1.69	7.0E-51	AW285603.1	EST_HUMAN	UI-H-BWO-elip-b-05-0-UI.s1 NCJ CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2729817 3'
11534	23982	37053	1.65	7.0E-51	AF161449.1	NT	Homo sapiens HSPC331 mRNA, partial cds
1575	14168	26899	17.64	6.0E-51	6678763	NT	Homo sapiens putative DNA binding protein (M96), mRNA
2022	14604	27169	5.19	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
3520	16125	28605	17.1	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
4397	16982	29428	1.09	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
4397	16982	29427	1.09	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
6142	18758	31514	57.08	6.0E-51	X01788.1	NT	Human hemoglobin related (Hpr) gene exon 3
6152	18765	31527	11.76	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6152	18765	31528	11.76	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6858	19592	32424	1.05	6.0E-51	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
6972	19549	32373	0.71	6.0E-51	11416751	NT	Homo sapiens non-kinase Cdc42 effector protein SPEC2 (LOC56990), mRNA
7044	18064	30454	2.22	6.0E-51	11429865	NT	Homo sapiens cerebral cell adhesion molecule (LOC51148), mRNA
9064	21601	34530	0.68	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
9064	21601	34531	0.68	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
9801	22101	35084	1.79	6.0E-51	7681535	NT	Homo sapiens B9 protein (B9), mRNA
9877	22176	35151	1.35	6.0E-51	U50093.1	NT	Human ankyrin (ANK1) gene, exon 2
11136	23644	36684	1.83	6.0E-51	11526289	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA
11403	23854	36919	1.58	6.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
11403	23854	36920	1.58	6.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
824	13441	25948	6.74	5.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
836	13452	25982	1.38	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1028	15431	26153	1.01	5.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1651	14243	26777	0.99	5.0E-51	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
2629	15191	27759	8.09	5.0E-51	AJ007558.1	NT	Homo sapiens mRNA for nucleoporin 155
4017	16615	26088	1.21	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4017	16615	26089	1.21	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5231	17795	30214	1.68	5.0E-51	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11069	23581	36621	2.02	5.0E-51	BE501320.1	EST_HUMAN	741a02.x1 NCJ CGAP_GC6 Homo sapiens cDNA clone IMAGE:3221258 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11160	23667	36712	4.75	5.0E-51	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
140	12805	25284	15.48	3.0E-51	AI587348.1	EST_HUMAN	tr1c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1218	13818	26833	34.32	3.0E-51	AI587348.1	EST_HUMAN	tr1c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
4420	17005	28448	2.04	3.0E-51	AL159142.1	NT	Novel human gene mapping to chromosome 22
7579	20095	32972	1.16	3.0E-51	R15914.1	EST_HUMAN	ye47c08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M14123_cds4 RETROVIRUS-RELATED POLYPROTEIN (HUMAN); contains LTR5 repetitive element;
8773	21312		6.15	3.0E-51	M29083.1	NT	Human hnRNP C2 protein mRNA
8968	25124		0.6	3.0E-51	AW583777.1	EST_HUMAN	la04d08.y1 Human Pancreatic Islets Homo sapiens cDNA 5'
12348	24529		2.15	3.0E-51	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
389	13035	25524	2.03	2.0E-51	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
717	13338	25824	0.94	2.0E-51	BE391063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
717	13338	25825	0.94	2.0E-51	BE391063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1726	14317	26860	5.61	2.0E-51	AA233352.1	EST_HUMAN	z30a05.r1 Stralagene NT2 neuronal precursor 637230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR:G233228 G233228 RTVL-H PROTEIN; contains LTR7.13 LTR7 repetitive element;
3795	16395	28860	2.71	2.0E-51	AI492415.1	EST_HUMAN	tr27g03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3'
4592	17175	29621	1.73	2.0E-51	AW137628.1	EST_HUMAN	ULH-B1-adj-d-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716851 3'
5630	18259	30730	0.78	2.0E-51	AI732851.1	EST_HUMAN	db34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
5630	18259	30731	0.76	2.0E-51	AI732851.1	EST_HUMAN	db34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
6166	18778	31542	3.29	2.0E-51	BE782015.1	EST_HUMAN	6014704448F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873563 5'
7350	19876		0.77	2.0E-51	AF219927.1	NT	Homo sapiens diacylglycerol kinase Iota (DGKI) gene, exon 23
7480	20002	32897	1	2.0E-51	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
8632	21171	34088	2.06	2.0E-51	BE901994.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959813 5'
8632	21171	34089	2.06	2.0E-51	BE901994.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959813 5'
8964	21502	34424	0.95	2.0E-51	11037084	NT	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA
9431	21957	34905	1.48	2.0E-51	AI917078.1	EST_HUMAN	ts74a07.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR;
9521	22021	34978	5.22	2.0E-51	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9537	22037	34997	0.61	2.0E-51	AB007926.1	NT	Homo sapiens mRNA for KIAA0457 protein, partial cds
10329	22823	35819	1.73	2.0E-51	AV682474.1	EST_HUMAN	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5'
10368	22862	35855	1.03	2.0E-51	AA378559.1	EST_HUMAN	EST91298 Synovial sarcoma Homo sapiens cDNA 5' end
11207	18259	30730	11.47	2.0E-51	AI732851.1	EST_HUMAN	ob34f09.x5 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35438 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
11207	18259	30731	11.47	2.0E-51	AI732851.1	EST_HUMAN	ob34f09.x5 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35438 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
12343	24524	30924	2.6	2.0E-51	11419159	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4), mRNA
119	12790	25272	27.93	1.0E-51	4503528	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1541	14133	29531	28.47	1.0E-51	AV742248.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone CBFCC12 5'
4408	17082	29531	1	1.0E-51	4759071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
4498	17082	29532	1	1.0E-51	4759071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
5588	18219	30669	2.68	1.0E-51	T18862.1	EST_HUMAN	ic39g02.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2089106 3'
7645	20157	33044	0.85	1.0E-51	AI572532.1	EST_HUMAN	ic39g02.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:3844091 3' similar to TR:P87892 P87892 PROTEASE ;
7844	20386	33289	7	1.0E-51	BF434359.1	EST_HUMAN	7a96b02.x1 NCL CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2089106 3'
11613	25129		3.01	1.0E-51	AV760590.1	EST_HUMAN	AV760590 MDS Homo sapiens cDNA clone MDSCB802 5'
10568	23104	36118	1.71	9.0E-52	R91838.1	EST_HUMAN	Yq10h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196567 5' similar to SP:YGAF_ECOLI_P37339 HYPOTHETICAL PROTEIN IN GABP 3'REGION ;
10568	23104	36119	1.71	9.0E-52	R91838.1	EST_HUMAN	Yq10h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196567 5' similar to SP:YGAF_ECOLI_P37339 HYPOTHETICAL PROTEIN IN GABP 3'REGION ;
12105	24367		6.53	9.0E-52	AA777621.1	EST_HUMAN	z195a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR13 THR repetitive element ;
163	12826	25313	8	8.0E-52	AA720574.1	EST_HUMAN	rw21g02.s1 NCL CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13 THR repetitive element ;
1543	14135	26869	1.32	8.0E-52	X94900.1	NT	H sapiens mRNA for laminin-5, alpha3b chain
1694	14286	26821	2.12	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1694	14286	26822	2.12	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4066	14286	26821	6.96	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4066	14286	26922	6.96	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
7528	20048	32916	1.8	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
7528	20048	32916	1.8	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
8943	21481	34403	1.39	7.0E-52	W56471.1	EST_HUMAN	zz59a06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326378 5' similar to contains Alu repetitive element.
1228	13828		0.85	6.0E-52	BE072409.1	EST_HUMAN	QV3-BT0537-271299-049-007 BT0537 Homo sapiens cDNA
1732	14323	26865	2.63	6.0E-52	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5902	18524	31249	2.12	6.0E-52	AI208794.1	EST_HUMAN	q944f04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838047 3'
11088	23568	36835	1.83	6.0E-52	BE048172.1	EST_HUMAN	tz48h04.y1 NCL_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291671 5' similar to SW:PGBM_MOUSE Q05793 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR;
4535	17119	29568	1.77	5.0E-52	Z78898.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment; SC6pA18H7
1702	14285	26830	1.27	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1823	14412	26957	1.35	4.0E-52	4758843	NT	Homo sapiens nucleoporin 155kD (NUP155) mRNA
4000	16598	28070	0.82	4.0E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4949	17427	28878	0.77	4.0E-52	AI766814.1	EST_HUMAN	w89b02.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400459 3'
5490	18124	30531	1.2	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
5490	18124	30532	1.2	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
7982	20524	33430	1.83	4.0E-52	BE622032.1	EST_HUMAN	601440687F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915836 5'
8471	21011	33928	5.51	4.0E-52	11417035	NT	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
11933	24267		5.12	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12458	24589		13.96	4.0E-52	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12801	24687		1.57	4.0E-52	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
4166	18757		12.28	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10875 (FLJ10875), mRNA
588	13218	25694	4.18	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
588	13218	25695	4.18	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1793	14383	26928	2.84	2.0E-52	AB007899.1	NT	Homo sapiens KIAA0439 mRNA, partial cds
2544	15108	27681	1.1	2.0E-52	BE207575.1	EST_HUMAN	b566b07.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:X16493 M.musculus mRNA for Zpf-1 zinc finger protein (MOUSE);
2764	15318		5.55	2.0E-52	BF677892.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
5113	17685	30121	3.51	2.0E-52	AL137188.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5981	18503	31228	3.32	2.0E-52	AW848041.1	EST_HUMAN	IL3-CT0214-231289-053-E12 CT0214 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8505	19105	31890	1.86	2.0E-52	11141888	NT	Homo sapiens interleukin 21 receptor (IL21R), mRNA
8814	19405	32221	0.89	2.0E-52	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7022	19556	32381	0.68	2.0E-52	AI792146.1	EST_HUMAN	os45d12.y5 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1608311 5'
8587	21126		10.89	2.0E-52	AF147880.1	NT	Macaca mulatta beta-tubulin mRNA, complete cds
8866	21405	34329	0.82	2.0E-52	AA778795.1	EST_HUMAN	z445g05.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:453272 3'
9400	21823		1.25	2.0E-52	4758789	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) (NDUFS5) mRNA
10024	22519	35514	5.62	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10024	22519	35515	5.62	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
11083	23595	36630	6.08	2.0E-52	AI831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408150 3' similar to contains THR.b2 THR repetitive element ;
11083	23595	36631	6.08	2.0E-52	AI831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408150 3' similar to contains THR.b2 THR repetitive element ;
11094	23606	36646	3.85	2.0E-52	AV715377	EST_HUMAN	AV715377 DGB Homo sapiens cDNA clone DCBAIE03 5'
11231	23762		1.87	2.0E-52	W70260.1	EST_HUMAN	z449g12.r1 Soares_fetal_heart_NBPH19W Homo sapiens cDNA clone IMAGE:344038 5'
11484	23933		3.4	2.0E-52	11417990	NT	Homo sapiens LIM domain kinase 2 (LIMK2), mRNA
11741	25099	30500	14.03	2.0E-52	AW236297.1	EST_HUMAN	xn72e07.x1 NCI_CGAP_GML1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu repetitive element; contains element LTR2 repetitive element ;
12154	24396		3.83	2.0E-52	AI808985.1	EST_HUMAN	wf67d05.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2360649 3' similar to TR.Q16859 Q16859 CARBOXYLESTERASE ;
558	13189	25668	1.59	1.0E-52	AA634445.1	EST_HUMAN	zu75h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'
1414	14007	26535	11.81	1.0E-52	4504028	NT	Homo sapiens glutamate-ammonia ligase (glutamine synthase) (GLUL) mRNA
2573	15136		1.75	1.0E-52	4502238	NT	Homo sapiens arylsulfatase D (ARSD), transcript variant 1, mRNA
3095	15710	28181	1.65	1.0E-52	S61070.1	NT	pod=reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 660 nt]
5536	18168	30582	4.64	1.0E-52	M29426.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
6527	19127	31921	2.18	1.0E-52	U38964.1	NT	Human PMS2 related (hPMSR2) gene, complete cds
7458	19881	32846	2.21	1.0E-52	X07292.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
8401	20941		1.24	1.0E-52	AL193227.2	NT	Homo sapiens chromosome 21 segment HS21C027
9116	21652	34593	0.81	1.0E-52	AF078778.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10469	22863		1.13	1.0E-52	AW020370.1	EST_HUMAN	df08g05.y1 Morton_Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483145 5'
10479	22973		0.78	1.0E-52	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10846	23178	36191	10.04	1.0E-52	U48296.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds
10716	23244		2.37	1.0E-52	11426321	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3859	18457	28920	1.13	9.0E-53	4506084	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
5186	17751	30182	0.91	9.0E-53	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
11987	24287		3.79	7.0E-53	BF238485.1	EST_HUMAN	601904771F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4132793 5'
12432	24969		5.2	7.0E-53	AI421782.1	EST_HUMAN	if44f07.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2099077 3' similar to contains THR.t1 THR repetitive element;
4174	18765	29213	4.45	5.0E-53	4758543	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
5364	17824	30338	1	5.0E-53	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
12035	24324		1.58	5.0E-53	AW813563.1	EST_HUMAN	RC3-ST0197-151099-011-g10 ST0197 Homo sapiens cDNA
53	12733	25200	1.15	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
53	12733	25201	1.15	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4947	17922	29884	0.99	4.0E-53	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
9337	21851		0.68	4.0E-53	AI613037.1	EST_HUMAN	ly08h04.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2278327 3'
9871	22170		0.71	4.0E-53	F13080.1	EST_HUMAN	HSC3ID041 normalized infant brain cDNA Homo sapiens cDNA clone c-3id04
11091	23603	36842	3.98	4.0E-53	BF128701.1	EST_HUMAN	601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
11091	23603	36843	3.98	4.0E-53	BF128701.1	EST_HUMAN	601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
2684	15242	27810	2.09	3.0E-53	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3794	16394	28859	1.19	3.0E-53	AW050836.1	EST_HUMAN	wz22c07.x1 Soares_Dieckgreffe_colon_NHCD Homo sapiens cDNA clone IMAGE:2658798 3'
4691	17273	29721	0.85	3.0E-53	AW803563.1	EST_HUMAN	IL2-UM0081-240300-055-D03 UM0081 Homo sapiens cDNA
5618	18247	30698	0.89	3.0E-53	AF001212.1	NT	Homo sapiens 26S proteasome subunit 9 mRNA, complete cds
5808	18433	31154	0.91	3.0E-53	11528297	NT	Homo sapiens MIL1 protein (MIL1), mRNA
6341	18947	31724	0.89	3.0E-53	BE160025.1	EST_HUMAN	GV1-HT0412-280300-123-c04 HT0412 Homo sapiens cDNA
7155	19687	32530	0.92	3.0E-53	Y10388.3	NT	H. sapiens graf gene
7155	19687	32531	0.92	3.0E-53	Y10388.3	NT	H. sapiens graf gene
8246	20787	33706	10.03	3.0E-53	S72043.1	NT	GLF=growth inhibitory factor [human, brain, Genomic, 2015 nt]
8793	21332	34256	0.51	3.0E-53	10835090	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
8987	21525		7.06	3.0E-53	5901953	NT	Homo sapiens FGFR1 oncogene partner (FOP), mRNA
11867	24221		1.27	3.0E-53	11428423	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
483	13116		32.96	2.0E-53	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
2365	14936	27508	5.15	2.0E-53	U78027.1	NT	Homo sapiens Brulon's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2574	15137		12.23	2.0E-53	4502316	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD, Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2752	15307	27871	0.9	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
2752	15307	27872	0.9	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
3255	15867	28347	0.65	2.0E-53	7705887	NT	Homo sapiens leucine aminopeptidase (LOC51056), mRNA
3282	15893	28372	0.87	2.0E-53	AF083822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
4133	16725	29178	2.15	2.0E-53	M61873.1	NT	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds
5619	18248	30699	3.27	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0396-170800-001-q03 CT0396 Homo sapiens cDNA
5619	18248	30700	3.27	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0396-170800-001-q03 CT0396 Homo sapiens cDNA
7812	20355	33263	0.84	2.0E-53	AW975598.1	EST_HUMAN	EST387707 MAGE resequences, MAGN Homo sapiens cDNA
7849	20481		0.83	2.0E-53	AA095652.1	EST_HUMAN	15429 seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9320	21843		17.91	2.0E-53	AW245676.1	EST_HUMAN	2822665.Sprfme NIH_MGC.7 Homo sapiens cDNA clone IMAGE:2822665 5'
1495	14087	26627	1.88	1.0E-53	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
3456	16063	28538	1.4	1.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4220	16808	28258	0.87	1.0E-53	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBAWF09 5'
5099	17671	30110	1.08	1.0E-53	BE296386.1	EST_HUMAN	601176725F1 NIH_MGC.17 Homo sapiens cDNA clone IMAGE:3531919 5'
6784	19385	32201	1.34	1.0E-53	BF364201.1	EST_HUMAN	CM4-NN1029-150800-543-e02 NN1029 Homo sapiens cDNA
7285	19823	32882	0.93	1.0E-53	BE012071.1	EST_HUMAN	RC5-BN1058-270400-031-D01 BN1058 Homo sapiens cDNA
7876	20418	33326	0.5	1.0E-53	AA249072.1	EST_HUMAN	119571.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9018	21555	34483	15.04	1.0E-53	X78536.1	NT	H. sapiens mRNA for hnRNPcore protein A1
3290	15901	28361	0.57	9.0E-54	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5505	24743	30549	5.34	9.0E-54	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
221	12882	25367	3.54	8.0E-54	BE386785.1	EST_HUMAN	601272863F1 NIH_MGC.20 Homo sapiens cDNA clone IMAGE:3614031 5'
1875	14481	27018	1.62	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
4841	17419	28871	0.9	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
4841	17419	28872	0.8	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
6092	18708	31458	20.41	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
407	13082	25574	1.55	7.0E-54	AA812537.1	EST_HUMAN	a179c12.s1 Soares, testis_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.13 MER30 repetitive element;
1870	14456	27013	2.37	7.0E-54	Y16845.1	NT	Homo sapiens mRNA for monocytic chemotactic protein-2
2248	14820	27395	5.06	7.0E-54	N27177.1	EST_HUMAN	yw68d12.s1 Soares, placenta_8to9weeks_2NbHP86c9W Homo sapiens cDNA clone IMAGE:257399 3' similar to contains LTR7.b3 LTR7 repetitive element;
4894	17276		23.4	7.0E-54	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10034	22529	35524	2.32	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA
11171	23878						qb57g03.x1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to
26	12705	25163	7.41	7.0E-54	AI160189.1	EST_HUMAN	contains OFR.t1 OFR repetitive element:
408	13083	25575	2.31	6.0E-54	AB003618.1	NT	Homo sapiens DNA for MICB, exon 4, 5 and partial cds
408	13083	25575	1.14	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
1917	14502	27058	1.14	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
1917	14502	27058	1.44	6.0E-54	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
3322	15932	28409	1.44	6.0E-54	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
4076	16872	28133	1.06	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
4561	17144	28591	35.06	6.0E-54	4502872	NT	Homo sapiens chloride channel 6 (CLCN6) mRNA
4969	17543	28985	0.88	6.0E-54	AV754746.1	EST_HUMAN	AV754746 TP Homo sapiens cDNA clone TPGAAC10 5'
5001	17574		1.07	6.0E-54	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
5140	17574		1.81	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p66 isoform
11328	23027	36036	2.28	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p66 isoform
2195	14771	27345	3.33	6.0E-54	AW813567.1	EST_HUMAN	RC3-ST0197-151099-011-08 ST0197 Homo sapiens cDNA
195	12855		2.41	5.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
			111.77	4.0E-54	AF110103.1	NT	Tupala belangeri beta-actin mRNA, partial cds
981	13603	26117					EST177686 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1841	14429	26981	69.58	4.0E-54	AA306764.1	EST_HUMAN	Human mRNA for KIAA0077 gene, partial cds
1841	14429	26982	2.97	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3238	15850		2.97	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
97	12773	25255	1.45	4.0E-54	AI935086.1	EST_HUMAN	wd26d11.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2329286 3' similar to TR:O02711
2604	15166	27733	0.97	3.0E-54	AA313487.1	EST_HUMAN	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
6083	18890	31422	0.97	3.0E-54	AL110383.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
7422	18946	32811	1.44	3.0E-54	AA844061.1	EST_HUMAN	DKFZp434E0731_r1 434 (synonym: hsc3) Homo sapiens cDNA clone DKFZp434E0731 5'
7422	18946	32812	1.54	3.0E-54	AA844061.1	EST_HUMAN	Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA
10964	23479	36504	1.54	3.0E-54	BF345600.1	EST_HUMAN	ai92c08.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
			4.52	3.0E-54			ai92c08.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
							602019408F1 NCJ_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155121 5'
11247	23777	36834					z707012.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315
11844	24206	31040	4.44	3.0E-54	AA393382.1	EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ;
11895	25059		2.75	3.0E-54	AW954559.1	EST_HUMAN	EST366628 MAGC resequences, MAGC Homo sapiens cDNA
			4.05	3.0E-54	AW748965.1	EST_HUMAN	RC1-BT0313-131199-011-b09 BT0313 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
670	13284	25774	29.57	2.0E-54	5031900	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
1409	14002	26530	1.59	2.0E-54	4507164	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
1595	14188	26719	1.03	2.0E-54	AA855008.1	EST_HUMAN	nt78a09.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element ;
2577	15139	27709	0.88	2.0E-54	AW163175.1	EST_HUMAN	au82q03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to SW-CUL1_HUMAN Q13616 CULLIN HOMOLOG 1 ;
2635	15195	27768	1.28	2.0E-54	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2920	15537	28012	1.26	2.0E-54	AW057524.1	EST_HUMAN	wy60b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
3602	16206		5.09	2.0E-54	AA532925.1	EST_HUMAN	nt45g09.s1 NCI_CGAP_Pr8 Homo sapiens cDNA clone IMAGE:995488 similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN);
3915	16513	28975	0.82	2.0E-54	4506376	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
3915	16513	28976	0.82	2.0E-54	4506376	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4283	16869		2.42	2.0E-54	4502642	NT	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA
4536	17120		1.11	2.0E-54	AF208161.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
4541	17125		3.09	2.0E-54	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5666	18293	30773	2.15	2.0E-54	4759089	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA
5788	18413	31130	0.88	2.0E-54	BE047864.1	EST_HUMAN	tz43c11.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291348 5'
5935	18558	31284	3.66	2.0E-54	11426657	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
6022	18641	31381	11.65	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6022	18641	31382	11.65	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6763	19356	32165	0.88	2.0E-54	AF008915.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
7177	19709	32557	8.13	2.0E-54	11426544	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA
8547	22047	35008	3.27	2.0E-54	AB001025.1	NT	Homo sapiens mRNA for brain tyrosine receptor, complete cds
8922	22418	35392	1.45	2.0E-54	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10028	22523	35519	0.88	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
10028	22523	35520	0.88	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
11573	24020		3.33	2.0E-54	7657454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
12368	24539	30903	2.87	2.0E-54	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
4564	17147		1.23	1.0E-54	BF315418.1	EST_HUMAN	601899230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
8664	21203	34121	0.64	1.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA
10152	22647	35640	0.56	1.0E-54	AA412409.1	EST_HUMAN	zu10e09.11 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731484 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1489	14082	26022	1.12	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1561	14153		1.02	4.0E-55	BF081411.1	EST_HUMAN	7152b10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L1.13 L1 repetitive element ;
2071	14651	27222	1.47	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2071	14651	27223	1.47	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2132	14710	27281	8.27	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2132	14710	27282	8.27	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2349	14920	27495	1.64	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
3318	15028	28405	1.01	4.0E-55	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
8285	20826		7.61	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11108	23618		4.93	4.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
11845	24207		1.88	4.0E-55	BF303941.1	EST_HUMAN	601866575F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
8710	19304	32108	0.83	3.0E-55	AA077156.1	EST_HUMAN	7809A09 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B09A09
10224	22719	35709	0.46	3.0E-55	AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
11780	24167		6.76	3.0E-55	BE178519.1	EST_HUMAN	PM1-HT0603-090300-001-g08 HT0603 Homo sapiens cDNA
12663	24663		1.63	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
400	13044	25535	2.16	2.0E-55	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
577	13207		2.15	2.0E-55	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
677	13301	25783	3.11	2.0E-55	4507296	NT	Homo sapiens syntaxin-binding protein 1 (STXB1) mRNA, and translated products
2986	15602	28082	0.93	2.0E-55	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4888	17463	29617	2.37	2.0E-55	BE171988.1	EST_HUMAN	CM1-HT0876-150800-357-g03 HT0876 Homo sapiens cDNA
7515	24785	32902	0.87	2.0E-55	AW501988.1	EST_HUMAN	UI-HF-BN0-aks-f-06-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078275 5'
8995	21533	34462	0.46	2.0E-55	BF224452.1	EST_HUMAN	hr76h08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134463 3'
8995	21533	34463	0.46	2.0E-55	BF224452.1	EST_HUMAN	hr76h08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134463 3'
9087	21623		3.77	2.0E-55	A1002836.1	EST_HUMAN	am88h06.s1 Stratiotes schizobrain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element ;
9165	21700		0.7	2.0E-55	BE007859.1	EST_HUMAN	QVO-BN0147-280400-213-g08 BN0147 Homo sapiens cDNA
10144	22639	35629	0.47	2.0E-55	AI439401.1	EST_HUMAN	QVO-BN0147-280400-213-g08 BN0147 Homo sapiens cDNA clone IMAGE:2140479 3'
10828	23349	36365	2.22	2.0E-55	AU119344.1	EST_HUMAN	h03h08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:3134463 3'
100	12776	25258	1.25	1.0E-55	4505060	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
203	12864	25348	84.41	1.0E-55	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
600	13229	25702	0.86	1.0E-55	AI026718.1	EST_HUMAN	ov65509.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644160 3'

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1189	13780	28301	6.18	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1993	14575	27134	1.21	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:2967027 5'
1993	14575	27135	1.21	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:2967027 5'
2363	14934		2.58	1.0E-55	5803174	NT	Homo sapiens SMA3 (SMA3), mRNA
2376	15399	27519	1.04	1.0E-55	AF000990.1	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
2558	15122	27691	10.31	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2590	15152	27718	4.82	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2590	15152	27719	4.82	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2642	15201	27774	1.88	1.0E-55	L54057.1	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4061	16658	29120	4.09	1.0E-55	AL163267.2	NT	Homo sapiens CLP mRNA, partial cds
4382	18969	29417	1.24	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C067
4837	17415		1.17	1.0E-55	N77261.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
4954	17529	29870	1.81	1.0E-55	AB037163.1	NT	y44g03.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:245620 5'
4954	17529	29871	1.81	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
5311	17873	30285	1.03	1.0E-55	8923125	NT	Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA
5689	18315	30814	8.13	1.0E-55	AF118856.1	NT	Homo sapiens PRO1851 mRNA, complete cds
6417	18020	31804	7.22	1.0E-55	11433046	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6417	18020	31805	7.22	1.0E-55	11433046	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
7930	20472	33381	2.11	1.0E-55	11432994	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
7930	20472	33382	2.11	1.0E-55	11432994	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8026	20568	33471	0.97	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
8026	20568	33472	0.97	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
10791	23314	36322	4.95	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
10791	23314	36323	4.95	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11322	23020	36028	2.23	1.0E-55	U50950.1	NT	Human infant brain unknown product mRNA, complete cds
11342	23040	36049	1.68	1.0E-55	T10045.1	EST_HUMAN	seq1575 b4HB3MA CofB-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F61 5' similar to similar to Chinese Hamster DHFR-coamplified protein mRNA
11448	23898	36864	1.81	1.0E-55	10587821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
7401	18928	32791	1.97	9.0E-56	BE378074.1	EST_HUMAN	601237702F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3609552 5'
2761	15316	27882	3.95	7.0E-56	H19934.1	EST_HUMAN	yH62903.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element
7636	20148	33031	2.11	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231069-013-b07 CT0252 Homo sapiens cDNA
7636	20148	33032	2.11	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231069-013-b07 CT0252 Homo sapiens cDNA
1730	14321	26883	1.59	5.0E-56	AW997712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9088	21624	34559	0.8	5.0E-56	AW015507.1	EST_HUMAN	UI-H-B10p-eau-a-05-0-U1.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2710544 3'
10289	22764		1.35	5.0E-56	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12020	25048	30509	3.74	5.0E-56	H55099.1	EST_HUMAN	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'
30	12709	25166	22.23	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
30	12709	25167	22.23	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2733	15288	27855	7.6	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2733	15288	27856	7.6	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2838	13183	25661	3.4	4.0E-56	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
6405	19008	31789	5.85	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
6405	19008	31780	5.85	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
10400	22894	35889	1.2	4.0E-56	AF043348.1	NT	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
10803	23326	36335	8.31	4.0E-56	AF498066.1	EST_HUMAN	bm85g12.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163048 3'
10803	23326	36336	8.31	4.0E-56	AF498066.1	EST_HUMAN	bm85g12.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163048 3'
1386	13980	26507	2.12	3.0E-56	8924028	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
1801	14391	26936	4.33	3.0E-56	6912743	NT	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
3159	15773	28240	1.88	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3159	15773	28241	1.88	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3903	16502		2.38	3.0E-56	AF035086.1	NT	Homo sapiens MHC class 1 region
3991	16589	28061	0.9	3.0E-56	BE393512.1	EST_HUMAN	601310203F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631848 5'
4477	17062	29512	0.62	3.0E-56	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
4515	17089	28546	5.15	3.0E-56	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
4873	17255	29707	2.57	3.0E-56	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
4925	17500		1.14	3.0E-56	BE893572.1	EST_HUMAN	601438154F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3923100 5'
5280	17842	30269	0.6	3.0E-56	6912593	NT	Homo sapiens phosphatidylinositol transfer protein, beta (PITPNB), mRNA
5346	17842	30269	0.59	3.0E-56	6912593	NT	Homo sapiens phosphatidylinositol transfer protein, beta (PITPNB), mRNA
5863	18485	31208	1.4	3.0E-56	4759163	NT	Homo sapiens sparco/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
5863	18485	31209	1.4	3.0E-56	4759163	NT	Homo sapiens sparco/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
6956	18533	32358	6.22	3.0E-56	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
8750	21289	34209	5.2	3.0E-56	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9727	22225	35202	0.88	3.0E-56	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10375	22869	35862	1.63	3.0E-56	11434956	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11194	23699	36749	6.31	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NP1P), mRNA
11194	23699	36750	6.31	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NP1P), mRNA
11883	24230	31002	1.3	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
11883	24230	31003	1.3	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
550	13181		2.35	2.0E-56	AA189818.1	EST_HUMAN	Zq52a08.s1 Stratiogene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:845208 3'
762	15424	25878	1.37	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
762	15424	25879	1.37	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
2426	14994	27567	1.32	2.0E-56	M26061.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds
2426	14994	27568	1.32	2.0E-56	M26061.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds
3017	15633	28110	1.33	2.0E-56	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3358	15966		1.2	2.0E-56	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3588	16190	28674	1.34	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ABCFC10 5'
7147	19680	32521	1.9	2.0E-56	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1016	13628		12.77	1.0E-56	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3737	16338	28603	1.67	1.0E-56	AW589833.1	EST_HUMAN	Hg23c11.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2946452 3'
3737	16338	28604	1.67	1.0E-56	AW589833.1	EST_HUMAN	Hg23c11.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2946452 3'
9866	22363		0.71	1.0E-56	AL183203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9861	22456	35439	1.57	1.0E-56	AW845987.1	EST_HUMAN	RC2-CT0163-220998-001-E02 CT0163 Homo sapiens cDNA
653	13276		1.74	9.0E-57	AW880885.1	EST_HUMAN	QV0-OT0033-070300-152-h03 OT0033 Homo sapiens cDNA
11089	23609	36849	1.92	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11089	23609	36850	1.92	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11397	23849	36915	2.01	9.0E-57	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
15	12694	25150	0.88	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
319	12673	25462	2.71	8.0E-57	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
917	13530	26048	8.64	8.0E-57	AW264599.1	EST_HUMAN	x05d10.x1 NCI_CGAP_Bm63 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U05875
1852	14440	26987	1.52	8.0E-57	AA498108.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
3428	16036	28516	1	8.0E-57	4758279	NT	z55b12.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757151 5'
3428	16036	28517	1	8.0E-57	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
5187	17752	30183	0.6	8.0E-57	BE238916.1	EST_HUMAN	Homo sapiens EphA4 (EPHA4) mRNA
5450	24958	30831	3.17	8.0E-57	11416185	NT	600944440F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860864 5'
6590	19187	31989	12.5	8.0E-57	AB023177.1	NT	Homo sapiens acinosa 2, mitochondrial (ACO2), mRNA
6590	19187	31990	12.5	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7728	20237	33128	2.72	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7729	20237	33129	2.72	8.0E-57	AB020844.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
11351	12694	25150	3.59	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
12271	24477	30936	1.41	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1261	13858	26375	1.18	7.0E-57	AJ003100.1	NT	Homo sapiens GYS2 gene, exon 14
3287	15898	28376	1.08	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3287	15898	28377	1.08	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3309	15920	28397	1	7.0E-57	6005979	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3948	16544	28011	2.3	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
3948	16544	28012	2.3	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
4524	17108		1.06	7.0E-57	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
12634	24992		5.12	5.0E-57	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3817	18417	28880	1.88	4.0E-57	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
837	13453	25963	1.03	3.0E-57	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1376	13969		39.52	3.0E-57	AA230279.1	EST_HUMAN	nc13107.s1 NCI_CGAP_P71 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN
2434	15001	27573	1.01	3.0E-57	AA348335.1	EST_HUMAN	P46783 40S RIBOSOMAL PROTEIN S10. ;
2727	15282	27849	0.93	3.0E-57	BE676822.1	EST_HUMAN	EST54770 Hippocampus II Homo sapiens cDNA 5' end
2727	15282	27850	0.93	3.0E-57	BE676822.1	EST_HUMAN	733b10.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H8C.2
3618	18221	28699	0.93	3.0E-57	AF232708.1	NT	CE20283 ;
3760	18361		60.31	3.0E-57	AW853964.1	EST_HUMAN	733b10.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H8C.2
6180	18790	31559	1.34	3.0E-57	11226808	NT	Homo sapiens cell-line tA201a chloride ion current inducer protein (Cln) gene, complete cds
6272	18880	31648	3.17	3.0E-57	BE796537.1	EST_HUMAN	RC3-CT0254-110300-027-d10 CT0254 Homo sapiens cDNA
8087	20828	33542	3.09	3.0E-57	W28130.1	EST_HUMAN	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
8111	20852	33560	2.27	3.0E-57	11545798	NT	601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
8111	20852	33561	2.27	3.0E-57	11545798	NT	42f6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8223	20764	33681	0.61	3.0E-57	11427757	NT	Homo sapiens hypothetical protein FLJ11856 (FLJ11856), mRNA
8368	20908	33827	1.18	3.0E-57	J05262.1	NT	Homo sapiens hypothetical protein FLJ11856 (FLJ11856), mRNA
8792	21331	34255	4.05	3.0E-57	AU117659.1	EST_HUMAN	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
9174	21751	34696	0.63	3.0E-57	11545798	NT	Human farnesyl pyrophosphate synthetase mRNA, complete cds
							AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
							Homo sapiens hypothetical protein FLJ11856 (FLJ11856), mRNA

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8174	21751	34697	0.63	3.0E-57	11545788	NT	Homo sapiens hypothetical protein FLJ11658 (FLJ11658), mRNA
10787	23311	36318	3.02	3.0E-57	AW248374.1	EST_HUMAN	2820473.5 prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'
11890	25068	30513	7.99	3.0E-57	W23871.1	EST_HUMAN	zb45d11.1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306549 5'
12272	24882		1.69	3.0E-57	AW178575.1	EST_HUMAN	RCO-HT0112-080999-001-C06 HT0112 Homo sapiens cDNA
1480	14073	26612	0.88	2.0E-57	AI478904.1	EST_HUMAN	hm28c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157618 3' similar to contains Alu repetitive element
1548	14140	26873	0.96	2.0E-57	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1548	14140	26874	0.96	2.0E-57	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
2444	15011	27583	1.15	2.0E-57	BE172526.1	EST_HUMAN	MRO-HT0559-010400-009-h10 HT0559 Homo sapiens cDNA
2758	15311	27877	4.79	2.0E-57	AA845419.1	EST_HUMAN	ak02b02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to contains Alu repetitive element; contains element MER22 repetitive element
3486	16091		2.28	2.0E-57	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3605	16209	28688	0.71	2.0E-57	R07702.1	EST_HUMAN	ye98h01.1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
3605	16209	28689	0.71	2.0E-57	R07702.1	EST_HUMAN	ye98h01.1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
4004	16602	29078	0.62	2.0E-57	BE073284.1	EST_HUMAN	MRO-BT0551-060300-103-b03 BT0551 Homo sapiens cDNA
4608	17181	29637	8.02	2.0E-57	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
5849	18473		1.57	2.0E-57	AA016131.1	EST_HUMAN	zs31c05.1 Soares_retina_N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.L3 L1 repetitive element
6184	18784		29.73	2.0E-57	BF115286.1	EST_HUMAN	7n80f04.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570966 3' similar to contains TAR1.t1
6307	18914	31688	0.73	2.0E-57	11431281	NT	MER22 repetitive element
8566	21105	34024	1.22	2.0E-57	AF045452.1	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 22 (SCYA22), mRNA
9760	22558	35241	2.55	2.0E-57	AF057722.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
11150	23658	36701	2.05	2.0E-57	11424084	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4
11150	23658	36702	2.05	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11192	23697	36746	1.84	2.0E-57	AJ245503.1	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11192	23697	36747	1.84	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
8528	21165		3.5	1.0E-57	BE043031.1	EST_HUMAN	Homo sapiens partial mRNA for PEX5 related protein
12049	24333		0.35	1.0E-57	AW470791.1	EST_HUMAN	ho32808.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3039062 3' similar to TR:O00246 O00246 HYPOTHETICAL 9.3 KD PROTEIN
5857	18480	31203	1.02	9.0E-58	AA297847.1	EST_HUMAN	hs33d08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3
12335	24518	30922	2.62	9.0E-58	BE395081.1	EST_HUMAN	THR repetitive element
615	13242		3.87	8.0E-58	BE688715.1	EST_HUMAN	EST11348 Uterus Homo sapiens cDNA 5' end
							601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
							601445948F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
682	13306	25789	3.77	8.0E-58	AI798376.1	EST_HUMAN	t34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
682	13306	25790	3.77	8.0E-58	AI798376.1	EST_HUMAN	t34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
1897	14482	27041	2.82	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1897	14482	27042	2.82	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
3003	15619		2.94	8.0E-58	7706132	NT	Homo sapiens DHG1 protein (LOC51304), mRNA
10735	23260		6.42	7.0E-58	5174542	NT	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B), mRNA
10809	23332	36344	3.77	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BNO-ali-g-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
10809	23332	36345	3.77	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BNO-ali-g-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
2414	14982	27558	3.39	6.0E-58	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
2928	15542	28017	1.26	8.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
2828	15542	28018	1.28	8.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
6318	18925	31702	1.15	6.0E-58	AF106911.1	NT	Homo sapiens chemokine MIP-2 gamma (MIP-2 gamma) mRNA, complete cds
10211	22708	35700	0.99	6.0E-58	11434748	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
12150	24393		1.87	6.0E-58	11628291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
322	12978	25464	3.26	5.0E-58	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
739	13359	25853	5.81	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-160600-016-b05 NT0057 Homo sapiens cDNA
1236	13635	26350	3.59	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1236	13635	26351	3.59	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1237	13635	26350	2.7	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1237	13635	26351	2.7	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3365	15973	28450	4.17	5.0E-58	AA988183.1	EST_HUMAN	cr98e07.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603908 3'
4345	16932	28673	0.78	5.0E-58	AI636745.1	EST_HUMAN	ts89e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2238468 3' similar to SW:PRO2_ACACA P18984 PROFILIN II ;
5105	17677		1.12	5.0E-58	AW848834.1	EST_HUMAN	IL3-CT0214-090300-081-F06 CT0214 Homo sapiens cDNA
5811	18435		2.08	5.0E-58	11496282	NT	Homo sapiens placenta-specific 1 (PLACT1), mRNA
6325	18931	31707	5.73	5.0E-58	H23072.1	EST_HUMAN	ym51h07.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:52071 5'
6528	19128	31922	0.87	5.0E-58	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6597	19194	31999	1.24	5.0E-58	11421330	NT	Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA
7161	19993	32539	0.72	5.0E-58	4885400	NT	Homo sapiens holo-cytochrome c synthase (cytochrome c heme-lyase) (HCCS), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7910	20452	33359	9.67	5.0E-58	8922693	NT	Homo sapiens hypothetical protein FLJ10826 (FLJ10826), mRNA
8294	20835	33757	0.74	5.0E-58	AB046837.1	NT	Homo sapiens mRNA for KIAA1617 protein, partial cds
9263	21789	34739	0.72	5.0E-58	5231227	NT	Homo sapiens ribonuclease 6 precursor (RNASE6PL) mRNA
9263	21789	34740	0.72	5.0E-58	5231227	NT	Homo sapiens ribonuclease 6 precursor (RNASE6PL) mRNA
9771	22289	35253	0.74	5.0E-58	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
10030	22525	35521	1.39	5.0E-58	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10300	22794	35784	0.59	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10300	22794	35785	0.59	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
11859	24987		6.17	5.0E-58	11526283	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
12331	25016		1.81	5.0E-58	11426423	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
12577	24673		1.34	5.0E-58	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12653	24725	30853	1.37	5.0E-58	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12653	24725	30854	1.37	5.0E-58	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
396	13042	25532	5.55	4.0E-58	4502302	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA
829	13446	25953	1.76	4.0E-58	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
1517	14109	26945	1.88	4.0E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2611	15173	27741	1.13	4.0E-58	AF285555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
2660	15219	27760	1.75	4.0E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3367	15975	28452	1.62	4.0E-58	D16470.1	NT	Human mRNA, Xq terminal portion
3803	16403	28867	1.26	4.0E-58	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
11221	23724	36779	9.32	4.0E-58	11424059	NT	Homo sapiens E1B-55kDa-associated protein 5 (E1B-AP5), mRNA
357	13006		1.77	3.0E-58	R17879.1	EST_HUMAN	X010602.1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31693 5'
1433	14026	28554	2.23	3.0E-58	4758981	NT	Homo sapiens peptide YY (PYY) mRNA
3059	15675		0.73	3.0E-58	R17879.1	EST_HUMAN	X010602.1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31693 5'
3212	15824	28300	3.1	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
3212	15824	28301	3.1	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
6407	19010	31792	0.72	3.0E-58	BE039508.1	EST_HUMAN	QV0-BT0702-170400-194-099 BT0702 Homo sapiens cDNA
6572	19170	31967	0.98	3.0E-58	F07058.1	EST_HUMAN	HSC1T G081 normalized infant brain cDNA Homo sapiens cDNA clone c-1g08
8751	19344	32151	1.25	3.0E-58	AV712977.1	EST_HUMAN	AV712977 DCA Homo sapiens cDNA clone DCAAZG04 5'
976	13588	26103	8.92	2.0E-58	AF098824.1	NT	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1333	13927		30.8	2.0E-58	BE208532.1	EST_HUMAN	ba08b07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69391.60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
5539	18171	30588	0.75	2.0E-58	AW074831.1	EST_HUMAN	xa08a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567704 3'
5560	24745	30607	4.01	2.0E-58	BE907188.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5560	24745	30637	4.01	2.0E-58	BE907188.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
6207	18817	31588	1.26	2.0E-58	BF513488.1	EST_HUMAN	U1-H-BW1-ems-g-11-Q-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071060 3'
							am57402.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539674 3' similar to WP.ZK328.1 CE05065 UBIQUITIN CONJUGATING ENZYME; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN;
6270	18878	31646	2.1	2.0E-58	AI124874.1	EST_HUMAN	yq08h08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196379 5'
6302	18909	31681	0.88	2.0E-58	R92567.1	EST_HUMAN	qm84d01.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1895424 3'
7006	19504	32323	1	2.0E-58	AI291407.1	EST_HUMAN	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7210	19741	32594	2.91	2.0E-58	AF134638.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7210	19741	32595	2.91	2.0E-58	AF134638.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
10920	23152	36164	19.73	2.0E-58	BF307745.1	EST_HUMAN	601890312F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131891 5'
10844	23365	36381	2.67	2.0E-58	AW872641.1	EST_HUMAN	hm25708.x1 NCI_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3'
751	13371	25865	4.83	1.0E-58	M85134.1	NT	Human complement component C5 mRNA, 3' end
1106	13710	26219	5.91	1.0E-58	6274549	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1372	13968	26492	1.24	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGe resequences, MAGD Homo sapiens cDNA
1372	13966	26493	1.24	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGe resequences, MAGD Homo sapiens cDNA
1440	14033	26561	2.04	1.0E-58	AJ238083.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1704	14297	26834	0.9	1.0E-58	BE468132.1	EST_HUMAN	hy10f08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3198935 3'
2828	15380	27950	1.17	1.0E-58	4759169	NT	Homo sapiens steroid regulatory element binding transcription factor 2 (SREBF2) mRNA
3590	16194	28679	0.62	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3590	16194	28680	0.62	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3783	16383	28848	0.57	1.0E-58	4507628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNIP1) mRNA
5108	17878	30117	8.64	1.0E-58	AI141063.1	EST_HUMAN	oz43h01.x1 Soares_NhiHMPu_S1 Homo sapiens cDNA clone IMAGE:1678129 3'
6007	18627	31362	1.2	1.0E-58	BE081880.1	EST_HUMAN	RC1-BT0254-290100-015-e01 BT0254 Homo sapiens cDNA
6948	19523	32345	0.73	1.0E-58	11422031	NT	Homo sapiens myothesin (LOC51280), mRNA
8803	21342	34268	0.7	1.0E-58	4505314	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
8912	21450	34371	0.83	1.0E-58	AV751001.1	EST_HUMAN	AV751001 NPC Homo sapiens cDNA clone NPCACH09 5'
9010	21547	34475	0.65	1.0E-58	AA412397.1	EST_HUMAN	z89f05.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
9010	21547	34476	0.65	1.0E-58	AA412397.1	EST_HUMAN	z89f05.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit : BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10089	22584	35577	0.55	1.0E-58	11432994	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
11610	24053		5.43	1.0E-58	XG3392.1	NT	H. sapiens Immunoglobulin kappa light chain variable region L14
2273	14847	27423	18.05	8.0E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
8121	20662	33572	2.08	8.0E-59	AI761963.1	EST_HUMAN	wh50406.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384171 3'
190	15409		2.18	6.0E-59	BF035327.1	EST_HUMAN	601438331F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
8188	20729	33641	0.59	6.0E-59	AI750970.1	EST_HUMAN	cn08h02.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn08h02 random
1790	14380	26924	1.32	5.0E-59	AW157281.1	EST_HUMAN	au83h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to TR:O75786 O75786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
1790	14380	26925	1.32	5.0E-59	AW157281.1	EST_HUMAN	au83h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to
3161	15775	28243	7.81	5.0E-59	AI807484.1	EST_HUMAN	TR:O75786 O75786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
4762	17343	29781	4.42	5.0E-59	XG3497.1	NT	wt48c11.x1 Soares NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836 3'
5886	18509	31235	0.81	5.0E-59	6005698	NT	H. sapiens DNA for ZNF80-linked ERV9 long terminal repeat
7064	18083	30440	8.32	5.0E-59	AW162304.1	EST_HUMAN	Homo sapiens alazin 2 related protein (AZLP), mRNA
8741	21280	34203	1.35	5.0E-59	11421778	NT	au66c07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TARI repetitive element ;
9821	22121	35085	1.85	5.0E-59	AV762869.1	EST_HUMAN	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA
10786	23310	36317	3.47	5.0E-59	11434608	NT	AV762869 MDS Homo sapiens cDNA clone MDSEIC12 5'
828	13443	25951	2.85	4.0E-59	DB0006.1	NT	Homo sapiens hypothetical protein (LOC57143), mRNA
5728	18354	31058	1.22	4.0E-59	11034810	NT	Human mRNA for KIAA0184 gene, partial cds Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
12004	24917		5.54	4.0E-59	AF057720.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
10	12689		4.75	3.0E-59	AW965524.1	EST_HUMAN	EST377582 MAGE resequences, MAGI Homo sapiens cDNA
245	12904	25385	3.86	3.0E-59	7662247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
1748	14338	26884	8.2	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
1748	14338	26885	8.2	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2174	14751	27320	7.15	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2174	14751	27321	7.15	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2798	15477	27920	1.29	3.0E-59	AF232298.1	NT	Homo sapiens NF1-2 pseudogene, exon 17
3074	15889	28161	0.77	3.0E-59	TI18965.1	EST_HUMAN	h020171 Testis 1 Homo sapiens cDNA clone h02017 5' end
3074	15889	28162	0.77	3.0E-59	TI18965.1	EST_HUMAN	h020171 Testis 1 Homo sapiens cDNA clone h02017 5' end
3163	15777	28247	4.67	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3163	15777	28248	4.87	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3897	16486	28958	1.12	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4798	17374	29828	0.98	3.0E-59	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4967	17541	29984	1.33	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
6369	18973	31751	2.1	3.0E-59	8924074	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA
7395	19920	32785	1.87	3.0E-59	5454137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA
7872	20414	33321	1.26	3.0E-59	X12556.1	NT	Human mRNA for dbi proto-oncogene
7872	20414	33322	1.26	3.0E-59	X12556.1	NT	Human mRNA for dbi proto-oncogene
9957	22452	35433	1.04	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
9957	22452	35434	1.04	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
11980	24291		1.26	3.0E-59	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12130	24386		9.09	3.0E-59	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
6044	18663	31402	0.98	2.0E-59	BF509383.1	EST_HUMAN	UI-H-BI4-ay-b-02-Q-UI.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086522 3'
6044	18663	31403	0.98	2.0E-59	BF509383.1	EST_HUMAN	UI-H-BI4-ay-b-02-Q-UI.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086522 3'
9555	22055		5.27	2.0E-59	AA309774.1	EST_HUMAN	EST180833 Jurkat T-cells V Homo sapiens cDNA 5' end
10419	22613		1.34	2.0E-59	BF365554.1	EST_HUMAN	RCO-NT0036-100700-032-a07 NT0036 Homo sapiens cDNA
10710	23238	36252	2.49	2.0E-59	AW410898.1	EST_HUMAN	fh07h04.x1 NIH_MGC.17 Homo sapiens cDNA clone IMAGE:2981654 5'
10710	23238	36253	2.49	2.0E-59	AW410898.1	EST_HUMAN	fh07h04.x1 NIH_MGC.17 Homo sapiens cDNA clone IMAGE:2981654 5'
11879	24228	31046	5.76	2.0E-59	AI631809.1	EST_HUMAN	Q86542 RTVL-H PROTEIN, contains LTR7.b1 LTR7 repetitive element;
12437	24943	30821	2.86	2.0E-59	L11845.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
174	12837		18.31	1.0E-59	BE298411.1	EST_HUMAN	601176757F1 NIH_MGC.17 Homo sapiens cDNA clone IMAGE:3531927 5'
2516	15080	27652	1.02	1.0E-59	AI139341.1	EST_HUMAN	qc21c08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1710254 3'
2516	15080	27653	1.02	1.0E-59	AI139341.1	EST_HUMAN	qc21c08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1710254 3'
							ca56h11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309029 3' similar to TR:Q13537
2849	15208		1.45	1.0E-59	AA748468.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
7563	20080	32956	1.98	1.0E-59	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
7703	20212	33100	0.93	1.0E-59	BE256814.1	EST_HUMAN	601111951F1 NIH_MGC.16 Homo sapiens cDNA clone IMAGE:3352692 5'
7703	20212	33101	0.93	1.0E-59	BE256814.1	EST_HUMAN	601111951F1 NIH_MGC.16 Homo sapiens cDNA clone IMAGE:3352692 5'
9307	21907	34855	1.2	1.0E-59	11418630	NT	Homo sapiens zinc finger protein 275 (ZNF275), mRNA
9522	22022	34979	0.82	1.0E-59	11428849	NT	Homo sapiens 3-hydroxybutyryl-Coenzyme A hydrolase (HIBCH), mRNA
9522	22022	34980	0.82	1.0E-59	11428849	NT	Homo sapiens 3-hydroxybutyryl-Coenzyme A hydrolase (HIBCH), mRNA
10734	20080	32956	9.52	1.0E-59	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
795	13413	25917	1.28	8.0E-60	AW977845.1	EST_HUMAN	EST389849 IMAGE resequences, MAGO Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1520	14112	26648	3.21	8.0E-60	4759159	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
2216	14791	27394	1.95	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
2216	14791	27395	1.95	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
6135	18749	31506	1.01	8.0E-60	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6628	19224	32029	1.85	8.0E-60	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog (human, plasma, mRNA, 2408 nt)
7684	20195	33083	0.76	8.0E-60	11420841	NT	Homo sapiens phosphate cytidylyltransferase 1, choline, beta isoform (PCYT1B), mRNA
7908	20448	33355	2.66	8.0E-60	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
8969	21408	34332	4.03	8.0E-60	11428949	NT	Homo sapiens S-antigen; retina and pineal gland (arrestin) (SAG), mRNA
9392	21815	34794	0.98	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9392	21815	34795	0.98	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10465	22959	35989	0.68	8.0E-60	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10712	23240	36255	5.93	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
10712	23240	36256	5.93	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
784	13403	25907	12.12	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region
785	13403	25907	52.6	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region
848	13464	25972	1.28	7.0E-60	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
2173	14750	27319	1.95	7.0E-60	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
4258	16844	29293	2.74	7.0E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
9328	21842	34784	3.6	7.0E-60	H58041.1	EST_HUMAN	yr1204.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element;
11243	23773	36830	1.87	7.0E-60	H58041.1	EST_HUMAN	yr1204.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element;
8376	20816		7.56	6.0E-60	H52456.1	EST_HUMAN	yr78109.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201863 5' similar to contains OFR repetitive element;
87	12763	25245	1.13	5.0E-60	AB07917.1	EST_HUMAN	wf52c07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
87	12763	25246	1.13	5.0E-60	AB07917.1	EST_HUMAN	wf52c07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
3000	15616		1.47	4.0E-60	AA289037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
7390	19915	32779	0.7	4.0E-60	BF196068.1	EST_HUMAN	h8105.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE Q61085 GTP-RHO BINDING PROTEIN 1;
8034	21591		0.82	4.0E-60	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1899	14484	27044	5.26	3.0E-60	BE562611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1899	14484	27045	5.26	3.0E-60	BE562611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1910	14495		2.4	3.0E-60	6031190	NT	Homo sapiens prohibitin (PHB) mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4556	17139	29587	1.88	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5822	18446	31186	2.04	3.0E-60	AW836196.1	EST_HUMAN	RC3-LT0023-200100-012-401 LT0023 Homo sapiens cDNA
7034	18054	30477	1	3.0E-60	A1792814.1	EST_HUMAN	060h11.y6 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1534053 5' similar to SW:UDP_MOUSE P52624 URIDINE PHOSPHORYLASE ;
8341	20882	33802	5.3	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8341	20882	33803	5.3	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8519	21058	33881	0.51	3.0E-60	A1040295.1	EST_HUMAN	ox56409.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1660337 3' similar to SW:FORM_MOUSE Q05860 FORMIN ;
8677	21216	34136	4.75	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
12520	24980		1.71	3.0E-60	AA485286.1	EST_HUMAN	ab07h04.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:840151 5' similar to contains LTR10.11 LTR10 repetitive element ;
33	12712	25171	2.84	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1470	14082	26597	2.86	2.0E-60	Z11694.1	NT	H. sapiens 41kDa protein kinase related to rat ERK2
1759	14349	28893	1.24	2.0E-60	M24603.1	NT	Human bcr protein mRNA, 5' end
3638	16241	28717	0.72	2.0E-60	4757867	NT	Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
3987	16595	29056	0.78	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4203	16792		0.65	2.0E-60	BF513458.1	EST_HUMAN	U1-H-BW1-ams-e-05-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070952 3'
6443	18045	31833	0.94	2.0E-60	A1791852.1	EST_HUMAN	nn01112.y6 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.11 THR repetitive element ;
6818	19215	32020	1.65	2.0E-60	AF004877.1	NT	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
6816	19407	32224	0.89	2.0E-60	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
6934	18042	30486	2.08	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
6934	18042	30487	2.08	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7164	19696	32542	8.14	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7164	19696	32543	8.14	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7628	20140		1.05	2.0E-60	BF512808.1	EST_HUMAN	U1-H-BW1-ams-e-02-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071210 3'
7947	20499	33399	1.05	2.0E-60	X85597.1	EST_HUMAN	HS15BEST human adult testis Homo sapiens cDNA clone CAM_IEST15
8801	21340	34267	3.38	2.0E-60	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
9888	22385	35382	2.67	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
9888	22385	35383	2.67	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
12168	24407		3.98	2.0E-60	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12309	24908		1.71	2.0E-60	AF088757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12311	24503		1.88	2.0E-60	11418068	NT	Homo sapiens similar to HSPC022 protein (H. sapiens) (LOC83504), mRNA
12328	24515		1.95	2.0E-60	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
548	13179	25657	0.92	1.0E-60	BE178598.1	EST_HUMAN	PM3-HT0605-270200-001-008 HT0605 Homo sapiens cDNA
3970	16568	28037	0.95	1.0E-60	AU143388.1	EST_HUMAN	AU143388 Y79AA1 Homo sapiens cDNA clone Y79AA1001854 5'
5091	17684	30104	1.32	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
7889	20431	-33340	0.73	1.0E-60	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
8690	21229		2.93	1.0E-60	AA244041.1	EST_HUMAN	nc04e12.1 NCI_CGAP_Py1 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.1 L1 repetitive element
8717	21268	34176	1.51	1.0E-60	AV764031.1	EST_HUMAN	AV754081 TP Homo sapiens cDNA clone TPGAED05 5'
1138	13741	28250	2.37	9.0E-61	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
2894	15251	27821	1.11	8.0E-61	AW006478.1	EST_HUMAN	w05b10.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2506555 3'
2894	15251	27822	1.11	8.0E-61	AW006478.1	EST_HUMAN	w05b10.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2506555 3'
2878	15594		2.53	8.0E-61	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
7836	20378	33284	0.79	8.0E-61	AA583988.1	EST_HUMAN	nm59q06.st NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088218 3'
133	12789	25286	0.89	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
133	12789	25287	0.89	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
287	12943	25428	3.39	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
844	13460	25969	2.13	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1366	13960	26485	13.81	6.0E-61	AF119880.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1672	14264	26798	0.91	6.0E-61	BE257400.1	EST_HUMAN	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
1689	14281	26816	2.23	6.0E-61	AA566033.1	EST_HUMAN	nm68h09.st NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'
2172	14749	27318	0.93	8.0E-61	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
3347	15957	28433	11.6	6.0E-61	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
6182	18792	31591	3.06	6.0E-61	S79249.1	NT	Ig-beta/B29=CD79b (alternatively spliced) [human, B cells, mRNA Partial, 375 nt]
7380	19806	32771	1.71	6.0E-61	U2498.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene
7614	20127	33004	1.95	6.0E-61	AF035737.1	NT	Homo sapiens general transcription factor 2-1 (GTF2I) mRNA, complete cds
12065	13460	25969	1.38	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
236	12896	25379	2.06	5.0E-61	8922990	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
236	12896	25380	2.06	5.0E-61	8922990	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
382	13029	25517	0.61	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1718	14310	26849	2.36	5.0E-61	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3071	15886	28158	1.9	5.0E-61	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4053	16650		1.91	5.0E-61	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
5144	13028	25517	0.69	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
11856	24215		4.95	4.0E-61	AV731140.1	EST_HUMAN	AV731140 HTP Homo sapiens cDNA clone HTFAR801 5'
4292	16878	29325	0.98	3.0E-61	BE396279.1	EST_HUMAN	601309785F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3831220 5'
8390	20900	33821	0.63	3.0E-61	AF150190.1	EST_HUMAN	AF150190 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAGB04
8829	21168	34083	0.51	3.0E-61	AA301233.1	EST_HUMAN	EST14323 Testis tumor Homo sapiens cDNA 5' end
8629	21168	34084	0.51	3.0E-61	AA301233.1	EST_HUMAN	EST14323 Testis tumor Homo sapiens cDNA 5' end
524	13158	25838	1.29	2.0E-61	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1254	13851	26368	1.98	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1254	13851	26369	1.98	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1705	14298	26835	1.22	2.0E-61	N53039.1	EST_HUMAN	y53d11.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:246453 3' similar to gb:U25444 60S RIBOSOMAL PROTEIN L35A (HUMAN);
2697	15225		1.54	2.0E-61	N93937.1	EST_HUMAN	y93f11.1 Soares melanocyte 2NbmH Homo sapiens cDNA clone IMAGE:270189 5'
6557	19155	31951	0.85	2.0E-61	11426166	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP8N1A), mRNA
8945	21483	34408	1.01	2.0E-61	AV694317.1	EST_HUMAN	AV694317 GKC Homo sapiens cDNA clone GKCELG08 5'
9481	21890		1.55	2.0E-61	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
9836	22334	35316	1.59	2.0E-61	AW500256.1	EST_HUMAN	UI-HF-BN0-akd-k-12-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078774 5'
10149	22844	35636	1.99	2.0E-61	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA
10764	23288		9.83	2.0E-61	11419729	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
480	13094		0.91	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
805	13422	25928	1.25	1.0E-61	5453829	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1443	14036	26565	0.98	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1898	14483	27043	3.87	1.0E-61	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2238	14813	27385	1.55	1.0E-61	AW827281.1	EST_HUMAN	xn11b09.y1 NCL_CGAP_L15 Homo sapiens cDNA clone IMAGE:2693369 5' similar to contains element MSR1 repetitive element;
3422	16030	28511	0.88	1.0E-61	7682319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
4534	17118	29564	1.48	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4534	17118	29565	1.48	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4982	17556	29988	10.61	1.0E-61	AW298181.1	EST_HUMAN	UI-H-BW0-ajl-b-06-0-UI.st1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4982	17556	29989	10.61	1.0E-61	AW298181.1	EST_HUMAN	UI-H-BW0-ajl-b-06-0-UI.st1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
5888	18490	31216	0.89	1.0E-61	7682303	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
6043	18682	31401	1.17	1.0E-61	11416891	NT	Homo sapiens survival of motor neuron 1, telomeric (SMN1), mRNA
6981	19479	32300	8.17	1.0E-61	M30135.1	NT	Human P40 T-cell and mast cell growth factor (HP40) gene, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7148	19681	32522	0.73	1.0E-61	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
7242	19771	32627	1.54	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
7242	19771	32628	1.54	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8075	20617	33531	6.29	1.0E-61	11034840	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
8255	20798	33713	3.19	1.0E-61	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9206	21723		2.29	1.0E-61	AW999726.1	EST_HUMAN	MR0-BN0070-040400-010-h01 BN0070 Homo sapiens cDNA
9279	21805	34756	1.1	1.0E-61	11416280	NT	Homo sapiens cadherin 18 (CDH18), mRNA
9942	22437	35414	5.76	1.0E-61	11428892	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
10514	23052	36063	2.82	1.0E-61	11425578	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
11751	24966		1.58	1.0E-61	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
11793	24955	30629	3.23	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
11793	24955	30630	3.23	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12173	24412	30945	1.61	1.0E-61	M20809.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr1) variable region (subgroup V kappa I)
12494	24822	30891	17.77	1.0E-61	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
10259	22754	35742	1.82	9.0E-62	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
4649	17231	29688	1.03	8.0E-62	AA830420.1	EST_HUMAN	cc66h11.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVRK P31785 POL POLYPROTEIN ;
12652	24724		1.59	8.0E-62	AA768861.1	EST_HUMAN	n275g01.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1301328 3'
1146	13749	26258	1.31	7.0E-62	AV714334.1	EST_HUMAN	AV714334 DGB Homo sapiens cDNA clone DCBAMA08 5'
3554	18158	28641	0.7	7.0E-62	P17480	SWISSPROT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-90)
6075	18692	31438	0.96	7.0E-62	11427965	NT	Homo sapiens hypothetical protein (FLJ20261), mRNA
11229	23760	36816	5.72	7.0E-62	A1208681.1	EST_HUMAN	qg56a04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839150 3' similar to TR:O15103 O15103 HYPOTHETICAL 27.3 KD PROTEIN. ;
3029	15945		1.6	6.0E-62	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
3431	16039		4.97	6.0E-62	11418285	NT	Homo sapiens CGI-56 protein (CGI-56), mRNA
7621	20134	33011	3.43	6.0E-62	A1762801.1	EST_HUMAN	w04402.x1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:2389251 3'
7621	20134	33012	3.43	6.0E-62	A1762801.1	EST_HUMAN	w04402.x1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:2389251 3'
8030	20572		0.75	6.0E-62	AW501124.1	EST_HUMAN	UI-HF-BP0p-aid-409-0-J1r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072833 5'
8200	20741	33654	1.35	6.0E-62	11431139	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
9276	21802	34752	3.92	6.0E-62	AW814383.1	EST_HUMAN	MR3-ST0203-130100-025-a09 ST0203 Homo sapiens cDNA
441	13074	25599	1.99	5.0E-62	A1950528.1	EST_HUMAN	wx51e07.x1 NCL CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95 ; contains element MER22 repetitive element ;

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2451	15018	27589	3	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
2451	15018	27590	3	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
2626	15188	27755	0.87	5.0E-62	U39487.1	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
2626	15188	27756	0.87	5.0E-62	U39487.1	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
3468	16073	28548	2.52	5.0E-62	4508758	NT	Homo sapiens ryanodine receptor 3 (RYSR3) mRNA
4421	17006	29449	2.23	5.0E-62	AA431093.1	EST_HUMAN	zw78e09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT
4657	17239		0.95	5.0E-62	AW905887.1	EST_HUMAN	P47245 NARDILYSIN
8485	21024	33941	0.64	5.0E-62	4508758	NT	RCS-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
9436	21962	34911	5.85	5.0E-62	AW410687.1	EST_HUMAN	Homo sapiens ryanodine receptor 3 (RYSR3) mRNA
11144	23652	36693	2.54	5.0E-62	11425574	NT	h07g09.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861616 5'
11144	23652	36694	2.54	5.0E-62	11425574	NT	Homo sapiens muscle specific gene (M9), mRNA
873	13488	26003	4.05	4.0E-62	AW161479.1	EST_HUMAN	Homo sapiens muscle specific gene (M9), mRNA
873	13488	26004	4.05	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
874	13488	26003	3.94	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
874	13488	26004	3.94	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1511	14103		1.01	4.0E-62	AA311281.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
2498	15062	27636	1.7	4.0E-62	AB27900.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2498	15062	27637	1.7	4.0E-62	AB27900.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
3446	18054		7.95	4.0E-62	4557887	NT	EST182043 Jurkat T-cells Y Homo sapiens cDNA 5' end
6081	18698	31445	1.79	4.0E-62	4506978	NT	EST182043 Jurkat T-cells Y Homo sapiens cDNA clone IMAGE:2350359 3' similar to
8439	19041	31829	2.58	4.0E-62	11420654	NT	gb:X57138_ma1 HISTONE H2B.2 (HUMAN);
7223	19754	32609	1.86	4.0E-62	11421041	NT	wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
7630	20142	33021	2.5	4.0E-62	7657057	NT	gb:X57138_ma1 HISTONE H2B.2 (HUMAN);
7630	20142	33022	2.5	4.0E-62	7657057	NT	Homo sapiens keratin 18 (KRT18) mRNA
8112	20653	33552	0.95	4.0E-62	11428973	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA
							Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
							Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA
							Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
							Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
							Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8780	21319	34243	5.44	4.0E-62	AB033089.1	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
10890	23411	36428	2.16	4.0E-62	Z78766.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
10890	23411	36430	2.16	4.0E-62	Z78766.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
11148	23654	36696	2.05	4.0E-62	AW023559.1	EST_HUMAN	df5g04.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487751 5'
12003	24912		1.89	4.0E-62	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
12420	24606	30887	1.78	4.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
12475	24600	30884	15	4.0E-62	11417802	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12475	24600	30885	15	4.0E-62	11417802	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12528	24642	30898	2.66	4.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
78	12755	25236	0.85	3.0E-62	4557794	NT	Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2) mRNA
3082	15697	28169	0.93	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3082	15697	28170	0.93	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3761	16362	28830	5.68	3.0E-62	X52858.1	NT	Human cyclophilin-related processed pseudogene
8477	21016	33932	3.98	3.0E-62	A1632733.1	EST_HUMAN	wa3304.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2299903 3' similar to contains THR 12
1274	13870	26390	2.31	2.0E-62	AL163284.2	NT	THR repetitive element
8709	21248	34170	4.31	2.0E-62	BF329911.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
8709	21248	34171	4.31	2.0E-62	BF329911.1	EST_HUMAN	RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
10078	22571		3.84	2.0E-62	AF224669.1	NT	RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
11537	23885		19.58	2.0E-62	BF330676.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
1082	13687	26199	1.74	1.0E-62	AF248540.1	NT	(UBE2D3) genes, complete cds
1592	14185	26717	9.15	1.0E-62	L78810.1	NT	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
1834	14422	26972	1.05	1.0E-62	AA625207.1	EST_HUMAN	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
2939	15555	28031	1.22	1.0E-62	AL030044.1	EST_HUMAN	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4825	17208	29658	1.46	1.0E-62	8923201	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
5305	17867	30290	0.74	1.0E-62	AA148822.1	EST_HUMAN	Homo sapiens NHPMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1
7188	19720	32597	1.01	1.0E-62	AA490060.1	EST_HUMAN	CE034433
7199	19730	32581	3	1.0E-62	AA722878.1	EST_HUMAN	DKFZp566F104_r1 566 (synonym: htkd2) Homo sapiens cDNA clone DKFZp566F104 5'
7199	19730	32582	3	1.0E-62	AA722878.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
8692	21231	34151	0.71	1.0E-62	AA280050.1	EST_HUMAN	z06b08.r1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:491511 5' similar to
8988	21528	34455	1.64	1.0E-62	7662289	NT	SW:CS61_BOVIN P:0897 CYTOCHROME B561.1

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8888	21528	34458	1.84	1.0E-62	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9030	21567	34495	2.39	1.0E-62	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9030	21567	34498	2.39	1.0E-62	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9476	21875	34822	2.95	1.0E-62	AA465170.1	EST_HUMAN	aa33408.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:815055 3'
11245	23775	36832	2.49	1.0E-62	Z78698.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA14D8
12289	24490		8.66	1.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
12508	24630	30894	2.04	1.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
360	13009	25492	1.88	9.0E-63	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
2383	14952		2.15	9.0E-63	C18159.1	EST_HUMAN	C18159 Human placenta cDNA (Tfujlwara) Homo sapiens cDNA clone GEN-558C10 5'
4114	16708	29182	9.09	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4114	16708	29183	9.09	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
5453	18022	37142	3.93	9.0E-63	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
5657	18284	30762	1.55	9.0E-63	Y15056.1	NT	Homo sapiens mRNA for PKB kinase
7234	19764	32620	3.66	9.0E-63	11428895	NT	Homo sapiens nucleoporin 88kD (NUP88), mRNA
8268	20809	33729	1.12	9.0E-63	11421160	NT	Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), mRNA
2382	14951	27524	1.5	8.0E-63	4557734	NT	Homo sapiens monamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2412	14980	27555	2.47	8.0E-63	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3508	16113	28580	4.62	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3508	16113	28591	4.62	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4352	16939	28381	3.64	8.0E-63	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
684	13575		2.31	7.0E-63	AB182137.1	EST_HUMAN	wm55g1.1 x1 NCI_CGAP_UJ2 Homo sapiens cDNA clone IMAGE:2438908 3'
5542	18174		34.88	6.0E-63	AA420803.1	EST_HUMAN	nc63f02.1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S
8807	21346	34270	0.5	5.0E-63	11528484	NT	RIBOSOMAL PROTEIN (HUMAN);
3363	15971	28449	0.81	4.0E-63	AL163276.2	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
3881	16479	28940	0.98	4.0E-63	AB014607.1	NT	Homo sapiens chromosome 21 segment HS21C078
3881	16479	28941	0.98	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
6573	19171	31868	5.46	4.0E-63	AW750372.1	EST_HUMAN	Homo sapiens mRNA for KIAA0707 protein, partial cds
6573	19171	31869	5.46	4.0E-63	AW750372.1	EST_HUMAN	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
11012	23528	36561	2.3	4.0E-63	AW134709.1	EST_HUMAN	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
11012	23528	36562	2.3	4.0E-63	AW134709.1	EST_HUMAN	UI-H-B11-abq-e-02-0-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
1879	14582	27121	1.75	3.0E-63	AB018260.1	NT	UI-H-B11-abq-e-02-0-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
2807	15359	27826	1.58	3.0E-63	J00310.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
							Human Mat-IRNA-1 gene 1

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2848	13877	28398	11.17	3.0E-63	6005963	NT	Homo sapiens zinc finger protein 144 (Mef-18) (ZNF144), mRNA
6600	19197	32002	29.68	3.0E-63	11545810	NT	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC83928), mRNA
9622	22122	35086	0.77	3.0E-63	BE876158.1	EST_HUMAN	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
9622	22122	35087	0.77	3.0E-63	BE876158.1	EST_HUMAN	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
205	12866	25351	3.47	2.0E-63	U07804.1	NT	Human DNA topoisomerase I mRNA, partial cds
212	12873	25359	1.4	2.0E-63	4885228	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
523	13155		5.21	2.0E-63	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
859	13475	25988	6.6	2.0E-63	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1612	14205	28739	3.37	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1612	14205	28740	3.37	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1803	14393	26938	1.08	2.0E-63	BE410739.1	EST_HUMAN	601301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636103 5'
2128	14706	27277	1.33	2.0E-63	AI883861.1	EST_HUMAN	wf54b02.x1 NCI_LGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406603 3' similar to gp.M57609 GLI3 PROTEIN (HUMAN);
3192	15804	28277	1	2.0E-63	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3324	15934	28411	1.7	2.0E-63	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
3976	16574	29044	2.09	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4980	17564	30009	1.18	2.0E-63	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5467	24742	30420	1.95	2.0E-63	11419428	NT	Homo sapiens similar to eukaryotic pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
6045	18684	31404	2.51	2.0E-63	BF373541.1	EST_HUMAN	QV1-F10170-040700-265-c05 F10170 Homo sapiens cDNA
6045	18684	31405	2.51	2.0E-63	BF373541.1	EST_HUMAN	QV1-F10170-040700-265-c05 F10170 Homo sapiens cDNA
6333	18939	31715	1.04	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6333	18939	31716	1.04	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV7S2A1N4T, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
6803	18394	32210	1.82	2.0E-63	U66059.1	NT	Homo sapiens MIST mRNA, partial cds
6844	19434	32249	0.87	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
6844	19434	32250	0.87	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7135	19474	32295	1.43	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7135	19474	32296	1.43	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7755	20263	33158	0.89	2.0E-63	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
8470	21010	33927	2.91	2.0E-63	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8984	21522	34449	1.12	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
8984	21522	34450	1.12	2.0E-63	11420948	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
9852	22350	35331	0.9	2.0E-63	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10825	23157	36170	22.7	2.0E-63	N78945.1	EST_HUMAN	zb18b05.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:302385 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN);
10852	23184	36198	2.83	2.0E-63	AF099810.1	NT	Homo sapiens neuritin III-alpha gene, partial cds
10852	23184	36199	2.83	2.0E-63	AF099810.1	NT	Homo sapiens neuritin III-alpha gene, partial cds
11886	24851	30702	6.92	2.0E-63	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
12823	24701	30864	1.4	2.0E-63	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
4434	17020	29460	3.52	1.0E-63	F08485.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4434	17020	29461	3.52	1.0E-63	F08485.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
5555	18187	30602	1.32	1.0E-63	A1271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
5943	18563	31293	1.38	1.0E-63	AW582266.1	EST_HUMAN	QVO-S10215-060100-083-b09 ST0215 Homo sapiens cDNA
8408	20948		2.21	1.0E-63	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12581	24970		17.03	1.0E-63	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6122	18737	31489	1.06	9.0E-64	AW401433.1	EST_HUMAN	UIHF-BKO-aad-b-09-0-UI.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3053153 5'
7808	20351	33259	4.35	9.0E-64	A1478186.1	EST_HUMAN	hm50b07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161525 3'
1084	13889		13.09	8.0E-64	BE280796.1	EST_HUMAN	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
6289	18997	31688	3.17	8.0E-64	BE885755.1	EST_HUMAN	601508988F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910338 5'
11894	24108		1.48	8.0E-64	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
11752	24148		3.56	8.0E-64	T60651.1	EST_HUMAN	y598802.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:79179 5'
3592	16186		0.84	7.0E-64	BE394321.1	EST_HUMAN	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4838	17418	29868	2.85	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
4838	17418	29869	2.85	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
7766	20274	33172	0.68	7.0E-64	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
8946	22441	35418	4.54	7.0E-64	Y07848.1	NT	Homo sapiens EWS, gar22, rrp22 and bam22 genes
1760	14350	26894	2.4	5.0E-64	A1851992.1	EST_HUMAN	wb51e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1760	14350	26895	2.4	5.0E-64	A1851992.1	EST_HUMAN	wb51e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3156	15770	28236	4.46	6.0E-64	AW026445.1	EST_HUMAN	wt13e03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529436 3'
3156	15770	28237	4.46	6.0E-64	AW026445.1	EST_HUMAN	wt13e03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529436 3'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5805	18430	31149	3.71	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5805	18430	31150	3.71	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5923	18447	31169	5.6	6.0E-64	NT13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
7286	19814	32870	2.45	6.0E-64	11525879	NT	Homo sapiens mesenchyme homoeo box 1 (MEOX1), mRNA
7286	19814	32871	2.45	6.0E-64	11525879	NT	Homo sapiens mesenchyme homoeo box 1 (MEOX1), mRNA
8250	21778	34727	8.24	6.0E-64	11420555	NT	Homo sapiens acetyl-CoA synthetase (LOC55902), mRNA
8425	21834	34883	2	6.0E-64	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
9634	22134	35099	2.23	6.0E-64	S76475.1	NT	trkC [human, brain, mRNA, 2715 nt]
10849	23181	36184	7.87	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
10849	23181	36195	7.87	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
10896	15770	28238	1.84	6.0E-64	AW026445.1	EST_HUMAN	w13e03 x1 NCI_CGAP_Bn23 Homo sapiens cDNA clone IMAGE:2528436 3'
10898	15770	28237	1.64	6.0E-64	AW026445.1	EST_HUMAN	w13e03 x1 NCI_CGAP_Bn23 Homo sapiens cDNA clone IMAGE:2528436 3'
11903	24242	31008	2.45	6.0E-64	11528198	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
853	13469	25979	3.09	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
853	13469	25980	3.09	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1393	13977	26504	0.95	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1467	14059	26593	2.55	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1467	14059	26594	2.55	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1749	14339	26886	1.52	5.0E-64	U89358.1	NT	Human I(3)mbt protein homolog mRNA, complete cds
2853	14120	26657	3.5	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2853	14120	26658	3.5	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
4032	16630	28099	7.79	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
4181	16771	29220	0.68	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
10692	23222	36235	3.91	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
10692	23222	36236	3.91	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
2239	14814	27386	3.14	3.0E-64	C18895.1	EST_HUMAN	C18895 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-569E02 5'
3293	15904	28384	0.78	3.0E-64	BE794381.1	EST_HUMAN	601589565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
3491	16096	28570	2.57	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
3491	16096	28571	2.57	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
6232	18841	31613	1.53	3.0E-64	Z6273.1	NT	H. sapiens isoform 1 gene for L-type calcium channel, exon 28
6619	19216	32021	3.11	3.0E-64	BF370000.1	EST_HUMAN	RC6-FN0019-280600-011-G11 FN0019 Homo sapiens cDNA
8402	20942	33864	1.83	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8402	20942	33865	1.83	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8432	20972	33885	4.49	3.0E-64	BE206521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb.L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
8432	20972	33886	4.49	3.0E-64	BE206521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb.L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
9348	21862	34810	1.23	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9348	21862	34811	1.23	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9433	21959	34907	0.72	3.0E-64	AW977384.1	EST_HUMAN	EST389493 MAGe resequences, MAGO Homo sapiens cDNA
9433	21959	34908	0.72	3.0E-64	AW977384.1	EST_HUMAN	EST389493 MAGe resequences, MAGO Homo sapiens cDNA
11118	23627	36669	1.83	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11118	23627	36670	1.83	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11539	23987	37058	4.89	3.0E-64	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1127	13730	26241	1.26	2.0E-64	AA606940.1	EST_HUMAN	af094008.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031151 3'
1441	14034	26562	8.3	2.0E-64	475770.1	NT	Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA
2566	15130		1.88	2.0E-64	AI927030.1	EST_HUMAN	wo87b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element
2570	15133	27702	1.25	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2570	15133	27703	1.25	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3174	15787	28259	1.17	2.0E-64	4504068	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2); nuclear gene encoding mitochondrial protein, mRNA
3855	18453	28916	0.63	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGe resequences, MAGe Homo sapiens cDNA
3855	18453	28917	0.63	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGe resequences, MAGe Homo sapiens cDNA
6157	18770	31534	2.28	2.0E-64	AU124387.1	EST_HUMAN	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5'
6389	18992	31772	1.52	2.0E-64	AF113708.1	NT	Homo sapiens angioopoietin 4 (ANG4) mRNA, partial cds
6611	19208	32016	4.45	2.0E-64	BF668537.1	EST_HUMAN	60212347F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280395 5'
6708	19301	32105	1.38	2.0E-64	AI078387.1	EST_HUMAN	oz29b03.x1 Soares_talal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1678717 3'
6802	18393	32209	53.03	2.0E-64	M77185.1	NT	H1.sapiens dopamine receptor D5 pseudogene 1, partial cds
8603	21142	34055	1.98	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA
8603	21142	34056	1.98	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA
9157	21692	34636	1.14	2.0E-64	AU132570.1	EST_HUMAN	AU132570 NT2RP4 Homo sapiens cDNA clone NT2RP4000109 5'
9889	22386	35364	0.48	2.0E-64	T06397.1	EST_HUMAN	EST042868 Feal brain, Stralagene (cat8938206) Homo sapiens cDNA clone HFBDS88
9889	22386	35365	0.48	2.0E-64	T06397.1	EST_HUMAN	EST042868 Feal brain, Stralagene (cat8938206) Homo sapiens cDNA clone HFBDS88
10643	23175	36187	2.38	2.0E-64	BF528114.1	EST_HUMAN	602042882F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4180556 5'
10929	23447	36468	5.36	2.0E-64	AI922911.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452211 3'
10929	23447	36469	5.36	2.0E-64	AI922911.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452211 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11112	23622	36663	1.79	2.0E-64	AW864773.1	EST_HUMAN	PM2-SN0018-220300-002-e12 SN0018 Homo sapiens cDNA
11828	24194	31034	1.5	2.0E-64	8567397	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
12285	24487		2.44	2.0E-64	H55162.1	EST_HUMAN	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
279	12936	25421	1.64	1.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1815	14405	26949	9.93	1.0E-64	AI929419.1	EST_HUMAN	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gbl21696 cds1 PROTHYMOSIN ALPHA (HUMAN); contains element MSR1 repetitive element ;
3045	15661	28142	0.62	1.0E-64	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
3561	16165	28648	5.94	1.0E-64	AF196779.1	NT	Homo sapiens transcription factor 1GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
3644	16247	28722	1.14	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3844	16247	28723	1.14	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3968	16566	29035	0.67	1.0E-64	8922828	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
8976	22471	35454	0.84	1.0E-64	AA042975.1	EST_HUMAN	zk53108.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486567 3'
11798	24178		1.37	1.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2316	14897	27462	1.02	9.0E-65	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2315	14887	27463	1.02	9.0E-65	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
11410	23661		35.61	9.0E-65	BF330676.1	EST_HUMAN	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
11383	23835	36897	14.63	8.0E-65	AI929244.1	EST_HUMAN	au58h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to SW:RL21_HUMAN P46778 60S RIBOSOMAL PROTEIN L21. ;
10059	22554	35550	2.06	7.0E-65	BE081653.1	EST_HUMAN	QV2-BT0635-240400-162-c02 BT0635 Homo sapiens cDNA
1094	13699	26209	1.68	6.0E-65	AV721898.1	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTBBZC06 5'
1998	14550		5.21	6.0E-65	AA550829.1	EST_HUMAN	nj86410.s1 NCI CGAP P111 Homo sapiens cDNA clone IMAGE:999379 similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);
8681	21220	34140	2.24	6.0E-65	AW083252.1	EST_HUMAN	xc07b09.x1 NCI CGAP_Co21 Homo sapiens cDNA clone IMAGE:2583545 3' similar to TR:Q63306 Q63306 LONG INTERSPERSED REPEITIVE DNA CONTAINING 7 ORF'S ; contains L1.b2 L1 repetitive element ;
8941	21479	34400	4.18	6.0E-65	AA427878.1	EST_HUMAN	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
8941	21479	34401	4.18	6.0E-65	AA427878.1	EST_HUMAN	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
9004	21541	34471	1.04	6.0E-65	A1085314.1	EST_HUMAN	qf18h05.x1 NCI CGAP_Bin25 Homo sapiens cDNA clone IMAGE:1750425 3'
9004	21541	34472	1.04	6.0E-65	A1085314.1	EST_HUMAN	qf18h05.x1 NCI CGAP_Bin25 Homo sapiens cDNA clone IMAGE:1750425 3'
10752	23276	36289	12.35	6.0E-65	BE567816.1	EST_HUMAN	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:368267 5'
11135	23643	36683	1.73	6.0E-65	AW206752.1	EST_HUMAN	UI-H-B1-efq-d-10-0-UJ.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722626 3'
11369	23821	36683	4.4	6.0E-65	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
659	13282	25762	0.75	5.0E-65	AF084604.1	NT	Homo sapiens KE03 protein mRNA, partial cds
1397	13991	26518	1.8	5.0E-65	7661961	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1397	13991	26519	1.8	5.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2200	14776	27349	0.87	5.0E-65	AB033768.1	NT	Homo sapiens hPAD-cclony10 mRNA for peptidylarginine deaminase type I, complete cds
3294	15905	28385	2.39	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3294	15905	28386	2.39	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
10384	22858	35850	0.99	5.0E-65	AF006668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
207	12868	25354	2.15	4.0E-65	AL120419.1	EST_HUMAN	DKFZp781G108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781G108 5'
775	13394	25894	1.3	4.0E-65	AI268488.1	EST_HUMAN	qm46e01.x1 Soares_placenta_81c9weeks_2NbHP81c9W Homo sapiens cDNA clone IMAGE:1891800 3'
775	13394	25895	1.3	4.0E-65	AI268488.1	EST_HUMAN	qm46e01.x1 Soares_placenta_81c9weeks_2NbHP81c9W Homo sapiens cDNA clone IMAGE:1891800 3'
1117	13720	26232	1.52	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1533	14125	26662	17.23	4.0E-65	4506638	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
2374	14944	27518	1.14	4.0E-65	BE221469.1	EST_HUMAN	hu25604.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
2374	14944	27517	1.14	4.0E-65	BE221469.1	EST_HUMAN	hu25604.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
6303	18910	31682	4.44	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6303	18910	31683	4.44	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
7171	19703	32550	0.85	4.0E-65	M19879.1	NT	Human clabidin 27 gene, exons 10 and 11, and L1 and Alu repeats
7271	19789	32658	2.39	4.0E-65	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7783	20326	33230	0.81	4.0E-65	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
7783	20326	33231	0.81	4.0E-65	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
9072	21609	34539	0.8	4.0E-65	11429127	NT	Homo sapiens Janus Kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10473	22967		2.55	4.0E-65	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
10833	23354	36369	1.93	4.0E-65	AV738764.1	EST_HUMAN	AV738764 CB Homo sapiens cDNA clone CBCBE05 5'
10877	23492	36522	3.39	4.0E-65	AF119846.1	NT	Homo sapiens PRO1474 mRNA, complete cds
12124	13720	28232	1.41	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
101	12778	25261	2.51	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
102	12778	25261	2.35	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1275	15393		11.57	3.0E-65	X78932.1	NT	H sapiens HZF9 mRNA for zinc finger protein
1505	14187	26729	0.98	3.0E-65	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1861	14449	27007	1	3.0E-65	AI000992.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838173 3' similar to contains element MSR1 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3019	15635	28111	0.8	3.0E-65	D87078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
3315	15925	28403	0.96	3.0E-65	4504950	NT	Homo sapiens laminin, beta 1 (LAMB1), mRNA
3784	16384	28849	1.19	3.0E-65	AI000892.1	EST_HUMAN	ov23103.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element;
4754	17335	29779	1.36	3.0E-65	6912385	NT	Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
9881	22476	35458	1.44	3.0E-65	BE787396.1	EST_HUMAN	601479886F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882405 5'
11287	23005	36013	13.23	3.0E-65	AA430006.1	EST_HUMAN	zw65a06.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781042 5'
3451	16058	28534	5.71	2.0E-65	BF680294.1	EST_HUMAN	60215502F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295986 5'
6957	19253		5.63	2.0E-65	BE263373.1	EST_HUMAN	601190983F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534741 5'
7186	19718	32565	25.57	2.0E-65	BF576922.1	EST_HUMAN	602134359F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289295 5'
8778	21318	34241	1.21	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ000056 protein, partial cds
8779	21318	34242	1.21	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ000056 protein, partial cds
11750	24147		6.58	2.0E-65	AA307804.1	EST_HUMAN	EST176755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' and similar to endogenous retrovirus
12241	24832		2.26	2.0E-65	BF246036.1	EST_HUMAN	601854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073769 5'
94	12770		0.76	1.0E-65	BF125544.1	EST_HUMAN	601763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5'
564	13195	25974	1.4	1.0E-65	7857495	NT	Homo sapiens putative Rab5 GTP/GTP exchange factor homologue (RABEX5), mRNA
2084	14865	27236	0.95	1.0E-65	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
3419	16027	28508	0.94	1.0E-65	BE466681.1	EST_HUMAN	h224e09.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:3208888 3'
4070	16668	29127	1.85	1.0E-65	4504082	NT	Homo sapiens glycican 4 (GPC4) mRNA
4070	16668	29128	1.85	1.0E-65	4504082	NT	Homo sapiens glycican 4 (GPC4) mRNA
4285	16871	29317	2.39	1.0E-65	AW029340.1	EST_HUMAN	wx09c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
4285	16871	29318	2.39	1.0E-65	AW029340.1	EST_HUMAN	wx09c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
5968	18295	30775	0.74	1.0E-65	AI243738.1	EST_HUMAN	qh88h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854109 3' similar to TR:Q07823
8196	20737	33648	4.11	1.0E-65	AW820481.1	EST_HUMAN	Q07823 MAC30 PROTEIN;
8196	20737	33649	4.11	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042-F12 ST0298 Homo sapiens cDNA
8222	20763	33679	0.56	1.0E-65	BE732118.1	EST_HUMAN	QV2-ST0298-140200-042-F12 ST0298 Homo sapiens cDNA
8222	20763	33680	0.56	1.0E-65	BE732118.1	EST_HUMAN	601566124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8261	20802	33719	2.05	1.0E-65	AI141293.1	EST_HUMAN	601566124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8261	20802	33720	2.05	1.0E-65	AI141293.1	EST_HUMAN	AU141285 THYRO1 Homo sapiens cDNA clone THYRO1000356 5'
8774	21313	34235	2.42	1.0E-65	BF698707.1	EST_HUMAN	AU141285 THYRO1 Homo sapiens cDNA clone THYRO1000356 5'
8950	21488	34410	2.86	1.0E-65	AI129040.1	EST_HUMAN	602126239F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4283313 5'
							AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8950	21488	34411	2.86	1.0E-65	AU128040.1	EST_HUMAN	AU128040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
8981	21499		2.54	1.0E-65	11431894	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
9398	21821	34770	5.09	1.0E-65	AI191716.1	EST_HUMAN	qd56a02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733450 3' similar to gb:M29581 ZINC FINGER PROTEIN 8 (HUMAN); contains MER19 t1 MER19 repetitive element;
9800	22298	35283	1.39	1.0E-65	AU153783.1	EST_HUMAN	AU153783 NT2RP3 Homo sapiens cDNA clone NT2RP3004016 3'
10203	22698	35692	0.65	1.0E-65	AA069559.1	EST_HUMAN	z75a04.t1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:382734 5'
10463	22957	35988	1.12	1.0E-65	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
10529	23088	36078	3.58	1.0E-65	M26167.1	NT	Human platelet factor 4 variation 1 (PF4var1) gene, complete cds
10656	23188	36204	22.3	1.0E-65	4506660	NT	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
11010	23524	36558	2.79	1.0E-65	BF688707.1	EST_HUMAN	602128239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'
11098	23600	36838	2.25	1.0E-65	AI621017.1	EST_HUMAN	ts78a08.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2237170 3' similar to gb:L15533_rna1 PANCRAITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);
11799	24179	31005	2.28	1.0E-65	11418041	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
11896	24238	31005	5.17	1.0E-65	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
75	12753	25232	4.57	9.0E-68	AL160311.1	NT	Novel human gene mapping to chromosome 22
75	12753	25233	4.57	9.0E-68	AL160311.1	NT	Novel human gene mapping to chromosome 22
1398	13992	26520	1.54	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1398	13992	26521	1.54	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1531	14123		4.45	9.0E-68	M87299.1	NT	Human transposon-like element, partial
4802	17390	29830	0.57	9.0E-68	AL137163.1	NT	Novel human gene mapping to chromosome X
4801	17379	29829	0.68	9.0E-68	AA424304.1	EST_HUMAN	zn90c05.r1 Soares_NHMRu_ST Homo sapiens cDNA clone IMAGE:787048 5'
11225	23756		1.78	7.0E-68	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
4455	17041	29483	1.11	6.0E-68	AI924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595;
4455	17041	29484	1.11	6.0E-68	AI924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595;
4455	17041	29485	1.11	6.0E-68	AI924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595;
8373	20913		0.48	6.0E-68	BE178563.1	EST_HUMAN	PM2-HT0604-030300-001-b08 HT0604 Homo sapiens cDNA
11038	23532	36587	7.01	6.0E-68	X69181.1	NT	H. sapiens mRNA for ribosomal protein L31
1411	14004	26532	1.25	5.0E-66	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
5278	17840	30266	0.57	5.0E-68	BE886844.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
5278	17840	30267	0.57	5.0E-68	BE886844.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
9218	21735	34877	14.1	5.0E-68	11420557	NT	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
823	13440	25947	1.13	4.0E-66	6879816	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
1771	14361	28906	0.87	4.0E-66	AW887798.1	EST_HUMAN	RC1-NN0063-100500-022-a02 NN0063 Homo sapiens cDNA
2319	14891	27468	1.64	4.0E-66	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2513	15077		2.35	4.0E-66	AJ223364.1	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
4898	17473		6.76	4.0E-66	9635487	NT	Human endogenous retrovirus, complete genome
5739	18365	31072	3.33	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methylenetetrahydrofolate cyclohydrolase (MTHFD2), mRNA
5918	18540	31268	0.9	4.0E-66	AW939119.1	EST_HUMAN	QV1-DT0069-110200-067-g10 DT0069 Homo sapiens cDNA
6940	18048	30470	4.62	4.0E-66	AW865473.1	EST_HUMAN	EST377546 IMAGE resequences, MAGI Homo sapiens cDNA
7185	19717	32564	7.41	4.0E-66	U78168.1	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
7625	18365	31072	1.05	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methylenetetrahydrofolate cyclohydrolase (MTHFD2), mRNA
8022	20564	33466	6.44	4.0E-66	11421838	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
8076	20618	33532	0.98	4.0E-66	X57147.1	NT	Human endogenous retrovirus PHE.1 (ERV9)
1473	14065	26801	11.5	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1473	14065	26602	11.5	3.0E-66	4502098	NT	(SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
2026	14608	27173	1	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares multiple sclerosis 2NBHMSP Homo sapiens cDNA clone IMAGE:284328 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1H2B.2. [2] PIR:B56612;
2026	14608	27174	1	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares multiple sclerosis 2NBHMSP Homo sapiens cDNA clone IMAGE:284328 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1H2B.2. [2] PIR:B56612;
2026	14608	27175	1	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares multiple sclerosis 2NBHMSP Homo sapiens cDNA clone IMAGE:284328 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1H2B.2. [2] PIR:B56612;
2732	15287	27854	3.43	3.0E-66	11141880	NT	Homo sapiens TGF(beta)-induced transcription factor 2 (TGIF2), mRNA
3151	15765	28232	6.89	3.0E-66	7662223	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
5658	18285	30783	0.9	3.0E-66	AB020699.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5948	18568	31296	2.07	3.0E-66	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
5948	18568	31297	2.07	3.0E-66	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
9444	21970	34919	0.59	3.0E-66	AK024453.1	NT	Homo sapiens mRNA for FLJ00045 protein, partial cds
9835	22135	35100	0.89	3.0E-66	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9985	22480	35464	0.8	3.0E-66	7019480	NT	Homo sapiens protocadherin beta 1 (PCDH-beta1), mRNA
10415	22909	35908	0.92	3.0E-66	AF155659.1	NT	Homo sapiens molybdenum cofactor biosynthesis protein E (MCBPE) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11384	23836	36898	9.34	3.0E-66	5453948	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
55	12735	25203	1.34	2.0E-66	7657334	NT	Homo sapiens Mitshapen/NIK-related kinase (MINK), mRNA
55	12735	25204	1.34	2.0E-66	7657334	NT	Homo sapiens Mitshapen/NIK-related kinase (MINK), mRNA
447	12876	25132	1.21	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
447	12876	25133	1.21	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
1866	14452	27011	1.73	2.0E-66	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
3002	15618	28096	1.55	2.0E-66	X68859.1	NT	H. sapiens pseudogene for the low affinity IL-8 receptor
3372	16176	28658	0.97	2.0E-66	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3828	16428	28889	0.72	2.0E-66	AL117233.1	NT	Novel human gene mapping to chromosome 1
4139	16731	28184	0.57	2.0E-66	AF108388.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
4760	17341	28788	16.35	2.0E-66	A1133287.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
4760	17341	28789	16.35	2.0E-66	A1133287.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
5982	18602	31336	0.8	2.0E-66	AW968854.1	EST_HUMAN	EST380930 MAGe resequences, MAGJ Homo sapiens cDNA
5982	18602	31337	0.8	2.0E-66	AW968854.1	EST_HUMAN	EST380930 MAGe resequences, MAGJ Homo sapiens cDNA
8781	21320	34244	2.24	2.0E-66	N45480.1	EST_HUMAN	yy69c02.r1 Soares_multiple_sclerosis_2NbHMSF Homo sapiens cDNA clone IMAGE:277826 5'
12132	25057		1.8	2.0E-66	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
2919	15536	28010	1.65	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
2919	15536	28011	1.65	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4474	15536	28010	3.57	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4474	15536	28011	3.57	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
5583	18214	30683	5.49	1.0E-66	BF673088.1	EST_HUMAN	60216296F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294151 5'
5952	18574	31307	0.68	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-118-E04 NT0101 Homo sapiens cDNA
5952	18574	31308	0.68	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-118-E04 NT0101 Homo sapiens cDNA
7018	19516	32338	0.95	1.0E-66	BF328623.1	EST_HUMAN	RC5-BN0193-010900-034-G06 BN0193 Homo sapiens cDNA
8395	20935	33857	1.6	1.0E-66	AA666858.1	EST_HUMAN	aa80604.st NCI CGAP GCBT Homo sapiens cDNA clone IMAGE:827282 3'
9347	21861	34809	0.74	1.0E-66	AA018828.1	EST_HUMAN	2657612.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363118 5'
10273	22768	35756	0.75	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10273	22768	35757	0.75	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10509	23003	36011	0.51	1.0E-66	BE044595.1	EST_HUMAN	hcd4702.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040563 3'
10821	23342	36357	1.96	1.0E-66	AF111187.2	NT	Homo sapiens jun dimerization protein gene, partial cds, cDNA, complete cds, and unknown gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11901	24240		3	8.0E-67	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
403	13078	25570	3.59	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb.M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1425	14018	26547	1.75	7.0E-67	AA383416.1	EST_HUMAN	EST66812 Testis 1 Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid ZK353
1601	14193	26724	1.25	7.0E-67	W85947.1	EST_HUMAN	zh56b03.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1601	14193	26725	1.25	7.0E-67	W85947.1	EST_HUMAN	zh56b03.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
2836	13078	25570	3.15	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb.M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
6231	18840	31612	0.98	7.0E-67	10190695	NT	Homo sapiens zinc finger protein 304 (ZNF304), mRNA
6416	18019	31802	1.79	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6416	18019	31803	1.79	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6823	19413	32230	1.03	7.0E-67	4855084	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP6N1A), mRNA
7627	20139	33018	0.99	7.0E-67	11418212	NT	Homo sapiens mitochondrial carrier family protein (LOC555972), mRNA
7627	20139	33019	0.99	7.0E-67	11418212	NT	Homo sapiens mitochondrial carrier family protein (LOC555972), mRNA
8012	20564	33457	0.49	7.0E-67	4826895	NT	Homo sapiens phosphodiesterase 1/nucleotide pyrophosphatase 3 (PDNPP3), mRNA
8285	20808	33724	0.8	7.0E-67	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2), mRNA
8862	21401	34326	0.78	7.0E-67	10835044	NT	Homo sapiens retinaldehyde dehydrogenase 2 (RALDH2), mRNA
11625	23973	37043	2.92	7.0E-67	U82486.1	NT	Human cytochrome oxidase subunit VIa (COX6A1P) pseudogene, complete cds
11675	24094	37147	2.95	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
11675	24094	37148	2.95	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12159	24399	30978	1.44	7.0E-67	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
585	13215	25892	1.84	6.0E-67	X89668.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
828	13445	25952	1.64	6.0E-67	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
1316	13910	26430	1.2	6.0E-67	Y14320.1	NT	Homo sapiens PMP69 gene, exons 3, 4, 5, 6 & 7
3485	16090	28562	1.47	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3485	16090	28563	1.47	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4205	16784	29240	0.74	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4205	16784	29241	0.74	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4815	17393	29845	3.86	6.0E-67	7637020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4815	17393	29846	3.86	6.0E-67	7637020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
3258	15870	28350	2.65	5.0E-67	AF009690.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
10863	23384		1.9	5.0E-67	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1373	13987	26494	1.16	4.0E-67	R90819.1	EST_HUMAN	Yn02d11.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:167253 5'
7964	20506	33413	0.68	4.0E-67	A1733032.1	EST_HUMAN	Q26c05.x3 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1493288 3' similar to SW:Z33A_HUMAN
8322	20863		1.3	4.0E-67	BF357321.1	EST_HUMAN	Q06730 ZINC FINGER PROTEIN 33A ; RCO-HT0934-150900-028-c03 HT0934 Homo sapiens cDNA
10842	23458		1.92	4.0E-67	AA714294.1	EST_HUMAN	hw08a01.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238472 3' similar to TR:O10385 O10385
2839	13284	25765	5.7	3.0E-67	AA333768.1	EST_HUMAN	PRO-POL-DUTPASE POLYPROTEIN ;
4804	17382	29832	3.38	3.0E-67	AW869159.1	EST_HUMAN	EST37803 Embryo, 9 week Homo sapiens cDNA 5' and
4831	17409		0.93	3.0E-67	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
8122	20663	33573	1.17	3.0E-67	BF196068.1	EST_HUMAN	hr81f05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
11139	23647		22.61	3.0E-67	AA927874.1	EST_HUMAN	Q61085 GTP-RHO BINDING PROTEIN 1 ; om18b07.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541365 3'
201	12862	25346	1.74	2.0E-67	BE348354.1	EST_HUMAN	hw18g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP:F23H11.9
878	13492	28010	4.98	2.0E-67	AW816405.1	EST_HUMAN	CE09617 ;
1144	13747		1.84	2.0E-67	AF167460.1	NT	QV4-ST0234-181199-037-405 ST0234 Homo sapiens cDNA
1928	14512	27069	1.5	2.0E-67	BE303037.1	EST_HUMAN	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4
1928	14512	27070	1.5	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:O94892 O94892
2428	14985	27570	2.84	2.0E-67	AF309561.1	NT	KIAA0798 PROTEIN. ;
2475	15042	27610	0.95	2.0E-67	4758795	NT	Homo sapiens KRAB zinc finger protein ZFQR mRNA, complete cds
3514	16119	28569	4.48	2.0E-67	AA825755.1	EST_HUMAN	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
4074	16670	29131	2.76	2.0E-67	AL163300.2	NT	zu81g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
6222	18831	31605	0.83	2.0E-67	AL049784.1	NT	Homo sapiens chromosome 21 segment HS21C100
8273	18881	31649	5.18	2.0E-67	BF240758.1	EST_HUMAN	Novel human gene mapping to chromosome 13
6438	19040	31627	2.25	2.0E-67	AB051763.1	NT	601875351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 5'
6438	19040	31628	2.25	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
8493	21032	33952	0.98	2.0E-67	AA334609.1	EST_HUMAN	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
8493	21032	33953	0.98	2.0E-67	AA334609.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to cerebellin
8927	21465	34381	1.09	2.0E-67	AW602635.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to cerebellin
8927	21465	34382	1.08	2.0E-67	AW602635.1	EST_HUMAN	RC4-BT0568-170100-011-c07 BT0568 Homo sapiens cDNA
9486	21943	34890	1.24	2.0E-67	AV731333.1	EST_HUMAN	RC4-BT0568-170100-011-c07 BT0568 Homo sapiens cDNA
9625	22125	35089	1.19	2.0E-67	AW296624.1	EST_HUMAN	AV731333 HTF Homo sapiens cDNA clone HTFARD03 5'
							UI-H-B12-ahn-0-10-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727283 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10781	23305	36313	1.57	2.0E-67	BF685788.1	EST_HUMAN	602140470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301705 5'
10934	25127		3.62	2.0E-67	11438448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
11107	23617	36859	1.85	2.0E-67	BE285714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
11330	23028	36037	2.01	2.0E-67	BF377169.1	EST_HUMAN	PM2-TN0103-040900-001-c02 TN0103 Homo sapiens cDNA
12034	24911	30714	2.53	2.0E-67	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12347	24528	30925	2.26	2.0E-67	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
274	12931	25418	3.31	1.0E-67	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
737	13357	25851	1.2	1.0E-67	AA702784.1	EST_HUMAN	z19b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
2220	14795	27388	1.73	8.0E-68	BE970732.1	EST_HUMAN	601448558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
3937	16535	29001	5.37	8.0E-68	AA209456.1	EST_HUMAN	zq82h10.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN ;
3937	16535	28002	5.37	8.0E-68	AA209456.1	EST_HUMAN	zq82h10.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN ;
8045	20587	33493	0.53	7.0E-68	AB10505.1	EST_HUMAN	wb99e03.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2312860 3'
10349	22840	35836	2.53	6.0E-68	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
12349	24530		3.32	6.0E-68	BE612554.1	EST_HUMAN	601452067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
835	15389	25960	0.67	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
835	15389	25961	0.67	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
852	13468	25977	4.54	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
852	13468	25978	4.54	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
2808	15360	27827	72.53	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3181	15794	28266	3.22	5.0E-68	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4260	16846		0.63	5.0E-68	4826987	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
4590	17173	29618	1.21	5.0E-68	AL157645.1	EST_HUMAN	DKFZp547D207_r1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D207 5'
5111	17683		8.92	4.0E-68	P04406	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
6118	18734	31487	0.76	4.0E-68	AF157063.1	NT	Homo sapiens sedlin (SEDL) gene, exon 4
6870	19604	32437	6.01	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
6870	19604	32438	6.01	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
7674	20185	33073	0.92	4.0E-68	7681683	NT	Homo sapiens DKFZP586L0724 protein (DKFZP586L0724), mRNA
8970	21608	34429	5.04	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
8970	21508	34430	5.04	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9106	21642	34582	2.9	4.0E-68	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
10882	23403	38420	5.14	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10882	23403	36421	5.14	4.0E-68	4508282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
12225	24448	30953	2.91	4.0E-68	11417968	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
3722	18323	28780	2.56	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
9378	20317		8.15	3.0E-68	A1342323.1	EST_HUMAN	qt38h02.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950291 3' similar to contains THR.L2 THR repetitive element ;
10396	22890	35884	1.77	3.0E-68	F28784.1	EST_HUMAN	HSPD18178 HM3 Homo sapiens cDNA clone s3000023D09
12571	24829		2.05	3.0E-68	AW939485.1	EST_HUMAN	QV1-DT0072-010200-056-h06 DT0072 Homo sapiens cDNA
2887	18011		27.71	2.0E-68	D00522.1	NT	Cricetus longicaudatus mRNA for EF-1 alpha, complete cds
4097	16692	29149	0.78	2.0E-68	BE675766.1	EST_HUMAN	711502.x1 NCI_CGAP CLL1 Homo sapiens cDNA clone IMAGE:3294747 3' similar to TR:O80828 O80828 HYPOTHETICAL 88.8 KD PROTEIN ;
4789	17369	29821	1.56	2.0E-68	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
6957	19334		8.86	2.0E-68	R45088.1	EST_HUMAN	y338g04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34898 3'
7123	19463	32280	4.81	2.0E-68	BF035316.1	EST_HUMAN	601458514F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862034 5'
8879	21417	34341	0.84	2.0E-68	Q05859	SWISSPROT	FORMIN 4 (LIMB DEFORMITY PROTEIN)
10494	22888	35986	0.46	2.0E-68	N78493.1	EST_HUMAN	y278c07.r1 Soares multiple sclerosis 2NbrIMSP Homo sapiens cDNA clone IMAGE:289185 5'
11792	25077		2.11	2.0E-68	BE697376.1	EST_HUMAN	601437367F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922192 5'
12839	24714		1.84	2.0E-68	AW018803.1	EST_HUMAN	UI-H-B10-eam-b-05-0-UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709824 3'
83	12759	25242	0.78	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
318	12972	25461	12.22	1.0E-68	AW816405.1	EST_HUMAN	QV4-ST0234-18189-037-05 ST0234 Homo sapiens cDNA
2294	14868	27443	0.89	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2294	14868	27444	0.89	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2785	15338	27809	1.12	1.0E-68	AW451832.1	EST_HUMAN	UI-H-B13-alk-t01-0-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737272 3'
5178	17745	30174	0.68	1.0E-68	AA897343.1	EST_HUMAN	al47g12.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460518 3'
5233	17787	30215	0.88	1.0E-68	BE296032.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'
5525	18157	30572	1.51	1.0E-68	7682349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0968), mRNA
10065	22560	35573	0.49	1.0E-68	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
10732	23258	36274	2.83	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
10732	23258	36275	2.83	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
10763	23307	36314	3.41	1.0E-68	L76416.1	NT	Homo sapiens MIF2 suppressor (HSM13) mRNA, complete cds
11072	23584	36825	1.72	1.0E-68	11433277	NT	Homo sapiens myosin IC (MYO1C), mRNA
11179	23685	36731	2.23	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11179	23685	36732	2.23	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11517	23965	37036	2.1	1.0E-68	11418431	NT	Homo sapiens CGI-78 protein (LOC51632), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11517	23965	37037	2.1	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
12330	12759	25242	2.37	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
12618	24697		1.62	1.0E-68	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
23	12702	25158	13.45	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF), mRNA
23	12702	25159	13.45	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF), mRNA
1065	13670	28180	1.44	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
1065	13670	28181	1.44	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
4208	16787	28245	0.69	9.0E-69	4757867	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF), mRNA
5384	17943	30356	0.9	9.0E-69	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
10769	23293		11.7	9.0E-69	AU117241.1	EST_HUMAN	AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA1000988 5'
3433	16041		1.56	8.0E-69	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
6493	18094	31878	5.18	7.0E-69	9966912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
7804	20347	33254	22.34	6.0E-69	A182764.1	EST_HUMAN	qe2h01.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gb:L11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
7804	20347	33255	22.34	6.0E-69	A182764.1	EST_HUMAN	qe2h01.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gb:L11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
8904	21442	34365	0.98	5.0E-69	AAB26039.1	EST_HUMAN	cd60a03.x1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1372300 3'
546	13177		1.07	4.0E-69	A1873630.1	EST_HUMAN	wm26h11.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437125 3'
5834	24751	31283	1.56	4.0E-69	BE561063.1	EST_HUMAN	601344705F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677641 5'
6009	18629	31364	4.7	4.0E-69	A1784973.1	EST_HUMAN	wh57506.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384819 3' similar to TR:O55137
6739	18333	32139	2.45	4.0E-69	4557732	NT	O55137 ACYL-COA THIOESTERASE. ;
6739	18333	32140	2.45	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2), mRNA
8845	21384	34309	0.99	4.0E-69	AU119634.1	EST_HUMAN	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2), mRNA
12663	24733		2.96	4.0E-69	A187952.1	EST_HUMAN	AU119634 HEMBA1 Homo sapiens cDNA clone HEMBA1006283 5'
409	13084	25577	4.92	3.0E-69	BE258012.1	EST_HUMAN	qe13105.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738881 3'
640	13263	25739	2.24	3.0E-69	AF221712.1	NT	60111037F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3351352 5'
							Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
1602	14194		1.13	3.0E-69	T80514.1	EST_HUMAN	yd08a02.11 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24880 5' similar to SP:A48836
2415	14983		1.34	3.0E-69	5728910	NT	A48836 SPEG II=EGF REPEAT-CONTAINING FIBROPELIN-LIKE PROTEIN - SEA URCHIN ;
4688	17270		0.77	3.0E-69	T98234.1	EST_HUMAN	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1), mRNA
5407	17270		0.81	3.0E-69	T98234.1	EST_HUMAN	ye48h04.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121015 5'
5452	18021	37141	1.37	3.0E-69	11418185	NT	ye48h04.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121015 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6894	19628		0.99	3.0E-68	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3)-deoxyribonucleotidase (dNT-2 gene), exons 1-5
7407	19932	32798	0.87	3.0E-68	AF085703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7449	19973	32840	1.42	3.0E-68	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojuncin (CTNND2) mRNA, partial cds
7554	20073	32949	7.75	3.0E-69	AF268075.1	NT	Homo sapiens TRAF6-binding protein T6BP mRNA, complete cds
8313	20854	33780	0.87	3.0E-69	AW138646.1	EST_HUMAN	UI-H-B11-acw-g-01-Q-UJ.s1 NCJ_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715840 3'
8703	21242		1.8	3.0E-69	AA376399.1	EST_HUMAN	EST88807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
8907	21445	34367	0.5	3.0E-69	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
9334	21848	34797	1.77	3.0E-69	X13223.1	NT	H. sapiens mRNA for N-acetylglucosaminide-(beta 1-4)-galactosyltransferase
9452	21978	34930	8.92	3.0E-69	X06233.1	NT	Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein
9743	22241	35222	0.55	3.0E-69	5730036	NT	Homo sapiens SEC10 (S. cerevisiae)-like 1 (SEC10L1), mRNA
10520	23058	36068	3.93	3.0E-69	11432120	NT	Homo sapiens ribosomal protein S15a (RPS15A), mRNA
10721	23249		12.34	3.0E-69	AA376399.1	EST_HUMAN	EST88807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
11813	24185		3.86	3.0E-69	11419157	NT	Homo sapiens HGC6.2 protein (HGC6.2), mRNA
134	13062	25556	1.07	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
134	13062	25557	1.07	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
429	13062	25558	5.07	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
429	13062	25557	5.07	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
1929	14513	27071	1.46	2.0E-69	BE257857.1	EST_HUMAN	601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5'
2869	15487		2.86	2.0E-69	AA431157.1	EST_HUMAN	zw7192.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781682 5'
8489	21028	33946	0.82	2.0E-69	AA114270.1	EST_HUMAN	zrn29g01.r1 Stralagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:527088 5'
1740	14330	26874	1.89	1.0E-69	AF053788.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
5173	17740		0.58	1.0E-69	BE409094.1	EST_HUMAN	601301284F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635781 5'
6201	18811	31580	0.76	1.0E-69	BE902501.1	EST_HUMAN	601875788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:39585532 5'
6201	18811	31581	0.76	1.0E-69	BE902501.1	EST_HUMAN	601875788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:39585532 5'
6717	19311	32114	4.38	1.0E-69	AW393969.1	EST_HUMAN	QV0-TT0010-031199-045-c07 TT0010 Homo sapiens cDNA
6908	19842	32478	1.4	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6908	19842	32479	1.4	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6924	19583	32412	3.33	1.0E-69	AB032873.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
6924	19583	32413	3.33	1.0E-69	AB032873.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
10077	22572	35566	5.1	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10077	22572	35567	5.1	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10169	22884	35659	1.41	1.0E-69	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
10313	22807	35798	0.47	1.0E-69	BF528429.1	EST_HUMAN	602043782F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4181325 5'
10751	23275		14.22	1.0E-69	4504918	NT	Homo sapiens keratin 8 (KRT8) mRNA
11745	24144	36768	1.61	1.0E-69	BF125887.1	EST_HUMAN	601762902F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025785 5'
12168	24408		4.69	1.0E-69	AI808994.1	EST_HUMAN	wf84e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2380390 3' similar to contains Alu repetitive element; contains element M1R repetitive element;
2370	15484	27513	1.52	8.0E-70	AA230303.1	EST_HUMAN	nc13d12.1f1 NCI_CGAP_Prl1 Homo sapiens cDNA clone IMAGE:1008023
4463	17049	29493	1.81	8.0E-70	L77586.1	NT	Homo sapiens DGS-1 mRNA, 3' end
1849	14437	26963	1.65	7.0E-70	AI497807.1	EST_HUMAN	tm8901.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1849	14437	26964	1.65	7.0E-70	AI497807.1	EST_HUMAN	tm8901.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1974	14558	27115	1.64	7.0E-70	AA282955.1	EST_HUMAN	215h04.1f1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713239 5'
2109	14687		3.14	7.0E-70	5031688	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA
4309	16895	29339	4.83	7.0E-70	4757723	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
5874	18301	30782	5.56	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
5874	18301	30783	5.56	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7004	18502	32321	3.22	7.0E-70	AJ000052.1	NT	Homo sapiens gene encoding splicing factor SF1, exons 2-8
7745	20253	33147	0.67	7.0E-70	11417306	NT	Homo sapiens titin immunoglobulin domain protein (myoblin) (TTID), mRNA
8370	20910	33829	2.67	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8370	20910	33830	2.67	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8656	21195	34114	3.59	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
8656	21195	34115	3.59	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
9084	21620	34555	3.99	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9084	21620	34556	3.99	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9356	20295	33194	3.84	7.0E-70	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
9382	20320	33223	2.01	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
9382	20320	33224	2.01	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
							Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
9575	22075	35038	1.33	7.0E-70	4557624	NT	Homo sapiens NDST4 mRNA for N-deacetylaseN-sulfotransferase 4, complete cds
10199	22694	35686	0.61	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylaseN-sulfotransferase 4, complete cds
10199	22694	35687	0.61	7.0E-70	AB036429.1	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant: spastin) (SPG4), mRNA
10953	23468	36492	1.59	7.0E-70	11429885	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant: spastin) (SPG4), mRNA
10953	23468	36493	1.59	7.0E-70	11429885	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant: spastin) (SPG4), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11468	23918	36986	2.2	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
11468	23918	36987	2.2	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
904	13518	26036	2	6.0E-70	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2182	14758	27328	1.02	6.0E-70	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2551	15115	27885	1.42	6.0E-70	8923689	NT	Homo sapiens CMP-N-acetylneuraminic acid synthase (LOC555907), mRNA
2588	15470	27715	1.68	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2588	15470	27716	1.68	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
11756	24151		3.78	5.0E-70	BE166034.1	EST_HUMAN	MR3-HT0487-150200-115-a06 HT0487 Homo sapiens cDNA
6851	19440	32255	153.56	4.0E-70	T06037.1	EST_HUMAN	EST03928 Fetal brain. Strategene (cat#936206) Homo sapiens cDNA clone HFB0N25
6887	19622	32456	0.79	4.0E-70	AW793226.1	EST_HUMAN	CM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA
6887	19622	32457	0.79	4.0E-70	AW793226.1	EST_HUMAN	CM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA
1633	14225	28756	1.19	3.0E-70	BE071796.1	EST_HUMAN	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
1633	14225	28757	1.19	3.0E-70	BE071796.1	EST_HUMAN	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
6100	18716	31467	0.9	3.0E-70	AI831975.1	EST_HUMAN	W60003.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2388005 3'
6511	19111	31887	2.36	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
6511	19111	31888	2.36	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
41	12720	25181	0.89	2.0E-70	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
718	13339	25826	11.56	2.0E-70	N42161.1	EST_HUMAN	Y07a10.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
718	13339	25827	11.56	2.0E-70	N42161.1	EST_HUMAN	Y07a10.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
734	13354	25850	3.41	2.0E-70	AI246899.1	EST_HUMAN	qx51h01.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1059	13684	26175	1.89	2.0E-70	8923689	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1226	13825	26340	1.29	2.0E-70	7681983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1226	13825	26341	1.29	2.0E-70	7681983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1778	14368	26912	1.48	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2359	14930		4.22	2.0E-70	AA054010.1	EST_HUMAN	ZF49g04.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A
3688	16289	28758	2.21	2.0E-70	H37988.1	EST_HUMAN	P03345 GAG POLYPROTEIN ;
3891	16480	28950	0.8	2.0E-70	AL133207.2	NT	Yp58S04.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:191599 5'
4123	16716	29172	5.05	2.0E-70	M69181.1	NT	Novel human gene mapping to chromosome X Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5706	18332	30836	8.49	2.0E-70	X72662.1	NT	H.sapiens gene for schwannomin (CS8)
5706	18332	30837	8.49	2.0E-70	X72662.1	NT	H.sapiens gene for schwannomin (CS8)
6351	18958	31735	1.22	2.0E-70	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
6745	19338	32144	1.97	2.0E-70	D12625.1	NT	Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds
6773	19365	32176	9.77	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6773	19365	32177	9.77	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
7070	18089	30446	1.94	2.0E-70	11422642	NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminidase alpha 2,3-sialyltransferase) (SIAT6), mRNA
7434	19958	32823	0.84	2.0E-70	AF288207.1	NT	Homo sapiens cysteinyl-RNA synthetase mRNA, complete cds, alternatively spliced
7859	20401	33307	6.42	2.0E-70	M21741.1	NT	Human guanine nucleotide-binding protein alpha-subunit gene (G-s-alpha), exons 4 and 5
8164	20705	33821	0.75	2.0E-70	11423599	NT	Homo sapiens amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), mRNA
8594	21133		0.87	2.0E-70	H47959.1	EST_HUMAN	yo79g02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193682 5'
8096	21632	34571	0.87	2.0E-70	11526355	NT	Homo sapiens dynactin p62 subunit (LOC51164), mRNA
10044	22539	35536	1.3	2.0E-70	AF123303.1	NT	Homo sapiens calcitriol-binding transporter mRNA, partial cds
10490	22884	35992	0.8	2.0E-70	AB033042.1	NT	Homo sapiens mRNA for KIAA1216 protein, partial cds
10950	23465	36487	3.48	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
10950	23465	36488	3.48	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
11497	23946	37016	7.73	2.0E-70	4503520	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (48kD) (EIF3S6) mRNA
12157	24397	30978	2.52	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12157	24397	30977	2.52	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3440	16048		2.73	1.0E-70	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
9204	21721		0.84	1.0E-70	W85795.1	EST_HUMAN	zh55g05.r1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:416024 5'
8714	22212		0.81	1.0E-70	AA442292.1	EST_HUMAN	zv54c03.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757444 5'
10814	23335	36348	15.93	1.0E-70	AV738538.1	EST_HUMAN	AV738538 CB Homo sapiens cDNA clone CBLG810 5'
6099	18715	31465	9.2	9.0E-71	AH143870.1	EST_HUMAN	q604f01.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
6099	18715	31466	9.2	9.0E-71	AH143870.1	EST_HUMAN	q604f01.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
7098	19669	32508	1.82	9.0E-71	A1654903.1	EST_HUMAN	wb52c05.x1 NC1_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
11399	19669	32508	5.11	9.0E-71	A1654903.1	EST_HUMAN	wb52c05.x1 NC1_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9000	21537		3.85	8.0E-71	AA171451.1	EST_HUMAN	zp21d11.r1 Strabagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:610101 5' similar to TR:G1143061 G1143061 STRAIN XA34 POL:
7410	19935	32800	7.39	7.0E-71	AA442230.1	EST_HUMAN	z60h06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:758075 5'
8812	21151	34065	1.34	7.0E-71	AA05457.1	EST_HUMAN	z91a06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462226 3'
11211	23714	36769	5.33	7.0E-71	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2251	14825	27401	7.82	5.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4197	18787	29238	1.17	5.0E-71	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
6041	18860	31399	1.72	5.0E-71	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6768	18361	32170	1.8	5.0E-71	11641408	NT	Homo sapiens keratin, hair, acidic, 7 (KRT47), mRNA
7000	19498	32318	0.8	5.0E-71	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7200	19731	32583	0.97	5.0E-71	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7520	20040	32909	2.64	5.0E-71	M38106.1	NT	Human neurofibromatosis protein type 1 mRNA, 3' end of cds
7693	20202	33089	0.72	5.0E-71	11526445	NT	Homo sapiens MAGUK protein p55T; Protein Associated with Lins 2 (LOC51676), mRNA
7716	20224	33113	20.65	5.0E-71	AF072810.1	NT	Homo sapiens transcription factor WSTF mRNA, complete cds
8460	21000	33916	0.69	5.0E-71	6453777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKKB) mRNA
8460	21000	33917	0.69	5.0E-71	5453777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKKB) mRNA
9825	22323		2.26	5.0E-71	X13467.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)
10513	23051	36062	1.57	5.0E-71	5726900	NT	Homo sapiens IGF-II mRNA-binding protein 3 (KOC1), mRNA
10859	23380	36399	4.63	5.0E-71	11436514	NT	Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP), mRNA
11071	23583	36624	2.24	5.0E-71	11438069	NT	Homo sapiens similar to hypothetical protein FLJ20163 (H. sapiens) (LOC833325), mRNA
11708	24119	37152	1.76	5.0E-71	11417682	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
108	12784	25267	1.08	4.0E-71	4507592	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
372	13021	25508	116.83	4.0E-71	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
372	13021	25507	116.83	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2911	15528	27998	3.25	4.0E-71	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4519	17103	28549	5.18	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
5123	17695	30132	6.54	4.0E-71	7657602	NT	Homo sapiens putative heme-binding protein (SOUL), mRNA
7677	20519		1.23	3.0E-71	AU135734.1	EST_HUMAN	AU135734 PLACE1 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5 repetitive element;
10572	23107	36121	4.09	3.0E-71	AA557683.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C006
1273	13669	26389	6.26	2.0E-71	AL183206.2	NT	Human mRNA for KIAA0272 gene, partial cds
5523	18155	30570	6.94	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
5523	18155	30571	6.94	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10478	22972	35979	2.97	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10478	22972	35980	2.97	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10574	23109	36122	3.75	2.0E-71	BE018477.1	EST_HUMAN	bb31a08.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW:R23B_HUMAN
11454	23904	36871	1.96	2.0E-71	R55826.1	EST_HUMAN	P54727 UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG B ;
11825	24183		10.18	2.0E-71	T95489.1	EST_HUMAN	y177c11.r1 Soares breast 2NblHBst Homo sapiens cDNA clone IMAGE:154772 5'
666	13280	25771	1.4	1.0E-71	A1077927.1	EST_HUMAN	y43e09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120520 5'
977	13589	26104	2.23	1.0E-71	7706281	NT	oy15e03.s1 Soares senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665918 3' similar to contains LOR1.b2 LOR1 repetitive element ;
1139	13742	26251	4.37	1.0E-71	AF205880.1	NT	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
1385	13979	26506	10.24	1.0E-71	AF012872.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
2129	14707	27278	1.38	1.0E-71	AB017007.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
2129	14707	27279	1.38	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2171	15274	27840	3.73	1.0E-71	7657153	NT	Homo sapiens PMS2L16 mRNA, partial cds
3549	16153	28635	1.24	1.0E-71	AF119665.1	NT	Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEYL), mRNA
3658	16259	28730	6.17	1.0E-71	AF246219.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3658	16259	28731	6.17	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3710	16311	28778	0.95	1.0E-71	BE122850.1	EST_HUMAN	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3710	16311	28778	0.95	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3804	16404	28868	2.11	1.0E-71	AF218904.1	NT	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
4569	17152	29598	2.19	1.0E-71	D28478.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 19
4695	17277	29723	0.61	1.0E-71	H23178.1	EST_HUMAN	Human mRNA for KIAA0045 gene, complete cds
6840	19430	32246	1.54	1.0E-71	11426182	NT	ym56h10.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52528 5'
7144	19877	32517	1.33	1.0E-71	AB011131.1	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA
7352	19878	32743	11.94	1.0E-71	U60753.1	NT	Homo sapiens mRNA for KIAA0559 protein, partial cds
8089	20630	33543	0.87	1.0E-71	AF105287.1	NT	Homo sapiens CAGL79 mRNA, partial cds
8110	20651	33559	2.11	1.0E-71	11426430	NT	Homo sapiens glypican-6 (GPC6) mRNA, complete cds
8383	20923	33842	3.93	1.0E-71	8922811	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
8383	20923	33843	3.93	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9155	21680	34634	0.97	1.0E-71	S72393.1	NT	CSNK2A1=casein kinase II (CKII) subunit alpha [human, Genomic, 18862 nt]
9920	22416	35391	7.06	1.0E-71	AY007643.1	NT	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, complete cds
9980	22475		4.9	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
10431	22825	35931	1.57	1.0E-71	11433142	NT	Homo sapiens activated leucocyte cell adhesion molecule (ALCAM), mRNA
10663	23165		6.4	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
10762	23288	36288	2.09	1.0E-71	11418903	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
11025	23539	36574	1.82	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
11025	23539	36575	1.82	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
12208	24432		15.2	1.0E-71	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
432	13065	25559	1.33	9.0E-72	A1857635.1	EST_HUMAN	wk95g03.x1 NC1_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:086705 O86705
432	13065	25560	1.33	9.0E-72	A1857635.1	EST_HUMAN	HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element
6259	18868	31638	0.87	8.0E-72	BF03752.1	EST_HUMAN	HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element
10950	23504	36533	2.04	8.0E-72	11424480	NT	601458747F1 NIH MGC 66 Homo sapiens cDNA clone IMAGE:3862451 5'
10990	23504	36534	2.04	8.0E-72	11424480	NT	Homo sapiens nuclear RNA helicase, DECD variant of DEAD box family (DDXL), mRNA
10990	23504	36535	2.04	8.0E-72	11424480	NT	Homo sapiens nuclear RNA helicase, DECD variant of DEAD box family (DDXL), mRNA
4190	18779	28225	1.48	7.0E-72	4501868	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4190	16778	28226	1.48	7.0E-72	4501868	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4190	16779	28227	1.48	7.0E-72	4501868	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
7178	19710	32558	3.23	7.0E-72	S41694.1	NT	(pseudogene) PTMAP2=prthymosin alpha [human, Genomic, 1192 nt, segment 2 of 3]
12339	24621		1.9	7.0E-72	F26259.1	EST_HUMAN	HSPD13670 HM3 Homo sapiens cDNA clone s400051G02
8324	20865		4.31	8.0E-72	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
67	12746	25223	1.56	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
67	12746	25224	1.56	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
68	12746	25223	10.23	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
68	12746	25224	10.23	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
1178	13780		2.72	5.0E-72	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
7030	19584	32391	1.36	5.0E-72	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8711	21250	34173	3.16	5.0E-72	AW161274.1	EST_HUMAN	au80c03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782564 5' similar to TR:Q99785 Q99785 HYPOTHETICAL 32.4 KD PROTEIN ;contains element MSR1 repetitive element ;
9871	22368	35346	0.62	5.0E-72	AV724632.1	EST_HUMAN	AV724632 HTB Homo sapiens cDNA clone HTBAK801 6'
11122	23630	36672	3.44	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-005 BT0598 Homo sapiens cDNA
11122	23630	36673	3.44	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-005 BT0598 Homo sapiens cDNA
11500	23949	37018	1.62	5.0E-72	BE208545.1	EST_HUMAN	ba08g08.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823806 5'
11500	23949	37019	1.62	5.0E-72	BE208545.1	EST_HUMAN	ba08g08.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823806 5'
11895	25047		2.89	5.0E-72	BE928645.1	EST_HUMAN	QV1-BT0632-280800-342-010 BT0632 Homo sapiens cDNA
4948	17523		1.21	4.0E-72	11034844	NT	Homo sapiens hypothetical protein dJ1057820.2 (DJ1057820.2), mRNA
5422	17978	30387	1.05	4.0E-72	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
5656	18283	30761	0.72	4.0E-72	AF170025.1	NT	Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternatively spliced, complete cds
6874	19270	32075	0.81	4.0E-72	T87947.1	EST_HUMAN	y483a01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP:A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
7439	19863	32829	3.01	4.0E-72	5729887	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
9699	22198	35171	1.64	4.0E-72	8923669	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
10318	22812	35807	0.98	4.0E-72	AJ248798.1	EST_HUMAN	qh87c02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849730 3' similar to TR:Q14498 Q14498 SPLICING FACTOR. [1] ;contains Alu repetitive element;contains element L1 repetitive element ;
11402	23853	36918	7.8	4.0E-72	H79421.1	EST_HUMAN	y428a03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:235084 5'
11528	23976	37046	2.48	4.0E-72	T81910.1	EST_HUMAN	y28a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109649 3'
12263	24473	30833	4.5	4.0E-72	AJ277548.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
22	12701	25157	3.55	3.0E-72	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
936	13549		1.46	3.0E-72	AA723823.1	EST_HUMAN	ah63a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1310290 3'
1196	13797	26307	7.76	3.0E-72	U16308.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1196	13797	26308	7.76	3.0E-72	U16308.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1235	13834	26348	1.33	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1235	13834	26349	1.33	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1567	14159	26690	0.88	3.0E-72	BE242161.1	EST_HUMAN	TCAAAP1E1252 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAAP1252
3110	15725	28196	13.29	3.0E-72	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3317	15927	28404	2.84	3.0E-72	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3895	18494	28955	2.71	3.0E-72	577589.1	NT	TCR V delta 2-C alpha = T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
4509	17083	28540	0.94	3.0E-72	AF143892.1	NT	[human, precursor B-cell line REH, mRNA Partial, 211 nt]
4509	17083	28541	0.94	3.0E-72	AF143892.1	NT	Homo sapiens thioredoxin-like protein (TXNL), gene, exon 3
4643	17225	28678	2.89	3.0E-72	11416198	NT	Homo sapiens thioredoxin-like protein (TXNL), gene, exon 3
5711	18337		1.07	3.0E-72	4758083	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
6134	18748	31504	1.88	3.0E-72	AF073387.1	NT	Homo sapiens semaphorin W (SEMAW) mRNA
6134	18748	31505	1.98	3.0E-72	AF073387.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10), gene, exon 5
6314	18921	31697	4.49	3.0E-72	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6314	18921	31698	4.49	3.0E-72	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6726	18320	32125	3.59	3.0E-72	4826987	NT	Homo sapiens ribosomal protein L3-like (RPL3L), mRNA
7585	20100	32975	1.92	3.0E-72	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44), gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8118	20857	33586	1.52	3.0E-72	5031892	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA
10328	22822	35818	1.67	3.0E-72	X98289.1	NT	Homo sapiens S100A12 gene for Calgranulin C, exon 2 and joined cds
12174	24413	30948	2.03	3.0E-72	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
6113	18729	31482	1.41	2.0E-72	11428671	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA
9025	21582	34490	0.76	2.0E-72	BF308560.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131481 5'
9025	21582	34491	0.76	2.0E-72	BF308560.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131481 5'
10619	23151	36163	2.52	2.0E-72	AA789277.1	EST_HUMAN	aj28809.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391609 3' similar to gb:X02067 H.sapiens mRNA for 7SL RNA pseudogene (HUMAN);
12260	24470	30930	4.78	2.0E-72	AF182714.1	NT	Rattus norvegicus putative phosphate/phosphoenolpyruvate translocator mRNA, complete cds
2120	14688	27287	1.03	1.0E-72	AA846225.1	EST_HUMAN	aj83d02.s1 Soares_parathyroid_tumor_NbH-PA Homo sapiens cDNA clone IMAGE:1387395 3'
5940	18560	31289	4.04	1.0E-72	7657676	NT	Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA
6676	19272	32076	1.18	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6676	19272	32077	1.18	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6744	24768	32143	1.3	1.0E-72	AV751818.1	EST_HUMAN	Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA
7633	20145	33026	3.81	1.0E-72	BE175434.1	EST_HUMAN	AV751818 NPd Homo sapiens cDNA clone NPDAIE11 5'
7633	20145	33027	3.81	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
9510	22010	34968	7.2	1.0E-72	AF222742.1	NT	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
9510	22010	34969	7.2	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
1508	14100	26637	1.28	9.0E-73	AW374968.1	EST_HUMAN	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
							MIR0-CT0063-071099-002-h11 CT0063 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6190	18800	31570	0.98	9.0E-73	11525883	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
10829	23350		27.89	9.0E-73	11424099	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
1076	13680	26180	1.62	8.0E-73	AW071755.1	EST_HUMAN	ws55c06.x1 NCJ_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2501098.3 similar to TR:Q569050 Q569050 HYPOTHETICAL PROTEIN MJ1656 ;
3332	15942	28417	0.61	8.0E-73	11435180	NT	Homo sapiens gephyrin (GPH), mRNA
5768	18394	31108	0.76	8.0E-73	4505788	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
6687	19283	32086	4.21	8.0E-73	11428469	NT	Homo sapiens lysosome homolog (LOC57151), mRNA
8039	20581	33488	2.58	8.0E-73	AF113129.1	NT	Homo sapiens vacuolar ATPase isoform VA68 mRNA, complete cds
9275	21801	34751	5.4	8.0E-73	BE019900.1	EST_HUMAN	bb82a06.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034.5 similar to gb:X04098_cds1 ACTIN, CYTOPLASMIC 2 (HUMAN); gb:M21495 Mouse cytoskeletal gamma-actin mRNA, complete cds (MOUSE);
9655	22154	35123	1.83	8.0E-73	11528037	NT	Homo sapiens Interleukin 12 receptor, beta 1 (IL12RB1), mRNA
9655	22154	35124	1.83	8.0E-73	11528037	NT	Homo sapiens Interleukin 12 receptor, beta 1 (IL12RB1), mRNA
12324	24511	30919	7.07	8.0E-73	11418189	NT	Homo sapiens thyroid autoantigen 70KD (Ku antigen) (G22P1), mRNA
1173	13775	26285	1.37	7.0E-73	8923280	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3340	15950	28426	1.27	7.0E-73	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
4298	16884	28329	2.59	7.0E-73	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21- hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes;>
5079	17652		1.84	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
169	12832		2.14	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
7224	19755	32610	3.52	6.0E-73	BE166574.1	EST_HUMAN	QV0-HT0494-020300-137-003 HT0494 Homo sapiens cDNA
5460	18095	30413	1.78	4.0E-73	11422159	NT	Homo sapiens HELG protein (FAM44A1), mRNA
1802	14487	27048	1.78	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
1902	14487	27048	1.78	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
6799	19390	32205	1.03	3.0E-73	AA139403.1	EST_HUMAN	zn95e04.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:565950.3 similar to gb:Z23064_cds1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HUMAN);
8693	21232	34152	0.83	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTC Homo sapiens cDNA clone HTCAAF071.5
8693	21232	34153	0.83	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTC Homo sapiens cDNA clone HTCAAF071.5
11478	23928		1.68	3.0E-73	AI004040.1	EST_HUMAN	ou11402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1625955.3
12578	24875		1.34	3.0E-73	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C045
12583	24877		1.67	3.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
884	13488	26016	2.4	2.0E-73	AF139897.1	NT	Homo sapiens BASS1 (BASS1) mRNA, partial cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1889	14571		2.46	2.0E-73	AW88081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
3215	15827	28305	2.05	2.0E-73	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3604	18208	28686	0.68	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
3604	18208	28687	0.68	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
6607	19204	32011	6.35	2.0E-73	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6801	19392	32207	1.52	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6801	19392	32208	1.52	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
9451	21977	34928	0.68	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
9451	21977	34929	0.68	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
10320	22814	35810	1.46	2.0E-73	4504168	NT	Homo sapiens glutathione synthetase (GSS) mRNA
10391	22885	35890	1.18	2.0E-73	11496990	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
10391	22885	35891	1.18	2.0E-73	11496990	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
10933	23451	36472	3.48	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
10933	23451	36473	3.48	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
10962	23477	36502	1.85	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
12096	14571		2.75	2.0E-73	AW88081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
12665	24735	30825	1.41	2.0E-73	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
1818	14408	26933	1.74	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
2525	15089	27681	0.97	1.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
6500	19100	31885	1.05	1.0E-73	BE151283.1	EST_HUMAN	CM1-HT0282-111199-042-h10 HT0282 Homo sapiens cDNA
9419	21928	34874	1.41	1.0E-73	AI147427.1	EST_HUMAN	qq61b07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839637 5' similar to contains element
11325	23023	36032	3.93	1.0E-73	BE385477.1	EST_HUMAN	MER22 repetitive element ;
770	13369	25888	2.42	8.0E-74	4557426	NT	6012/6071F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617105 5'
6073	18690	31435	1.87	8.0E-74	S83194.1	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
6073	18690	31436	1.87	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
1892	14574	27133	3.26	7.0E-74	AJ001689.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
3371	15979	28466	1.18	7.0E-74	AL163246.2	NT	Homo sapiens NKX2D gene, exon 10
9167	21744	34687	2.49	7.0E-74	BE987432.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
12323	24510	30918	6.87	7.0E-74	BE266305.1	EST_HUMAN	601649284F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932987 5'
1161	13764	28275	4.55	6.0E-74	AF109607.1	NT	601191927F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535855 5'
							Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1868	14261	26784	0.9	6.0E-74	AW263177.1	EST_HUMAN	xn78g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700638 3'
2355	14926	27469	10.83	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2355	14926	27500	10.83	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2889	15506	27977	1.22	6.0E-74	AW014039.1	EST_HUMAN	UI-H-B10-eah-h-03-O-UI.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
2889	15506	27978	1.22	6.0E-74	AW014039.1	EST_HUMAN	UI-H-B10-eah-h-03-O-UI.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
3775	16375	28840	1.64	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:312332 3'
3775	16375	28841	1.64	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:312332 3'
5177	17744	30172	0.85	6.0E-74	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
5177	17744	30173	0.85	6.0E-74	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
5588	18189	30647	3.28	6.0E-74	11056013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
938	13551	28067	1.37	5.0E-74	AW020986.1	EST_HUMAN	df17c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2726	15281	30682	4.42	5.0E-74	AW362756.1	EST_HUMAN	PMO-CT0289-271099-001-h07 CT0289 Homo sapiens cDNA
5603	18232	30682	1.98	5.0E-74	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
5981	18583	31317	11.6	5.0E-74	X89670.1	NT	H. sapiens mRNA for TPCP16 protein
6004	18624	31359	8.99	5.0E-74	4507866	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
6067	18684	31426	2.33	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6067	18684	31427	2.33	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6978	19552	32377	3.35	5.0E-74	7682263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7980	20522	33428	3.2	5.0E-74	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
10614	23147	36158	1.96	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
10614	23147	36159	1.96	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
301	12956	25446	2.66	4.0E-74	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
885	13499	26017	9.19	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
2005	14587	27146	2.26	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2005	14587	27147	2.26	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2117	14695	27263	2.03	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2117	14695	27264	2.03	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2178	14755	27325	1.21	4.0E-74	AB032894.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2471	15038	27608	0.89	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3127	15741	28210	4.58	4.0E-74	AJ008976.1	NT	Homo sapiens PLP gene
3580	16184	28668	1.14	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4136	16728	28181	1.01	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4655	17237	28682	1.71	4.0E-74	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4720	17301	28748	0.79	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
5168	17737	30184	0.81	4.0E-74	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
8486	21025		21.13	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to similar to ribosomal protein L37
8510	21049	33971	0.47	3.0E-74	9966912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
8284	21894	34841	2.47	3.0E-74	M76984.1	EST_HUMAN	EST01132 Subtracted Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCPE91
10241	22736	35728	2.42	3.0E-74	AA601493.1	EST_HUMAN	no17g05.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100984 3'
993	13605	26119	172.8	2.0E-74	7659491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
993	13605	26120	172.8	2.0E-74	7659491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1217	13817	26332	0.92	2.0E-74	AF020092.1	NT	Homo endogenous retrovirus HERV-K-147D
1287	13882	26407	1.64	2.0E-74	A1950528.1	EST_HUMAN	wc51e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN
1839	14231	26764	4.17	2.0E-74	4883198	NT	Q08379 GOLGIN-95, contains element MER22 repetitive element ; Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
1839	14231	26765	4.17	2.0E-74	4883198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
5149	17719	30148	2.97	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
5149	17719	30150	2.97	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
5155	17725	30156	3.93	2.0E-74	J02963.1	NT	Human platelet glycoprotein IIb mRNA, 3' end
5966	24752	31322	1.72	2.0E-74	BE711134.1	EST_HUMAN	RC6-HT0678-220500-011-C03 HT0678 Homo sapiens cDNA
6055	24755	31412	2.03	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6055	24755	31413	2.03	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6120	24755	31412	2.72	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6120	24755	31413	2.72	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
7160	19692	32538	1.3	2.0E-74	BF030788.1	EST_HUMAN	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
7881	20423	33331	1.56	2.0E-74	AB037816.1	NT	601557524F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827549 5'
8304	21904	34853	7.76	2.0E-74	AL163204.2	NT	Homo sapiens mRNA for KIAA1385 protein, partial cds
12033	24323		3.9	2.0E-74	AA198181.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
12605	24689	30882	1.99	2.0E-74	BF666568.1	EST_HUMAN	zp86a06.s1 Striatum muscle 937209 Homo sapiens cDNA clone IMAGE:628018 3'
57	12737	26207	2.04	1.0E-74	7657334	NT	602121428F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278569 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
359	13008	25491	4.11	1.0E-74	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
525	13157	25639	0.92	1.0E-74	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
532	13163	25644	10.17	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
627	13254	25728	1.88	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
1037	13647	26159	2.13	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
2268	14842	27419	3.73	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3173	15786	28258	2.7	1.0E-74	4756697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
3994	16592	29084	0.63	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3994	16592	29085	0.63	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4040	16638	29106	6.11	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4137	16729	29182	0.78	1.0E-74	BE083080.1	EST_HUMAN	RC2-BT0642-270300-019-008 BT0642 Homo sapiens cDNA
					h373h08.x1 NCI_CGAP_Lu24	Homo sapiens cDNA clone IMAGE:3213663 3' similar to WP.B0511.12	
4354	16941	29383	0.75	1.0E-74	BE487769.1	EST_HUMAN	OE17951
5351	17911	30328	1.67	1.0E-74	D83327.1	NT	Homo sapiens DGRR1 mRNA, partial cds
6806	19397	32211	1.51	1.0E-74	M89914.1	NT	Human neurofibromin (NF1) gene, complete cds
7622	20135	33013	1.23	1.0E-74	11417977	NT	Homo sapiens KIAA0852 protein (KIAA0852), mRNA
8000	20542	33444	0.74	1.0E-74	BE549105.1	EST_HUMAN	601070089F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
8000	20542	33445	0.74	1.0E-74	BE549106.1	EST_HUMAN	601070089F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
8740	21279	34202	7.81	1.0E-74	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
8768	21307	34230	0.81	1.0E-74	BF351951.1	EST_HUMAN	MRO-HT0559-230500-021-a03 HT0559 Homo sapiens cDNA
10376	22870	35863	1.37	1.0E-74	11420549	NT	Homo sapiens hypothetical protein FLJ10783 (FLJ10783), mRNA
11659	24086	37144	1.95	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
11746	24145		3.39	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
							Homo sapiens glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12400	24560		1.59	1.0E-74	AF240788.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
2670	15228		4.06	8.0E-75	AF176228.1	NT	Homo sapiens chromosome 21 segment HS21C002
12058	24339		2.18	8.0E-75	AL163202.2	NT	aj28c06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391626 3' similar to TR:Q15377 Q15377 Y-
5376	17935		1.01	6.0E-75	AA789285.1	EST_HUMAN	CHROMOSOME RNA RECOGNITION MOTIF PROTEIN ;
8939	21378	34301	2.15	5.0E-75	BE272325.1	EST_HUMAN	601126068F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2989865 5'
9045	21582	34511	0.62	5.0E-75	AA132811.1	EST_HUMAN	zo17e08.r1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 5'
9122	21658	34569	0.8	5.0E-75	BE561855.1	EST_HUMAN	601346909F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687458 5'
9122	21658	34600	0.8	5.0E-75	BE561855.1	EST_HUMAN	601346909F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687458 5'
9295	21895	34842	1.39	5.0E-75	BF690254.1	EST_HUMAN	602188816T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298738 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10133	22628	35616	2.5	5.0E-75	AI638623.1	EST_HUMAN	U31612.1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2242380 3' similar to TR:P97381 P97381 HYPOTHETICAL 20.1 KD PROTEIN:
117	12788	25270	1.81	4.0E-75	BE081333.1	EST_HUMAN	QV1-BT0632-210200-079-e02 BT0632 Homo sapiens cDNA
484	13117		1.21	4.0E-75	N36757.1	EST_HUMAN	y90h08.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:269055 5'
1602	14392	26937	1.43	4.0E-75	AW897230.1	EST_HUMAN	CMD-NND057-150400-335-g11 NN0057 Homo sapiens cDNA
2874	15492	27962	5.4	4.0E-75	BE409484.1	EST_HUMAN	601303866F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:36338344 5'
5720	18348	31048	0.71	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
5720	18348	31049	0.71	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6415	19018	31801	5.28	4.0E-75	5579457	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (110KD) (EIF3S8), mRNA
6856	19444	32260	1.84	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6856	19444	32261	1.84	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
10365	23101	38115	8.22	4.0E-75	7689505	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
1040	13650	26162	2.75	3.0E-75	AF157623.1	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
1041	13650	26162	9.08	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1876	14462	27019	2.54	3.0E-75	AB011153.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
2158	14735	27308	1.47	3.0E-75	4507334	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
2467	15034	27601	3.11	3.0E-75	4759153	NT	Homo sapiens synapjanin 1 (SYNJ1), mRNA
3056	15672	28148	0.65	3.0E-75	AL163201.2	NT	Homo sapiens synapjanin-associated protein, 29kD (SNAP29) mRNA
3223	15835	28313	1.12	3.0E-75	AB011153.1	NT	Homo sapiens chromosome 21 segment HS21C001
3393	16001	28480	0.83	3.0E-75	M72393.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3393	16001	28481	0.83	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4530	17114	28558	0.67	3.0E-75	7682421	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
5387	17927		0.61	3.0E-75	AL163209.2	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
5458	18093	30409	1.01	3.0E-75	11420956	NT	Homo sapiens chromosome 21 segment HS21C009
5458	18093	30410	1.01	3.0E-75	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
6967	19601	32432	1.42	3.0E-75	11528319	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
6967	19601	32433	1.42	3.0E-75	11528319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7189	19721	32568	4.6	3.0E-75	7662209	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7189	19721	32569	4.6	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7618	20131	33006	3.35	3.0E-75	4885632	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7618	20131	33007	3.35	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
8915	21453	34374	1.23	3.0E-75	11420804	NT	Homo sapiens Oncogene TIM (TIM) mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9598	22098	35059	0.85	3.0E-75	11420222	NT	Homo sapiens Drosophila Ketch like protein (DKELGHL), mRNA
10435	22929	35836	3.75	3.0E-75	11438430	NT	Homo sapiens syntaxin, alpha (non A4 component of amyloid precursor) (SNCA), mRNA
5853	18477		1.45	2.0E-75	AV734680.1	EST_HUMAN	AV734680 cDNA Homo sapiens cDNA clone cdABED02 5'
8685	21224	34144	2.43	2.0E-75	AI311783.1	EST_HUMAN	qq91e02.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386 POLJNV GENE:
2341	14912	27485	4.05	1.0E-75	AW188135.1	EST_HUMAN	xg60d02.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.11 PTR7 repetitive element:
2973	15589	28072	3.23	1.0E-75	X52221.1	NT	H. sapiens ERCC2 gene, exons 1 & 2 (partial)
5358	17918	30331	0.57	1.0E-75	BE894192.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
8353	20893		13.67	1.0E-75	AA398270.1	EST_HUMAN	z157h03.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:728485 3' similar to gb:M13932 40S
9349	21863	34812	4.14	1.0E-75	BF313645.1	EST_HUMAN	RIBOSOMAL PROTEIN S17 (HUMAN);
9349	21863	34813	4.14	1.0E-75	BF313645.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
10763	23287		6.58	1.0E-75	AA684377.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
10970	23485	36513	3.06	1.0E-75	AF223391.1	NT	ec77b08.s1 Stratagene lung (8937210) Homo sapiens cDNA clone IMAGE:968599 3'
11945	17918	30331	2.58	1.0E-75	BE894192.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
48	12728	25191	2.19	9.0E-76	AI652648.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
48	12728	25192	2.19	9.0E-76	AI652648.1	EST_HUMAN	w630b10.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;
9815	22313	35294	62.44	9.0E-76	M12637.1	NT	Human ferritin Heavy subunit mRNA, complete cds
154	12817	25305	9	8.0E-76	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
974	13586	26100	10.38	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
974	13586	26101	10.38	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2935	15551	28028	1.25	8.0E-76	7706724	NT	Homo sapiens mediator (Sur2), mRNA
8319	18928	31703	5.69	8.0E-76	11421442	NT	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA
7500	20022	32865	1.84	8.0E-76	11435215	NT	Homo sapiens LIM domain kinase 2 (STK2), mRNA
7567	20084	32980	0.94	8.0E-76	11419212	NT	Homo sapiens serine/threonine kinase 2 (STK2), mRNA
8237	20778	33689	0.81	8.0E-76	11416961	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
10280	22776	35764	1.25	8.0E-76	M13792.1	NT	Homo sapiens ALM-1 protein (LOC51151), mRNA
10346	23083	36097	7.29	8.0E-76	10442821	NT	Human adenosine deaminase (ADA) gene, complete cds
12305	24501		2.28	8.0E-76	11417862	NT	Homo sapiens baculoviral IAP repeat-containing 6 (BIRC6), mRNA
							Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							Homo sapiens dihydropyrimidinase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
808	13425	25931	2.84	7.0E-78	5016082	NT	
3333	15943	28418	3.23	7.0E-76	AFD56490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3339	15949	28425	5.78	7.0E-76	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
							Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
3379	15988	28467	1.89	7.0E-76	4757915	NT	
4481	17047	28490	6.32	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4481	17047	28491	6.32	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1277	13872		30.59	6.0E-76	BE396253.1	EST_HUMAN	601312010F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658757 5'
11340	23038	36047	2.97	6.0E-76	BE273201.1	EST_HUMAN	601142253F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506029 5'
1988	14568	27128	8.39	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1986	14588	27129	8.39	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1986	14588	27130	8.39	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
3242	15854	28338	0.88	4.0E-76	BE814096.1	EST_HUMAN	QV3-BN0047-270700-283-q06 BN0047 Homo sapiens cDNA
5474	18108	30427	1.22	4.0E-76	BE783412.1	EST_HUMAN	601471725F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874470 5'
9937	22432	35407	5.79	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (Tfujwara) Homo sapiens cDNA clone GEN-178G01 5'
9937	22432	35408	5.79	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (Tfujwara) Homo sapiens cDNA clone GEN-178G01 5'
657	13280	25759	1.63	3.0E-76	BF516262.1	EST_HUMAN	U1H-BW1-enz-b-04-0-U1.st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
657	13280	25760	1.63	3.0E-76	BF516262.1	EST_HUMAN	U1H-BW1-enz-b-04-0-U1.st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1643	14235	28769	7.45	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1643	14235	28770	7.45	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3476	16082	28555	5.2	3.0E-76	BF375889.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3478	16082	28558	5.2	3.0E-76	BF375889.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
5447	18018	37140	2.41	3.0E-76	Z41314.1	EST_HUMAN	HSCZQD042 normalized infant brain cDNA Homo sapiens cDNA clone c-zqd04 3'
							z073c07.r1 Stratagene pancreas (#637208) Homo sapiens cDNA clone IMAGE:592524 5' similar to gb:L32976 MIXED LINEAGE KINASE 1 (HUMAN);
5908	18530	31255	1.06	3.0E-76	AA160611.1	EST_HUMAN	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
6506	19108	31891	7.49	3.0E-76	AF286598.1	NT	
8091	20632	33545	1.03	3.0E-76	N42871.1	EST_HUMAN	yy20g10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:271842 5'
9632	22132	35097	2.91	3.0E-76	AW286353.1	EST_HUMAN	xs49h01.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2773009 3'
9658	22155	35125	1.11	3.0E-76	AA442309.1	EST_HUMAN	zv54d111.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757481 5'
9658	22155	35128	1.11	3.0E-76	AA442309.1	EST_HUMAN	zv54d111.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757481 5'
11649	24864	30706	1.73	3.0E-76	AW987984.1	EST_HUMAN	EST380059 MAGC resequences, MAGJ Homo sapiens cDNA
11760	25090	30501	4.85	3.0E-76	AW958455.1	EST_HUMAN	EST388525 MAGC resequences, MAGD Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
303	12958	25448	1.1	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
364	13013	25495	2.12	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
364	13013	25498	2.12	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
486	13119		1.12	2.0E-76	4557662	NT	Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA
616	13243	26717	1.45	2.0E-76	4503944	NT	Homo sapiens glucagon (GCG) mRNA
1068	13673	26186	1.57	2.0E-76	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1583	14176	26708	0.89	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1583	14176	26709	0.89	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1972	14558	27113	1.04	2.0E-76	AA253954.1	EST_HUMAN	zs60h1.1.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701925 3'
2867	15485	27958	2.64	2.0E-76	P23266	SWISSPROT	OLFATORY RECEPTOR-LIKE PROTEIN F5
3336	15946	28422	2.3	2.0E-76	AA445992.1	EST_HUMAN	zw64602.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN
3336	15946	28423	2.3	2.0E-76	AA4445992.1	EST_HUMAN	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ;
3832	16431	28893	0.7	2.0E-76	AA400700.1	EST_HUMAN	zw64602.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN
4215	12958	25448	0.62	2.0E-76	D84295.1	NT	zw70g11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743396 5' similar to WP:R05D3.2
5082	17655	30096	7.33	2.0E-76	AW879818.1	EST_HUMAN	CE00281 ;
5512	18145		0.98	2.0E-76	AF127845.1	NT	Human mRNA for possible protein TPRDII, complete cds
5803	18428	31147	4.95	2.0E-76	AB029004.1	NT	QV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA
7442	19666	32833	0.72	2.0E-76	11421326	NT	Gorilla gorilla olfactory receptor (GGO18) gene, partial cds
7658	20170	33057	1.84	2.0E-76	11427410	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
10182	22677	35670	7.63	2.0E-76	11437211	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
10801	23324	36334	2.79	2.0E-76	7549807	NT	Homo sapiens TPCR88 protein (HSTPCR88P), mRNA
4365	16972	28420	4.17	1.0E-76	D63874.1	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63150), mRNA
4365	16972	28421	4.17	1.0E-76	D63874.1	NT	Homo sapiens HIRA interacting protein 4 (dnal-like) (HIRIP4), mRNA
5839	18288	30741	5.55	1.0E-76	BE796537.1	EST_HUMAN	Human mRNA for HMG-1, complete cds
6391	18994		0.7	1.0E-76	AA333207.1	EST_HUMAN	Human mRNA for HMG-1, complete cds
7003	19501	32320	4.41	9.0E-77	BE889525.1	EST_HUMAN	Human mRNA for HMG-1, complete cds
11115	23625	36667	1.68	9.0E-77	4508022	NT	Human mRNA for HMG-1, complete cds
12474	24599		1.9	9.0E-77	BE410354.1	EST_HUMAN	601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
200	12860	25344	1.36	8.0E-77	R83144.1	EST_HUMAN	EST37301 Embryo, 8 week 1 Homo sapiens cDNA 5' end
							601512435F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5'
							Homo sapiens protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C) mRNA
							601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636753 5'
							yp11h02.r1 Soares breast 3NbhBst Homo sapiens cDNA clone IMAGE:187155 5' similar to
							SP-ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1 ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4620	17203	28652	1.27	8.0E-77	BF205181.1	EST_HUMAN	60186626F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109503 5'
5644	19273	30747	2.93	8.0E-77	4606230	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mo34 homolog) (PSMD7) mRNA
11284	23792	36849	2.67	8.0E-77	AA019770.1	EST_HUMAN	ze62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
11284	23792	36850	2.67	8.0E-77	AA019770.1	EST_HUMAN	ze62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
12451	24585	30918	21.88	8.0E-77	R00245.1	EST_HUMAN	ye68f04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains MER10 repetitive element:
1973	14557	27114	2.58	7.0E-77	AA625755.1	EST_HUMAN	zu91g01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
2455	15022	27593	1.98	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2455	15022	27594	1.98	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
284	12940	25428	3.52	6.0E-77	4504600	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1181	13783	26293	3.04	6.0E-77	AW957753.1	EST_HUMAN	EST369823 MAGE resequences, MAGE Homo sapiens cDNA
1590	14183	26716	2.87	6.0E-77	AI204066.1	EST_HUMAN	q67h12.x1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1745063 3'
156	12819	25307	3.77	5.0E-77	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
156	12819	25308	3.77	5.0E-77	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
1279	13974	26394	1.69	5.0E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1404	13997	26526	1.53	5.0E-77	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2782	15345	27914	0.98	5.0E-77	4503160	NT	Homo sapiens cullin 1 (CUL1) mRNA
3574	16178	28661	1.03	5.0E-77	8394518	NT	Homo sapiens ubiquitin specific protease 18 (USP18) mRNA
4813	17391	28842	1.08	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
4813	17391	28843	1.08	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
5071	17644	30086	2.22	5.0E-77	AL043953.1	EST_HUMAN	DKFZp434G1728_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G1728 5'
5419	17978	30384	1.77	5.0E-77	AA861184.1	EST_HUMAN	ak33a05.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407728 3' similar to contains Alu repetitive element:contains element PTR7 PTR7 repetitive element:
6879	19813	32447	0.71	5.0E-77	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
7366	19892	32755	0.68	5.0E-77	X88286.1	NT	H. sapiens mRNA for ubiquitin hydrolase
7592	19892	32755	0.75	5.0E-77	X88286.1	NT	H. sapiens mRNA for ubiquitin hydrolase
8309	20850	33773	1.07	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
8309	20850	33774	1.07	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
9489	21945	34893	3.52	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
9489	21945	34894	3.52	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
10385	22879	35872	0.51	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0289 gene, partial cds
10385	22879	35873	0.51	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0289 gene, partial cds
2015	14597	27160	1.12	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA

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2015	14597	27161	1.12	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10189	22884	35875	0.82	3.0E-77	H65167.1	EST_HUMAN	U64g01.1r1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;
10189	22884	35876	0.82	3.0E-77	H65167.1	EST_HUMAN	U64g01.1r1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;
10493	22987	35994	0.51	3.0E-77	A017333.1	EST_HUMAN	ov31h07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638973 3'
10493	22987	35995	0.51	3.0E-77	A017333.1	EST_HUMAN	ov31h07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638973 3'
10754	23278	36291	4.39	3.0E-77	BF359917.1	EST_HUMAN	PM3-MT0078-080800-005-g03 MT0078 Homo sapiens cDNA
1398	13990	26517	1.82	2.0E-77	AV784617.1	EST_HUMAN	AV784617 MDS Homo sapiens cDNA clone MDSBTF10 5'
1479	14072	26611	3.43	2.0E-77	AW987712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
2138	14718	27268	1.24	2.0E-77	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2151	14728	27301	2.37	2.0E-77	7708315	NT	Homo sapiens CGI-79 protein (LOC51634), mRNA
2630	15471	27760	2.26	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2630	15471	27761	2.26	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4105	16889	28153	1.36	2.0E-77	BE044316.1	EST_HUMAN	h043b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4504	17088	28538	0.85	2.0E-77	A1613519.1	EST_HUMAN	Iw22g02.x1 NCL_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
4504	17088	28537	0.85	2.0E-77	A1613519.1	EST_HUMAN	Iw22g02.x1 NCL_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
4701	17283		1.38	2.0E-77	4504068	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
4883	17458	28910	4.3	2.0E-77	AA653025.1	EST_HUMAN	ns68g12.s1 NCL_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29. [1], contains element MSR1 repetitive element ;
6109	18725	31478	1.78	2.0E-77	BE288940.1	EST_HUMAN	601119852F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029436 5'
6320	18927	31704	1.68	2.0E-77	BE187143.1	EST_HUMAN	601476802F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879505 5'
7226	18757	32612	14.03	2.0E-77	A1833003.1	EST_HUMAN	ai74809.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311
8466	21006	33924	0.9	2.0E-77	A1362707.1	EST_HUMAN	Q13311 TAX1-BINDING PROTEIN TXBP151. [1];
9447	21973	34824	4.58	2.0E-77	U50321.1	NT	qy70c09.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2017360 3' similar to WP:F28D11.1
9447	21973	34825	4.58	2.0E-77	U50321.1	NT	CE03765 LOW DENSITY LIPID RECEPTOR-RELATED PROTEIN ;
9906	22403	35377	0.55	2.0E-77	BF310349.1	EST_HUMAN	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
							Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
							601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6806	22403	35378	0.55	2.0E-77	BF10349.1	EST_HUMAN	601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
47	12726	25187	1.39	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
47	12726	25188	1.39	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
284	12950	25437	2.09	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
284	12950	25438	2.09	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
908	15428	26041	2.96	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
908	15428	26042	2.96	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1863	14547	27104	1.41	1.0E-77	AW058119.1	EST_HUMAN	w83905.x1 Sceres, thymus_NHFTn Homo sapiens cDNA clone IMAGE:2536160 3'
2488	15053	27625	0.99	1.0E-77	AB028024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3081	15696	28168	2.82	1.0E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECRT1), mRNA
4445	17031	28472	3.95	1.0E-77	7706289	NT	Homo sapiens OGI-60 protein (LOC51626), mRNA
4822	17205	28854	20.39	1.0E-77	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4755	17336	29780	3.41	1.0E-77	6552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
5098	17180	28627	0.59	1.0E-77	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
5228	17792	30211	1.05	1.0E-77	7681849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
5228	17792	30212	1.05	1.0E-77	7681849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
5387	17948		4.13	1.0E-77	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6088	18702	31449	1.46	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6086	18702	31450	1.46	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6198	18908	31577	1.4	1.0E-77	M25844.1	NT	Human von Willebrand factor gene, exon 20
6575	19173	31972	1.45	1.0E-77	4885182	NT	Homo sapiens diaphanous (Drosophila, homodog) 1 (DIAPH1), mRNA
7114	19454	32270	15.68	1.0E-77	5881412	NT	Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA
7861	20173	33060	0.92	1.0E-77	11420159	NT	Homo sapiens cullin 1 (CUL1), mRNA
7740	20248	33141	0.78	1.0E-77	X04571.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
9189	21706	34649	1.31	1.0E-77	X94354.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
9189	21706	34650	1.31	1.0E-77	X94354.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
10416	22910	35909	1.01	1.0E-77	AB028396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
10416	22910	35910	1.01	1.0E-77	AB028396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
10956	23471	36496	2.82	1.0E-77	11433426	NT	Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA
10444	22938	35948	2.4	9.0E-78	AW753302.1	EST_HUMAN	RC3-CT0254-280999-011-b05 CT0254 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6574	19172	31970	4.74	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
6574	19172	31971	4.74	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
88	12785	25248	1.48	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
89	12785	25249	1.48	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
3358	15984	28441	0.72	6.0E-78	BF344101.1	EST_HUMAN	602016928F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4152511 5'
6877	19273		2.29	6.0E-78	11432710	NT	Homo sapiens GDNF family receptor alpha 1 (GFR1), mRNA
234	12894	25377	4.78	5.0E-78	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
2597	15159	27727	4.1	5.0E-78	AW673424.1	EST_HUMAN	ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to WP.Y4858A.6
3432	16040	28522	3.88	5.0E-78	M55586.1	NT	CE22121 ; Human collagenase type IV (CLG4) gene, exon 6
5807	18236	30688	2.29	5.0E-78	AF038538.1	NT	Homo sapiens Best's macular dystrophy related protein mRNA, partial cds
5764	18390	31102	24.58	5.0E-78	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68KD (TGFB1), mRNA
7208	19739	32593	2.2	5.0E-78	AW953120.1	EST_HUMAN	EST385190 MAGI2 resequencing, MAGB Homo sapiens cDNA
8012	21549	34478	6.88	5.0E-78	U60889.1	NT	Human lysosomal alpha-mannosidase (manB) gene, exon 7
9013	21550	34479	3.6	5.0E-78	BE960836.1	EST_HUMAN	601648081F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3931887 5'
1176	13778	26288	1.84	4.0E-78	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: hess3) Homo sapiens cDNA clone DKFZp434N0323 5'
1565	14157	26688	1.89	4.0E-78	AL355841.1	NT	Novel human gene mapping to chromosome 22
2357	14928	27502	2.97	4.0E-78	AF107405.1	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4414	16989	28441	1.23	4.0E-78	7656878	NT	Homo sapiens syncytin (LOC30816), mRNA
4887	17462	29915	1.91	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4887	17462	29916	1.91	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
5941	18501	31280	0.97	4.0E-78	11420732	NT	Homo sapiens SFRS3 protein kinase 2 (SRPK2), mRNA
7502	20024	32888	0.77	4.0E-78	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70KD, polypeptide 1 (RPS6KB1) mRNA
8787	21326	34250	1.51	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
8787	21326	34251	1.51	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
9280	21890	34837	0.61	4.0E-78	11417251	NT	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), mRNA
10341	22835	35829	2.03	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10341	22835	35830	2.03	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10841	23173	36185	1.67	4.0E-78	11428810	NT	Homo sapiens regulatory factor X-associated ankyrin-containing protein (RFXANK), mRNA
11297	23749	36806	2.09	4.0E-78	AF169148.1	NT	Homo sapiens e-CADHERIN (CABP1) mRNA, complete cds
11432	23892	36948	4.15	4.0E-78	X05844.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
12337	24520	30923	4.58	4.0E-78	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
172	12835	25318	2.42	3.0E-78	AF095901.1	NT	Homo sapiens eIF1 gene, complete cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
172	12835	25319	2.42	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
3827	16427		1.15	3.0E-78	AU140604.1	EST_HUMAN	AU140604 PLACES3 Homo sapiens cDNA clone PLACE3000373 5'
4180	16486	28947	0.76	3.0E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
10186	22681		5.76	3.0E-78	BE144758.1	EST_HUMAN	GM0-HTO180-041098-065-c07 HT0180 Homo sapiens cDNA
10860	23381	36400	5.65	3.0E-78	BE156318.1	EST_HUMAN	QVO-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
3155	15769		2.54	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
4088	16882		1.8	2.0E-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end
7483	20006	32870	1.38	2.0E-78	AW402306.1	EST_HUMAN	UI-HF-BK0-aag-g-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
7483	20006	32871	1.38	2.0E-78	AW402308.1	EST_HUMAN	UI-HF-BK0-aag-g-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
7714	20223	33110	3.47	2.0E-78	BF689800.1	EST_HUMAN	602186529F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4288599 5'
7984	20526	33432	1.73	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBBAW509 5'
8389	20929	33848	1.8	2.0E-78	AI557509.1	EST_HUMAN	P12.1_16_B07.r tumor2 Homo sapiens cDNA 3'
8389	20929	33849	1.8	2.0E-78	AI557509.1	EST_HUMAN	P12.1_16_B07.r tumor2 Homo sapiens cDNA 3'
10859	23474	36469	3.39	2.0E-78	AI197837.1	EST_HUMAN	q150105.x1 NCI CGAP_Bn25 Homo sapiens cDNA clone IMAGE:1659961 3' similar to W.P.R90.1
11003	23517	36552	3.47	2.0E-78	N66951.1	EST_HUMAN	CE08325 PROTEIN KINASE
5508	18141	30553	2.63	1.0E-78	11417304	NT	za4812.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:295823 3'
7035	18055	30478	1.91	1.0E-78	AV648699.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC51306), mRNA
8100	20841		2.25	1.0E-78	U52373.1	NT	AV648699 GLC Homo sapiens cDNA clone GLCBMCO1 3'
11832	24197	31037	2.17	1.0E-78	11430460	NT	Human serine/threonine kinase MNB (mtb) mRNA, complete cds
11826	24261	31014	1.41	1.0E-78	11435803	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4808	17386	28836	4.05	9.0E-79	11525891	NT	Homo sapiens similar to lymphocyte activation-associated protein (H. sapiens) (LOC63140), mRNA
4888	17582	30006	3.34	9.0E-79	BED00837.1	EST_HUMAN	Homo sapiens peptide YY (PYY), mRNA
5624	18253	30722	13.77	9.0E-79	AB028070.1	NT	RC2-BN0074-090300-014-c12 BN0074 Homo sapiens cDNA
6462	19083	31884	2.48	9.0E-79	5454145	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
6731	19325	32129	1.43	9.0E-79	11430822	NT	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E3) mRNA
7388	24781		0.98	9.0E-79	11424427	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
7575	20091	32868	0.89	9.0E-79	11421735	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7575	20091	32869	0.89	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
7612	20125	33002	0.72	9.0E-79	D30658.1	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
8287	20828	33748	0.56	9.0E-79	11417260	NT	Human T-cell mRNA for glycyl tRNA synthetase, complete cds
8287	20828	33749	0.56	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
8287	20828	33749	0.56	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8993	21531	34480	7.08	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
8993	21531	34481	7.08	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
8302	21802	34851	0.61	9.0E-79	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10267	22762	35749	0.59	9.0E-79	11438843	NT	Homo sapiens hypothetical protein FLJ20535 (FLJ20535), mRNA
10316	22810	35803	2.32	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
10316	22810	35804	2.32	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
10946	23482	36484	2.73	9.0E-79	AY008273.1	NT	Homo sapiens TRAF6-regulated IKK activator 1 beta Uev1A mRNA, complete cds
11388	23840	36904	3.26	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
11388	23840	36905	3.26	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
12549	24854	30900	2.05	9.0E-79	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3805	16405	28889	1.17	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11747	18035	30495	1.3	8.0E-79	8587387	NT	Homo sapiens perid (Drosophila) homolog 3 (PER3), mRNA
3291	15602	26382	10.29	7.0E-79	BE518648.1	EST_HUMAN	601472706T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875857 3'
11876	24095		2.07	6.0E-79	AA698828.1	EST_HUMAN	zfp4e04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462558 3' similar to
11368	23820	36882	3.85	5.0E-79	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
5159	17728	30157	2.24	4.0E-79	BF210869.1	EST_HUMAN	601874522FT NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101245 5'
335	12987	25474	2.46	3.0E-79	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
1014	13824	26139	4.44	3.0E-79	AF232708.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein (Cin) gene, complete cds
3133	15747	28216	1.91	3.0E-79	U08410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
5292	17854	30278	0.94	3.0E-79	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
5292	17854	30279	0.94	3.0E-79	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
5584	18195	30641	8.78	3.0E-79	AF110322.1	NT	Homo sapiens MSTP016 (MST016) mRNA, complete cds
5888	18520	31245	1.72	3.0E-79	AB020699.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5922	18544	31270	1.01	3.0E-79	BE789470.1	EST_HUMAN	601482143FT NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
5922	18544	31271	1.01	3.0E-79	BE789470.1	EST_HUMAN	601482143FT NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
5942	18562	31291	3.6	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
5942	18562	31292	3.6	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
5843	19433	32248	0.76	3.0E-79	BE256893.1	EST_HUMAN	601112055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352885 5'
7120	19460	32276	3.07	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
7120	19460	32276	3.07	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
8105	20646	33555	1.58	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
8324	21838	34789	0.71	3.0E-79	10835036	NT	Homo sapiens tetratricopeptide repeat domain 3 (TTC3), mRNA
10249	22744		0.62	3.0E-79	AV698115.1	EST_HUMAN	AV698115 GKCC Homo sapiens cDNA clone GKCAHE11 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10740	23265	36280	1.97	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
10740	23265	36281	1.97	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
309	12864		1.05	2.0E-79	H63129.1	EST_HUMAN	y48f03.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:208541 3'
662	13286	25767	1.38	2.0E-79	BE379926.1	EST_HUMAN	801159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:351107 5'
963	13574	26090	0.94	2.0E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA
1020	13630	26145	0.91	2.0E-79	4885234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
1020	13630	26146	0.91	2.0E-79	4885234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
1073	13678		1.06	2.0E-79	A1523747.1	EST_HUMAN	th18h07.x1 NCL_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2118685 3'
1824	14413	26958	1.21	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
1824	14413	26959	1.21	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
1918	14503	27060	1.01	2.0E-79	7662255	NT	Homo sapiens KIAA0703 gene product (KIAA0703), mRNA
2193	14789	27341	10.76	2.0E-79	4585883	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2193	14789	27342	10.76	2.0E-79	4585883	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2352	14923	27498	2.42	2.0E-79	AF244138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
2741	15298	27663	0.89	2.0E-79	AB023154.1	NT	Homo sapiens mRNA for KIAA0937 protein, partial cds
3985	16583	29054	0.65	2.0E-79	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
4245	16833	29284	1.24	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
4800	17378	29828	0.62	2.0E-79	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5851	18475		1.16	2.0E-79	AA312223.1	EST_HUMAN	EST162828 Jurkat T-cells V1 Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, cosmid B0303.15
5901	18523	31248	0.9	2.0E-79	11181769	NT	Homo sapiens X transporter protein 3 (XT3), mRNA
6390	18993	31773	1.1	2.0E-79	AB020637.1	NT	Homo sapiens mRNA for KIAA0830 protein, partial cds
7040	18060	30482	0.96	2.0E-79	AF263613.1	NT	Homo sapiens membrane-associated calcium-independent phospholipase A2 gamma mRNA, complete cds
7219	19750	32805	1.76	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
7219	19750	32806	1.76	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
8044	20586	33482	1.22	2.0E-79	4506442	NT	Homo sapiens retinoblastoma-like 1 (p107) (RBL1) mRNA
8454	20994	33912	2.52	2.0E-79	11427428	NT	Homo sapiens hypothetical protein FLJ11008 (FLJ11006), mRNA
8701	21240	34163	0.55	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
8701	21240	34164	0.55	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
8934	21472	34391	0.89	2.0E-79	11432184	NT	Homo sapiens similar to ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M8-9 (H. sapiens) (LOC63961), mRNA
10004	22499	35488	1.94	2.0E-79	S72869.1	NT	H4(D10S170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
10004	22499	35489	1.94	2.0E-79	S72869.1	NT	H4(D10S170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10808	23427	38444	5.07	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
10908	23427	38445	5.07	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
11716	18033	30493	5.59	2.0E-79	7662357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
11808	24181	31029	5.85	2.0E-79	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
12038	24326	30984	2.81	2.0E-79	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6701	24768		3.27	1.0E-78	BF363071.1	EST_HUMAN	MRO-NN0087-260600-017-b10 NN0087 Homo sapiens cDNA
8187	20728	33640	0.74	1.0E-78	BE394211.1	EST_HUMAN	601311517F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632909 5'
11487	23936	37006	2.11	1.0E-79	BF087405.1	EST_HUMAN	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA
11834	25021		1.84	1.0E-79	AI460115.1	EST_HUMAN	ar79a04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151438 3'
3180	15793	28264	5.7	8.0E-80	AA725848.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
3180	15793	28265	5.7	9.0E-80	AA725848.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
9928	22422	35386	1.33	9.0E-80	BE798603.1	EST_HUMAN	601581632F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936061 5'
11158	23863	36708	11.44	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
11158	23863	36709	11.44	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
3662	18264		1.19	8.0E-80	U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
7600	20113	32889	2.82	8.0E-80	11422847	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
7600	20113	32890	2.82	8.0E-80	11422847	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
9323	21837	34787	1.07	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9323	21837	34788	1.07	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
933	13546	26063	1.84	8.0E-80	AI422197.1	EST_HUMAN	tf58d02.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q18785 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
1685	14277	26810	2.29	6.0E-80	U64696.1	NT	Homo sapiens NRD convertase mRNA, complete cds
2337	14908	27479	2.88	6.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
2337	14908	27480	2.88	6.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4372	16959	29403	0.98	6.0E-80	AB032881.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
4372	16959	29404	0.98	6.0E-80	AB032881.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
5969	18590	31325	2.15	6.0E-80	11421462	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA
6228	18835	31608	3.18	6.0E-80	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
6376	18980	31759	4.09	6.0E-80	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
6418	18021		0.88	6.0E-80	7662393	NT	Homo sapiens KIAA0941 protein (KIAA0941), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8464	19065	31850	0.84	6.0E-80	M18533.1	NT	Homo sapiens dystrophin (DMD) mRNA, complete cds
8758	21297	34217	2.43	6.0E-80	11526464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
8758	21297	34218	2.43	6.0E-80	11526464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
8949	21487	34409	1.6	6.0E-80	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
9281	21807	34759	0.88	6.0E-80	AF161495.1	NT	Homo sapiens HSPC146 mRNA, complete cds
9775	22273	35258	1.49	6.0E-80	U20211.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha: subunit gene, exon 21
10820	23341	36358	2.68	6.0E-80	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
11103	23613	36853	22.81	6.0E-80	AF228730.1	NT	Homo sapiens Cy119 mRNA, complete cds
11593	24038	37105	1.93	6.0E-80	AF102265.1	NT	Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds
11817	24896		1.84	6.0E-80	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12019	24316		5.01	6.0E-80	AB028900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
12543	25028		1.95	6.0E-80	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
614	13241	25716	2.83	5.0E-80	4506228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
868	13483	25998	1.9	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
868	13483	25999	1.9	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
1231	13830		1.16	5.0E-80	X91647.1	NT	H. sapiens ncx1 gene (exon 12)
1503	14095		2.88	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2399	14987	27540	1.08	5.0E-80	U89358.1	NT	Human I(3)mbt protein homolog mRNA, complete cds
2474	15041	27609	2.56	5.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2820	15372	27941	2.67	5.0E-80	4504292	NT	Homo sapiens H3 histone family, member J (H3F-J) mRNA
4112	16706	29160	0.93	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4-mannosyltransferase, complete cds
4112	16706	29161	0.93	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4-mannosyltransferase, complete cds
5089	17662	30102	1.29	5.0E-80	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
8288	20839	33760	1.04	5.0E-80	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
9182	21759	34705	15.52	4.0E-80	F25915.1	EST_HUMAN	HSPD13155 HM3 Homo sapiens cDNA clone e4000045F03
233	12893		11.18	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5034	17608		6.93	3.0E-80	BE817465.1	EST_HUMAN	QV4-BN0263-040600-241-g10 BN0263 Homo sapiens cDNA
5986	18608	31340	2.04	3.0E-80	AI091675.1	EST_HUMAN	aa23e12.x1 Soares NSF_F8_9W_OT_PA_S1 Homo sapiens cDNA clone IMAGE:1567054 3' similar to
1833	14421	26871	6.34	2.0E-80	R35321.1	EST_HUMAN	TR:O35780 O35780 PIG-L.1
1900	14485	27046	1.4	2.0E-80	AI444821.1	EST_HUMAN	Yg58a08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:38080 5'
2100	14678	27247	5.6	2.0E-80	AL043116.2	EST_HUMAN	RET487 subcloned retina cDNA library Homo sapiens cDNA clone RET487
6393	18996	31775	0.71	2.0E-80	AI923972.1	EST_HUMAN	DKFZp434D1323 r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1323 5'
							wn49c10.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2448786 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6393	18986	31776	0.71	2.0E-80	A1823972.1	EST_HUMAN	wn49c10.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2448786 3'
6897	19631	32469	1.06	2.0E-80	AA582952.1	EST_HUMAN	nm80d01.s1 NCL_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1090177 3'
6983	19491	32312	1.89	2.0E-80	11421930	NT	Homo sapiens Golgi transport complex protein (80 kDa) (GTC80), mRNA
7298	19828	32885	1	2.0E-80	T75215.1	EST_HUMAN	yc86f12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22851 5' similar to SP:K1CR_XENLA P08802 KERATIN, TYPE I CYTOSKELETAL ENDO B ;
9088	21622	34558	1.25	2.0E-80	AW964270.1	EST_HUMAN	EST376343 MAGE resequences, MAGH Homo sapiens cDNA
9883	22182	35156	1.13	2.0E-80	AJ007378.1	NT	Homo sapiens GGT gene, exon 6
10748	23272	36287	7.28	2.0E-80	AA393362.1	EST_HUMAN	z170f12.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315
362	13011		1.44	1.0E-80	AL163303.2	NT	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN ;
832	13449	25956	1.39	1.0E-80	AF231820.1	NT	Homo sapiens chromosome 21 segment HS21C103
1987	14579		3.73	1.0E-80	A1732856.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
4945	17520	20962	0.71	1.0E-80	N98520.1	EST_HUMAN	nm01f12.x5 NCL_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.11 OFR repetitive element ;
5530	18162		6.77	1.0E-80	BE388615.1	EST_HUMAN	z339g07.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:294972 5' similar to contains Alu repetitive element;
6128	18741	31494	5.8	1.0E-80	L10347.1	NT	601274305F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615433 5'
6824	19221	32028	1.57	1.0E-80		NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
7258	19786	32642	1.39	1.0E-80	AJ224172.1	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA
7574	20080	32986	2.64	1.0E-80	A1948731.1	EST_HUMAN	Homo sapiens mRNA for lipophilin B
7574	20090	32987	2.84	1.0E-80	A1948731.1	EST_HUMAN	wq25c05.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472296 3'
8173	20714	33630	1.25	1.0E-80	11421211	NT	wq25c05.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472296 3'
8634	21173	34091	0.86	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
8634	21173	34092	0.96	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
9209	21726	34698	1.79	1.0E-80	AF245219.1	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
9209	21726	34699	1.78	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
10323	22817	35813	0.93	1.0E-80	D83479.2	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
10531	23068	36080	2.64	1.0E-80	11641276	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10531	23068	36081	2.64	1.0E-80	11641276	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
12091	24359	36967	2.04	1.0E-80	11417901	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
10584	23100	36113	3.56	8.0E-81	A1251752.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
10584	23100	36114	3.56	8.0E-81	A1251752.1	EST_HUMAN	qh80g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854296 3'
11033	23547	36582	6.13	8.0E-81	BE394525.1	EST_HUMAN	qh80g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854296 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7269	19827	32686	3.19	7.0E-81	AI822115.1	EST_HUMAN	zb91c08.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:269918 3'
4476	17061	29510	4.95	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3352840 5'
4476	17061	29511	4.95	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3352840 5'
5487	18121	30528	1.71	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5487	18121	30529	1.71	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
9162	21697	34841	1.22	6.0E-81	AA360017.1	EST_HUMAN	EST69129 Fetal lung II Homo sapiens cDNA 5' end
12240	24453	30955	2.16	6.0E-81	BF679022.1	EST_HUMAN	602153668F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
12240	24453	30956	2.16	6.0E-81	BF679022.1	EST_HUMAN	602153668F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
2258	14832	27410	2.66	5.0E-81	BE268042.1	EST_HUMAN	601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
8351	20892	33813	1.42	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8351	20892	33814	1.42	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9566	22066	35025	1.26	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
9566	22066	35026	1.26	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
11455	23905	36972	2.66	5.0E-81	9506634	NT	Homo sapiens hypothetical protein (FLJ11045), mRNA
238	12898	25381	1.3	4.0E-81	AF252257.1	NT	Homo sapiens ORP2 binding protein mRNA, partial cds
731	13351	25846	1.34	4.0E-81	AI521435.1	EST_HUMAN	th60612.x1 NCI_CGAP_OV23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:Q85560 Q85560
3208	15818	28294	4.76	4.0E-81	AB037786.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
3690	16291	28760	0.98	4.0E-81	AW004608.1	EST_HUMAN	ws90h03.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR:O43815 O43815
4240	16828	29277	2.39	4.0E-81	AF263308.1	NT	STRATIN ;
4240	16828	29278	2.39	4.0E-81	AF263308.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4481	17068	29516	1.08	4.0E-81	8923209	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
7321	19848	32708	0.86	4.0E-81	4757893	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
8229	20770	33689	1.71	4.0E-81	X06989.1	NT	Homo sapiens calcium channel, voltage-dependent, L type, alpha 2/delta subunit (CACNA2), mRNA
8482	21021	33936	3.39	4.0E-81	U20197.1	NT	Human mRNA for amyloid A4(751) protein
8482	21021	33937	3.39	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
9153	21688	34632	4.78	4.0E-81	AB018001.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
10012	22507	35498	1.79	4.0E-81	11425281	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
10075	22570	35564	0.57	4.0E-81	11439085	NT	Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA
10075	22570	35565	0.57	4.0E-81	11439085	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
11063	23575	36812	2.85	4.0E-81	4759085	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
11063	23575	36813	2.85	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
11063	23576	36813	2.85	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11708	24981	30834	11.8	4.0E-81	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
11708	24961	30635	11.8	4.0E-81	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12277	24481	30938	2.13	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
12277	24481	30939	2.13	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
12430	24572	30912	4.2	4.0E-81	11417974	NT	Homo sapiens transcobalamin II, macrocytic anemia (TCN2), mRNA
1310	13904	28422	9.81	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1310	13904	28423	9.81	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2409	14977	27551	1.66	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
3020	15636	28112	5.8	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
3020	15636	28113	5.8	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
5143	17714		2.95	3.0E-81	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2859	15478	27953	2.07	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121.5'
2859	15478	27954	2.07	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121.5'
3841	18440	28902	0.75	2.0E-81	AW811542.1	EST_HUMAN	hg85c01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384.3'
12591	18440	28902	2.77	2.0E-81	AW811542.1	EST_HUMAN	hg85c01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384.3'
1468	14060	26595	0.92	1.0E-81	W26539.1	EST_HUMAN	3313 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4813	17196	29642	1.81	1.0E-81	AA040370.1	EST_HUMAN	zk45h09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:485825.5' similar to PIR:S52437 S52437 CDP-diacylglycerol synthase - fruit fly
4750	17331	29774	8.65	1.0E-81	BE047896.1	EST_HUMAN	tz45c04.y1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291526.5'
5049	17622	30067	1.14	1.0E-81	AW182428.1	EST_HUMAN	xj42a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659852.3'
5446	18017	37139	3.85	1.0E-81	U87928.1	NT	Human aconitase hydratase (ACO2) gene, exon 3
5556	18188	30603	3.58	1.0E-81	11432968	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5556	18188	30604	3.58	1.0E-81	11432968	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5693	18319	30818	0.77	1.0E-81	AA255558.1	EST_HUMAN	zr85d06.r1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:682475.5' similar to SW:PRI2_HUMAN
5835	18459	31180	3.92	1.0E-81	U52351.1	NT	P49843 DNA PRIMASE 58 KD SUBUNIT
5835	18459	31181	3.92	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurexophilin (CTNND2) mRNA, partial cds
6295	18603	31674	1.82	1.0E-81	BF674641.1	EST_HUMAN	Homo sapiens arm-repeat protein NPRAP/neurexophilin (CTNND2) mRNA, partial cds
6836	19426	32242	0.73	1.0E-81	AJ133269.1	NT	602137864F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274536.5'
7748	20256	33151	7.93	1.0E-81	11432968	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7762	20270	33188	0.72	1.0E-81	AJ250408.1	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
							Homo sapiens GLI3 gene for GLI3 protein

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9691	22190	35163	13.75	1.0E-81	BE958278.1	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
9691	22190	35164	13.75	1.0E-81	BE958278.1	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
9679	22376	35353	4.13	1.0E-81	BE564367.1	EST_HUMAN	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685483 5'
							ac14d06.s1 Stratagene HeLa cell sc 937216 Homo sapiens cDNA clone IMAGE:856427 3' similar to SW:YB36_YEAST P38128 HYPOTHETICAL 60.5 KD PROTEIN IN RPS101-RPS13 INTERGENIC REGION.:
10014	22508	35500	1.16	1.0E-81	AA630784.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10016	22511	35502	2.84	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10018	22511	35503	2.84	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10402	22898	35892	1.47	1.0E-81	AW897550.1	EST_HUMAN	CM3-NN0059-140400-147-a12 NN0059 Homo sapiens cDNA
10867	23482	36508	2.02	1.0E-81	AW844986.1	EST_HUMAN	MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA
10867	23482	36509	2.02	1.0E-81	AW844986.1	EST_HUMAN	MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA
10871	23486	36514	1.57	1.0E-81	AW798167.1	EST_HUMAN	RC3-UM0046-290200-011-a08 UM0046 Homo sapiens cDNA
10871	23486	36515	1.57	1.0E-81	AW798167.1	EST_HUMAN	RC3-UM0046-290200-011-a08 UM0046 Homo sapiens cDNA
11152	18027	30489	2.07	1.0E-81	AW960658.1	EST_HUMAN	EST372729 MAGE resequences, MAGF Homo sapiens cDNA
11398	32850	36916	2.34	1.0E-81	BF204253.1	EST_HUMAN	601867714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
11920	24256	31012	3.39	1.0E-81	11418138	NT	Homo sapiens phorbol (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA
14	12683	25149	13.13	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
111	12683	25149	8.9	8.0E-82	AF161408.1	NT	Homo sapiens HSPC288 mRNA, partial cds
285	12941	25427	1.89	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
847	13463	25971	2.2	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
920	13533	26051	1.5	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
1337	14129	26865	1.12	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
							Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
1697	14280	28826	1.42	8.0E-82	5715801	NT	mRNA
4328	16914	29358	0.77	8.0E-82	8923432	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
1499	14091		1.45	7.0E-82	BF035327.1	EST_HUMAN	601458351F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
2794	15347	27916	1.21	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'
12395	24555		1.37	7.0E-82	AA155512.1	EST_HUMAN	n69e11.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:925196 3'
1710	14303	26840	20.15	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
5688	18314	30812	0.83	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-f08 HT0540 Homo sapiens cDNA
5688	18314	30813	0.83	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-f08 HT0540 Homo sapiens cDNA
							wp75609.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2467624 3' similar to TR:O75276 O75276 PKD1:
11583	24010	37080	5.53	4.0E-82	AI637300.1	EST_HUMAN	Homo sapiens presenilin-1 gene, exons 1 and 2
12178	24415		5.98	4.0E-82	AF028701.2	NT	

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
299	12955	25444	14.77	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
732	13352	25847	2.11	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010400-013-02 BN0120 Homo sapiens cDNA
820	13437	25944	8.87	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
903	13517	26035	3.37	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1099	13704		39.06	3.0E-82	AA725848.1	EST_HUMAN	ai23605.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
1398	13983	26522	1.11	3.0E-82	AW875073.1	EST_HUMAN	RC8-PT0001-190100-021-B02 PT0001 Homo sapiens cDNA
1515	14107	26843	2.15	3.0E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1945	14529	27085	1.59	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA
2050	14631	27202	1.18	3.0E-82	4501922	NT	Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) receptor type I (ADCYAP1R1) mRNA
3310	15921		2.54	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
5047	17020	30065	0.92	3.0E-82	AA135979.1	EST_HUMAN	zn83b04.r1 Striatagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565711 5' similar to SW:PAGT_BOVIN_Q07537 POLYPEPTIDE N-ACETYLGLACTOSAMINYL TRANSFERASE ;
8093	20834	33546	2.5	3.0E-82	11425206	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8491	21030	33949	0.82	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
8491	21030	33950	0.82	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
9738	22236	35215	5.16	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
9738	22236	35216	5.16	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
623	13250	25723	2.46	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
623	13250	25724	2.46	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1724	14315	26857	1.52	2.0E-82	AL046390.1	EST_HUMAN	DKFZp434M117_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434M117 5'
3837	16436	26898	1.47	2.0E-82	MB6876.1	NT	H. sapiens plasminogen-apolipoprotein (a) gene family, exon for 1st kringles 4 repeat
3973	16511	26973	1.03	2.0E-82	DB7675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4095	16690	29146	0.62	2.0E-82	U76833.1	NT	Human integral membrane serine protease Sepsin mRNA, complete cds
4317	16903	26347	0.66	2.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4656	17238	29693	1.38	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4656	17238	29694	1.38	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4895	17569	30013	2.59	2.0E-82	AF045555.1	NT	Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5239	17803	30223	1.36	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5239	17803	30224	1.36	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5320	17882	30301	1.3	2.0E-82	4502508	NT	Homo sapiens complement component 5 (C5) mRNA
5662	18289	30767	3.76	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
6322	18929	31705	4.77	2.0E-82	AF234882.1	NT	Homo sapiens FAM4A1 splice variant a (FAM4A1) mRNA, complete cds
7673	25121		1.02	2.0E-82	AI476428.1	EST_HUMAN	hm21g05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157272 3'
7771	20280	33177	0.71	2.0E-82	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8247	20788	33707	1.82	2.0E-82	11321570	NT	Homo sapiens slit (Drosophila) homolog 3 (SLIT3), mRNA
10018	22513	35505	1.45	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10018	22513	35508	1.45	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
11148	23657	36698	1.95	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11149	23657	36700	1.95	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11155	23662	36707	2.35	2.0E-82	11417105	NT	Homo sapiens 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMGCR), mRNA
11188	23693	36741	8.98	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11188	23693	36742	8.98	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11737	24140		4.92	2.0E-82	N94950.1	EST_HUMAN	zb31d10.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305203 3'
12299	24496		2.45	2.0E-82	AA011278.1	EST_HUMAN	z01g09.r1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429568 5'
618	13245	25718	1.59	1.0E-82	1154521	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1250	13847		1.25	1.0E-82	BE895106.1	EST_HUMAN	601510859F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5'
1329	13923	28443	2.7	1.0E-82	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
1330	13924	28444	0.84	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
8872	21411	34334	1.31	1.0E-82	AB037638.1	NT	Homo sapiens mRNA for KIAA1417 protein, partial cds
9571	22071	35032	0.48	1.0E-82	AB014582.1	NT	Homo sapiens mRNA for KIAA0662 protein, partial cds
10143	22638		1.19	1.0E-82	BF515838.1	EST_HUMAN	U1-H-BW1-80a-L03-Q-J1.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084053 3'
10824	23156	36169	2.41	1.0E-82	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10887	23408	36425	1.55	1.0E-82	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8949	21188	34106	4.39	9.0E-83	BF672220.1	EST_HUMAN	602150403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291561 5'
10175	22670	35964	0.78	9.0E-83	BE253347.1	EST_HUMAN	60117160F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3357734 5'
1459	14051	26583	4.53	8.0E-83	BE383973.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362 5'
1721	15394	26852	2.5	8.0E-83	N68951.1	EST_HUMAN	z848f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:285823 3'
1401	13995	26523	1	7.0E-83	AW385529.1	EST_HUMAN	QV4-LT0016-21299-068-h11 LT0016 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element
2890	15507		1.75	7.0E-83	AA584655.1	EST_HUMAN	7p37a07.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y316 Q9Y316
4940	17515		6.94	7.0E-83	BF221813.1	EST_HUMAN	DJ207H1.1;
6202	18812	31582	0.69	7.0E-83	11426657	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
428	13061	25555	3.97	6.0E-83	M3320.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
1822	14411	26956	2.07	6.0E-83	AW573088.1	EST_HUMAN	h131h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833525 3' similar to SW:YBEB_HAEIN P44471 HYPOTHETICAL PROTEIN H10034.;
3087	13702		0.81	6.0E-83	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3619	16222	28700	1.18	6.0E-83	11430241	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
5497	18131	30539	2.35	6.0E-83	4507868	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
6174	18785	31553	1.18	6.0E-83	AJ010770.1	NT	Homo sapiens hyperin gene, exons 1-50
7513	20034	32600	1.96	6.0E-83	11422024	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
9594	22094	35058	3.97	6.0E-83	4505314	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
9684	22183	35157	2.77	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Pp18 (PRP18), mRNA
9684	22183	35158	2.77	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Pp18 (PRP18), mRNA
11405	23856		6.84	6.0E-83	AA486105.1	EST_HUMAN	ab14e10.s1 Stratagene lung (837210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR 12 THR repetitive element ;
11685	24102		5.52	6.0E-83	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
982	13594		10.4	5.0E-83	U17883.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
2094	15397		1.12	5.0E-83	AF006305.1	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
3700	16301	28769	0.98	5.0E-83	AL133207.2	NT	Novel human gene mapping to chromosome X
3977	16575	28045	0.84	5.0E-83	4885190	NT	Homo sapiens deoxyribonuclease I (DNASE1), mRNA
4527	17111	29555	0.6	5.0E-83	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5238	17602	30221	13.17	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5238	17602	30222	13.17	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
668	13292	25773	1.34	4.0E-83	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3564	16168	28650	1.07	4.0E-83	BE888078.1	EST_HUMAN	601511580F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913195 5'
1035	13645		3.47	3.0E-83	AA368311.1	EST_HUMAN	EST70542 Placenta I Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9
6892	18288		0.88	3.0E-83	AI217223.1	EST_HUMAN	q73e06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755682 3'
1835	14423	26973	1.31	2.0E-83	AA883492.1	EST_HUMAN	q84g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614
1835	14423	26974	1.31	2.0E-83	AA909492.1	EST_HUMAN	q84g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614
1969	14553	27109	2.89	2.0E-83	NG6951.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216. ;
2876	15494	27984	1.06	2.0E-83	BE828694.1	EST_HUMAN	z948f12.s1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295923 3'

Single Exon Probes Expressed in Fetal Liver

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3307	15918		2.53	2.0E-83	11430834	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3842	18441		0.78	2.0E-83	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4429	17015	28457	4.01	2.0E-83	AF202879.1	NT	Homo sapiens hematopoietic progenitor cell antigen; CD34 precursor (CD34) mRNA, partial cds
4756	17337	29781	4.54	2.0E-83	7703398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
4756	17337	29782	4.54	2.0E-83	7703398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
5475	18109	30518	0.8	2.0E-83	U06678.1	NT	Human carcinoembryonic antigen gene family member 18 (CGM18) gene, exons A1 and B1
6119	18735	31488	1.28	2.0E-83	BE885401.1	EST_HUMAN	601507482F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906088 5'
7482	19885	32850	6.08	2.0E-83	AF129533.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds
7784	20327	33232	0.53	2.0E-83	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
7784	20327	33233	0.53	2.0E-83	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
7828	20470	33379	1.54	2.0E-83	U66707.1	NT	Rattus norvegicus desmin-180 mRNA, complete cds
8258	20787	33714	2.17	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
8258	20787	33715	2.17	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
8787	22285	35278	0.85	2.0E-83	BF128748.1	EST_HUMAN	601811127F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053894 5'
8947	22442	35419	2.41	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
8947	22442	35420	2.41	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
10025	22520	35516	1.12	2.0E-83	AU117659.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
10082	22587	35580	0.78	2.0E-83	AW505600.1	EST_HUMAN	UI-HF-BN0-amd-h-07-Q.U.I.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081852 5'
10729	23235	36271	4.98	2.0E-83	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
10806	23329	36340	1.95	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547J135 5'
10806	23329	36341	1.95	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547J135 5'
12342	24523		4.52	2.0E-83	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
1457	14049	26580	2.83	1.0E-83	4504328	NT	Homo sapiens hydroxacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1457	14049	26581	2.83	1.0E-83	4504328	NT	Homo sapiens hydroxacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1508	14098	26635	15.46	1.0E-83	AF105087.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
1506	14098	26636	15.46	1.0E-83	AF105087.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
2064	14844	27218	1.11	1.0E-83	4503652	NT	Homo sapiens fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1) mRNA
2681	15239	27807	1.08	1.0E-83	BE883690.1	EST_HUMAN	601507375F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908754 5'
3217	15828	28308	0.89	1.0E-83	7682349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0888), mRNA
3936	18534	29000	5.6	1.0E-83	AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
4328	18915	32356	2.45	1.0E-83	Z75822.1	NT	H. sapiens gene for mitochondrial dodecenoyl-CoA delta-isomerase, exon 3

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6797	19388	32204	1.58	1.0E-83	AI027614.1	EST_HUMAN	069b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1645431 3' similar to gb:M64241 QM PROTEIN (HUMAN);
3864	19462	28926	3.57	7.0E-84	BE901209.1	EST_HUMAN	601876023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958853 5'
1338	13932	28451	3.5	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
1338	13932	28452	3.5	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
2441	15008	27580	21.62	6.0E-84	AA776574.1	EST_HUMAN	ae88a03.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
5449	18019		2.84	6.0E-84	AL042863.2	EST_HUMAN	DKFZp434H0322_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0322 5'
5709	19335	30840	1.74	6.0E-84	AA807339.1	EST_HUMAN	al47g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460500 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
5841	18465	31189	1.06	6.0E-84	11428718	NT	Homo sapiens acyl LDL receptor; SREC=scavenger receptor expressed by endothelial cells (SREC); mRNA
5841	18465	31189	1.06	6.0E-84	11428718	NT	Homo sapiens acyl LDL receptor; SREC=scavenger receptor expressed by endothelial cells (SREC); mRNA
7489	20012	32878	3.2	6.0E-84	BE810371.1	EST_HUMAN	PM0-LT0019-190600-004-F02 LT0019 Homo sapiens cDNA
7679	20190	33079	0.93	6.0E-84	AF038391.1	NT	Homo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete cds
8018	20560	33461	1.85	6.0E-84	BE770199.1	EST_HUMAN	PM4-FT0054-160600-004-e10 FT0054 Homo sapiens cDNA
11409	23660		2	6.0E-84	AW369812.1	EST_HUMAN	IL0-BT0168-091199-139-e08 BT0168 Homo sapiens cDNA
743	13363	25858	0.69	5.0E-84	AA382811.1	EST_HUMAN	EST96094 Testis I Homo sapiens cDNA 5' end
3048	15684		1.4	5.0E-84	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
11419	23870	36931	2.7	5.0E-84	11428740	NT	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA
11506	23955	37024	1.95	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
11506	23955	37025	1.95	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
1456	14048	28579	2.3	4.0E-84	AI685321.1	EST_HUMAN	wa76c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN_043847 NARDILYSIN PRECURSOR;
5085	17658	30099	0.79	4.0E-84	4505928	NT	Homo sapiens polymerase (DNA-directed), alpha (70KD) (POLA2), mRNA
5086	17659	30100	1.62	4.0E-84	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5751	18377	31087	1.42	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5751	18377	31088	1.42	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
6414	19017	31800	2.16	4.0E-84	AF059650.1	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
7843	20155	33041	13.58	4.0E-84	11421326	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
8842	21381	34305	1.06	4.0E-84	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
8842	21381	34306	1.06	4.0E-84	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
10798	23321	36331	5.76	4.0E-84	AB032956.1	NT	Homo sapiens mRNA for KIAA1130 protein, partial cds
338	12990	25477	1.97	3.0E-84	AF026200.1	NT	Homo sapiens Bact1 protein homolog mRNA, partial cds

Table 4

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1184	13785	26304	0.86	3.0E-84	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2003	14585	27144	1.93	3.0E-84	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
2051	14632	27203	1.94	3.0E-84	AL086880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
3812	16411	28876	5.94	3.0E-84	AF014458.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLR51) mRNA, complete cds
10758	23282		10.76	3.0E-84	AI983801.1	EST_HUMAN	wu20d05.x1 Soares_Dieckgraebe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to gb:U05093.60S RIBOSOMAL PROTEIN L18A (HUMAN);
2153	14730	27304	6.66	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA
2153	14730	27305	6.66	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA
2970	15588	28068	11.6	2.0E-84	AF036943.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1-L) mRNA, complete cds
2989	15505	28085	1.3	2.0E-84	X89211.1	NT	H sapiens DNA for endogenous retroviral like element
5717	18343	30849	1.02	2.0E-84	BF511575.1	EST_HUMAN	U1-H-B14-ed-a-02-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084963 3'
5717	18343	30850	1.02	2.0E-84	BF511575.1	EST_HUMAN	U1-H-B14-ed-a-02-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084963 3'
6748	19341	32148	1.04	2.0E-84	H83370.1	EST_HUMAN	yf56a11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:209324 3'
8001	20543		1.51	2.0E-84	AI298674.1	EST_HUMAN	qm87c09.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1895728 3'
9269	21785	34744	0.89	2.0E-84	AU120280.1	EST_HUMAN	AU120280 HEMBB1 Homo sapiens cDNA clone HEMBB1000339 5'
9647	22146	35117	0.55	2.0E-84	H22841.1	EST_HUMAN	ym49e11.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:51383 5' similar to SP.APOH_RAT P26844 BETA-2-GLYCOPROTEIN I;
11954	24270	31021	1.89	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupskl_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756G23.1;
11954	24279	31022	1.89	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupskl_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756G23.1;
334	12986	25473	1.61	1.0E-84	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
575	13205	25885	7.74	1.0E-84	4507952	NT	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
749	13369		4	1.0E-84	11427631	NT	Homo sapiens complement component 5 (C5), mRNA
1336	13930	28449	3.89	1.0E-84	AA084379.1	EST_HUMAN	am85b11.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629885 3'
2099	14678	27246	2.49	1.0E-84	BE392137.1	EST_HUMAN	601308006F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3628257 5'
2265	14839	27415	1.21	1.0E-84	11427197	NT	Homo sapiens pericentriolar material 1 (PCM1), mRNA
2945	15561	28035	1.09	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
2945	15561	28036	1.09	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3814	16414	28878	2.92	1.0E-84	AA720851.1	EST_HUMAN	nw12606.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239106 3'
4508	17092	29539	6.06	1.0E-84	AJ226041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4809	17367	29837	3.09	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hlec3) Homo sapiens cDNA clone DKFZp434N0323 5'
4809	17387	29838	3.09	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hlec3) Homo sapiens cDNA clone DKFZp434N0323 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5037	17092	29539	3.8	1.0E-84	AJ228041.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6079	18696	31443	0.81	1.0E-84	114334422	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA
							uterine water channel=28 kda erythrocyte integral membrane protein homolog [human, uterus, mRNA, 1340 nt]
6337	18943	31722	1.46	1.0E-84	S73482.1	NT	Novel human gene mapping to chromosome 13
6981	19538	32361	1.63	1.0E-84	AL048784.1	NT	Novel human gene mapping to chromosome 13
6981	19538	32362	1.63	1.0E-84	AL048784.1	NT	Novel human gene mapping to chromosome 13
7162	18894	32540	2.39	1.0E-84	AL048784.1	NT	Novel human gene mapping to chromosome 13
7486	20009	32875	3.27	1.0E-84	8393894	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
7565	20082	32968	1.18	1.0E-84	11430846	NT	Homo sapiens NGFI-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
7598	20082	32998	2.45	1.0E-84	11430846	NT	Homo sapiens NGFI-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
8454	21880		4.5	1.0E-84	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PPI5), mRNA
8685	22184	35159	0.58	1.0E-84	AF224511.1	NT	Homo sapiens Ca ²⁺ -binding protein CABP3 (CABP3) gene, exon 6 and partial cds
9706	15561	28035	2.37	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
9706	15561	28036	2.37	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
11833	24198		2.44	1.0E-84	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
11943	24274	31017	3.97	1.0E-84	11418185	NT	Homo sapiens ecanitase 2, mitochondrial (ACO2), mRNA
1002	13613		4.54	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1111	13715	26224	6.29	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1111	13715	26225	6.29	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1424	14017	26546	1.35	9.0E-85	4759669	NT	Homo sapiens leupaxin (LDPL), mRNA
1622	14215	26746	9.44	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1622	14215	26747	9.44	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1714	14306	26845	2.45	9.0E-85	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA
4338	16925	29366	0.97	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5006	17579	30023	0.86	9.0E-85	5901979	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
5038	17611	30055	1.02	9.0E-85	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1175	13777	26287	10.28	7.0E-85	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
11499	23948		11.38	7.0E-85	AF113210.1	NT	Homo sapiens MSTP030 mRNA, complete cds
11294	23746	36803	3.15	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11294	23746	36804	3.15	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
2371	14941	27514	1.09	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084

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4525	17109		0.59	5.0E-95	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA1I) mRNA, complete cds
5642	18271	30744	1.42	5.0E-95	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862402 5'
5642	18271	30745	1.42	5.0E-95	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862402 5'
10698	23512	38545	1.95	5.0E-95	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12589	17109		3.17	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA1I) mRNA, complete cds
6297	18905	31675	1.63	4.0E-85	BF877910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
6297	18905	31676	1.63	4.0E-85	BF877910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
10484	22958		1.64	4.0E-85	BE079283.1	EST_HUMAN	RC1-BT0623-120200-011-c07 BT0623 Homo sapiens cDNA
1342	13937	26458	0.88	3.0E-85	AF096157.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1816	14406	26950	5.05	3.0E-85	T87495.1	EST_HUMAN	y53g09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121504 5'
4405	16990	29434	0.93	3.0E-85	BE267189.1	EST_HUMAN	601189704F2 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3533816 5'
5025	17599	30043	1.44	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
5025	17599	30044	1.44	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
6283	18891	31659	6.49	3.0E-85	7662309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
6283	18891	31660	6.49	3.0E-85	7662309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
7032	19568		7.22	3.0E-85	AJ404468.1	NT	Homo sapiens mRNA for dymin heavy chain (DNAH9 gene)
7428	19952	32817	0.95	3.0E-85	11416870	NT	Homo sapiens GTPase regulator associated with the focal adhesion kinase pp125(FAK); KIAA0821 protein (KIAA0821), mRNA
7813	20350	33264	1.55	3.0E-85	U44953.1	NT	Homo sapiens DENN mRNA, complete cds
8445	20985	33900	0.78	3.0E-85	11525828	NT	Homo sapiens CGI-81 protein (LOC51108), mRNA
8908	21447	34369	3.75	3.0E-85	11430889	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
9230	21952	34901	1.32	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B" (SNRNPB2), mRNA
9230	21952	34902	1.32	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B" (SNRNPB2), mRNA
10377	22871	35864	0.81	3.0E-85	AF098642.1	NT	Homo sapiens phospholipid scramblase mRNA, complete cds
11360	23832	36895	2.26	3.0E-85	5031660	NT	Homo sapiens EGF-like repeats and discordin 1-like domains 3 (EDL3), mRNA
12470	24595		2.19	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
988	13609	26124	3.12	2.0E-85	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1078	13683	26194	2.1	2.0E-85	AF248540.1	NT	Homo sapiens interectin 2 (SH3D1B) mRNA, complete cds
1450	14042	26570	3.85	2.0E-85	7706205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
1465	14057	26590	32.65	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1485	14057	26591	32.65	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2274	14848	27424	2.27	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2850	13978		8.53	2.0E-85	7857488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3057	15673	28149	1.18	2.0E-85	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4427	17013	29455	7.95	2.0E-85	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4884	17248	28700	8.24	2.0E-85	4826977	NT	Homo sapiens reelin (RELN) mRNA
5038	17610	30054	1.19	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5313	17875	30287	1.73	2.0E-85	4502212	NT	Homo sapiens arginase, liver (ARG1) mRNA
9197	21714	34658	1.33	2.0E-85	A1760820.1	EST_HUMAN	w167h08.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2398431 3' similar to contains element MSRI repetitive element;
9367	22067	35027	0.84	2.0E-85	A1914459.1	EST_HUMAN	w44903.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331461 3'
10163	22658	35654	1.38	2.0E-85	A1866384.1	EST_HUMAN	wm94d12.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443607 3'
2328	14897		2.43	1.0E-85	BE794306.1	EST_HUMAN	601591416F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5'
2437	15004	27576	8.29	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
2437	15004	27577	8.29	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
9898	22195	35168	2.03	1.0E-85	BE267817.1	EST_HUMAN	601109738F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350553 5'
10804	23327	36337	2.67	1.0E-85	AA778785.1	EST_HUMAN	Z45f03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
10804	23327	36338	2.67	1.0E-85	AA778785.1	EST_HUMAN	Z45f03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
10878	23397	36413	2.59	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
10878	23397	36414	2.59	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
10943	23459	36482	2.48	1.0E-85	Y00052.1	NT	Human mRNA for T-cell cyclophilin
11605	24048	37114	2.17	1.0E-85	A198420.1	EST_HUMAN	q158a07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1860468 3'
11838	24363	30869	4.42	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12098	24363	30969	5.48	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1475	14067		17.55	9.0E-88	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5'
6275	18983	31651	1.65	8.0E-86	11424140	NT	Homo sapiens similar to CDC28 protein kinase 1 (H. sapiens) (LOC63041), mRNA
11543	23991	37093	1.85	8.0E-86	4503224	NT	Homo sapiens cytochrome P450, subfamily IIF, polypeptide 1 (CYP2F1) mRNA
244	12903	25384	0.68	7.0E-86	7662247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
972	13593	26096	1.06	7.0E-86	AA860801.1	EST_HUMAN	aj88f08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
972	13583	26087	1.06	7.0E-86	AA860801.1	EST_HUMAN	aj88f08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
6343	18049	31726	1.01	7.0E-86	9968886	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6343	18049	31727	1.01	7.0E-86	9968886	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7053	18072	30463	5.8	7.0E-86	11421737	NT	Homo sapiens Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
8678	21218	34138	3.41	7.0E-86	L38557.1	NT	Homo sapiens galactose oxidase (GALC) gene, exon 15

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9816	22116		1.53	7.0E-86	5453987	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
9873	22172	35148	1.82	7.0E-86	11526307	NT	Homo sapiens DGeorge syndrome critical region gene 9 (DGC9), mRNA
10841	23362	36377	2.38	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
10841	23362	36378	2.38	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
11638	24077	37137	2.7	7.0E-86	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1337	13931	26450	2.34	6.0E-86	4505492	NT	Homo sapiens oxoglutarate dehydrogenase (lipoamide) (OGDH) mRNA
226	12886	25373	2.46	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
6185	18795	31563	10.86	4.0E-86	BE295843.1	EST_HUMAN	601176865F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3531953 5'
11120	12886	25373	1.86	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
4377	16964	26410	0.64	3.0E-86	BE867703.1	EST_HUMAN	601443262F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3647455 5'
5782	18407	31123	6.23	3.0E-86	AW340946.1	EST_HUMAN	z62h12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871719 3'
8205	20746	33658	1.15	3.0E-86	AV722329.1	EST_HUMAN	AV722329 HTB Homo sapiens cDNA clone HTBBD04 5'
10121	22616	36609	3.12	3.0E-86	BE868479.1	EST_HUMAN	601509696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
10121	22616	36607	3.12	3.0E-86	BE868479.1	EST_HUMAN	601509696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
11312	23010	36018	10.63	3.0E-86	AI659240.1	EST_HUMAN	lu1B02.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2251371 3'
11808	24893		3.18	3.0E-86	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638753 5'
288	12944	25429	2.06	2.0E-86	AA306264.1	EST_HUMAN	EST177232 Jurkat T-cells VI Homo sapiens cDNA 5' end
439	13072		2.33	2.0E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1232	13831	26345	2.18	2.0E-86	N58977.1	EST_HUMAN	yz19a08.r1 Soares multiple sclerosis 2NBMSP Homo sapiens cDNA clone IMAGE:283478 5'
2233	14808	27381	1.95	2.0E-86	9635487	NT	Human endogenous retrovirus, complete genome
3462	16069	28542	1.38	2.0E-86	AW966142.1	EST_HUMAN	EST378215 IMAGE resequences, MAGI Homo sapiens cDNA
3809	16408	28872	2.89	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3809	16408	28873	2.89	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
4113	16707		3.01	2.0E-86	AW515742.1	EST_HUMAN	hd87g08.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2916542 3'
4904	17479	29937	3.25	2.0E-86	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
6032	18651	31392	1.55	2.0E-86	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
6032	18651	31393	1.55	2.0E-86	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
7134	24773	32294	0.86	2.0E-86	11419429	NT	Homo sapiens similar to eukaryotic pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
7982	20494	33403	0.6	2.0E-86	U84744.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8453	20993		0.54	2.0E-86	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8509	21048	33969	2.19	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8509	21048	33970	2.19	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
8834	21373	34298	1.29	2.0E-86	10863876	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
9242	21768	34717	2.08	2.0E-86	11422084	NT	Homo sapiens chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA
10344	22838	35833	2.82	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10344	22838	35834	2.82	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10347	22841	35837	1.85	2.0E-86	11417120	NT	Homo sapiens hypothetical protein FLJ20125 (FLJ20125), mRNA
10397	22891	35885	0.85	2.0E-86	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
10784	23308	36315	1.94	2.0E-86	4759051	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5) mRNA
12269	24476	30935	3.82	2.0E-86	11418189	NT	Homo sapiens thyroid autotigen 70kD (Ku antigen) (G22P1), mRNA
12452	24586		3.38	2.0E-86	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
1641	14233	26767	1.33	1.0E-86	4826855	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA
3198	15810	28283	1.54	1.0E-86	5453849	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3272	15884	28366	3.1	1.0E-86	L20492.1	NT	Homo gamma-glutamyl transpeptidase mRNA, complete cds
3335	15945	28420	1.24	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3335	15945	28421	1.24	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4018	16816	29090	0.98	1.0E-86	7708181	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
4018	16816	29091	0.98	1.0E-86	7708181	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
4351	16938	29380	5.98	1.0E-86	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
5042	17615	30059	0.9	1.0E-86	AF100751.1	NT	Homo sapiens FK506-binding protein FKBP23 isoform mRNA, complete cds
5741	18367	31074	1.62	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5559	18191		1.72	9.0E-87	AI150703.1	EST_HUMAN	qb77c09.x1 Soares_fetal_hes1 NbHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE_P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
7472	18994	32857	1.78	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
7472	18994	32858	1.78	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
505	13137	25625	84.08	8.0E-87	X62245.1	NT	O. cuticulus mRNA for elongation factor 1 alpha
2335	14908	27477	2.29	7.0E-87	BF063211.1	EST_HUMAN	7h85f02.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3322779 3'
2335	14908	27478	2.29	7.0E-87	BF063211.1	EST_HUMAN	7h85f02.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3322779 3'
6533	18133	31926	0.86	7.0E-87	AF890336.1	EST_HUMAN	MR0-NT0039-020500-004-a11 NT0039 Homo sapiens cDNA
8130	20671	33581	2.87	7.0E-87	BF352778.1	EST_HUMAN	IL3-HT0619-080700-198-D10 HT0619 Homo sapiens cDNA
9375	20314	33216	0.67	7.0E-87	BE712861.1	EST_HUMAN	IL5-HT0702-160600-103-d08 HT0702 Homo sapiens cDNA
9983	22478	35460	3.7	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
9983	22478	35481	3.7	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10770	23284	36289	11	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A
10770	23284	36300	11	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A
3578	18183	28665	0.82	6.0E-87	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
6553	19151	31947	1.54	6.0E-87	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
10603	23137		8.8	6.0E-87	11432444	NT	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC63102), mRNA
1200	13801	26313	2.58	5.0E-87	AA382811.1	EST_HUMAN	EST06094 Testis 1 Homo sapiens cDNA 5' end
12100	13801	26313	2.47	5.0E-87	AA382811.1	EST_HUMAN	EST06094 Testis 1 Homo sapiens cDNA 5' end
1001	13612	26128	0.85	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1214	13814	26328	11.73	4.0E-87	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1476	14068	26605	3.14	4.0E-87	R78133.1	EST_HUMAN	y80f10.r1 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element
2466	15033	27599	2.57	4.0E-87	7706239	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
2468	15033	27600	2.57	4.0E-87	7706239	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
3511	16118	28595	1.82	4.0E-87	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) homoblog), translocated to, 4 (MLLT4) mRNA
5439	17994		0.92	4.0E-87	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5637	18268	30738	11.09	4.0E-87	O00321	SWISSPROT	ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2)
5925	18547	31273	0.72	4.0E-87	U85428.1	NT	Human transcription factor NFATx3 mRNA, complete cds
6198	18808	31575	4.42	4.0E-87	BE247284.1	EST_HUMAN	TCBAP1E4051 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4051
11044	23558	36504	5.04	4.0E-87	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
11623	24065	37130	2.12	4.0E-87	11417339	NT	Homo sapiens similar to heat shock 70kD protein 98 (mortalin-2) (H. sapiens) (LOC63184), mRNA
12202	24947	30623	1.81	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12202	24947	30624	1.81	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12371	24541		17.18	4.0E-87	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
2805	15357	27924	2.34	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA
2975	15591		1.1	2.0E-87	BF327820.1	EST_HUMAN	QVQ-BN0148-050860-254-a03 BN0148 Homo sapiens cDNA
3852	16450	28913	0.78	2.0E-87	AU116935.1	EST_HUMAN	AU116935 HEMBA1 Homo sapiens cDNA clone HEMBA1000307 5'
5039	17612	30056	0.6	2.0E-87	BF376311.1	EST_HUMAN	CMO-TN0038-150900-552-h08 TN0038 Homo sapiens cDNA
5842	18466	31191	12.69	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
5842	18466	31192	12.69	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
6488	19069		6.41	2.0E-87	BE567193.1	EST_HUMAN	6013471393F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3883348 5'
6800	19391	32206	2.12	2.0E-87	N48128.1	EST_HUMAN	yw21607.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6877	19811	32444	0.93	2.0E-87	AV654143.1	EST_HUMAN	AV654143 GLC Homo sapiens cDNA clone GLCDSG04.3'
7225	19756	32611	1.43	2.0E-87	BE284432.1	EST_HUMAN	601176032F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531511 5'
7277	19805	32684	0.76	2.0E-87	11433048	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
7476	19998	32663	31.97	2.0E-87	N48128.1	EST_HUMAN	yc21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
7676	20187	33075	33.12	2.0E-87	N48128.1	EST_HUMAN	yc21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
8334	20875	33787	15.53	2.0E-87	X52851.1	NT	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)
9700	22199		5.14	2.0E-87	BE531136.1	EST_HUMAN	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA
1224	15392		1.66	1.0E-87	7705983	NT	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
1478	14070	26607	1.21	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
1478	14070	26608	1.21	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
3772	16373	28838	6.15	1.0E-87	Y00052.1	NT	Human mRNA for T-cell cyclophilin
3798	16396	28861	2.65	1.0E-87	4758827	NT	Homo sapiens neuroxin III (NRXN3), mRNA
5283	17845	30272	1.14	1.0E-87	U50849.1	NT	Rattus norvegicus taste bud receptor protein TB 641 (TB 641) gene, complete cds
6374	18978	31758	2.17	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
6374	18978	31757	2.17	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
7229	19760	32816	0.72	1.0E-87	AF039517.1	NT	Homo sapiens corticotropin-releasing factor type 1 receptor gene, exon 8
7229	19760	32816	0.72	1.0E-87	AF039517.1	NT	Homo sapiens corticotropin-releasing factor type 1 receptor gene, exon 8
7235	19765	32821	1	1.0E-87	4508788	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
7430	19954	32819	1.18	1.0E-87	11431500	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
8059	20601	33511	10.74	1.0E-87	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
8840	21379	34302	1.01	1.0E-87	AB022818.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
8840	21379	34303	1.01	1.0E-87	AB022818.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
9551	22051	35013	3.71	1.0E-87	BE818183.1	EST_HUMAN	RC8-BN0278-050700-012-E02 BN0278 Homo sapiens cDNA
9551	22051	35014	3.71	1.0E-87	BE818183.1	EST_HUMAN	RC8-BN0278-050700-012-E02 BN0278 Homo sapiens cDNA
10275	22770	36758	0.89	1.0E-87	M34426.1	NT	Human L-plastin mRNA, 5' and
10911	23144	36155	2.84	1.0E-87	5728967	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
10978	23399		1.82	1.0E-87	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12198	25086		2.92	1.0E-87	7657632	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
955	13667	26081	5.21	9.0E-88	5453867	NT	Homo sapiens protease inhibitor 4 (kallistatin) (P14), mRNA
1145	13748	26257	8.79	9.0E-88	AF187465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1393	13987	26514	2.74	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
1393	13987	26515	2.74	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
3689	16280	28759	1.7	9.0E-88	AL193209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4356	16943	28385	3.11	9.0E-88	X91928.1	NT	H. sapiens ECE-1 gene (exon 9)

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4356	16943	29386	3.11	9.0E-88	X91929.1	NT	H.sapiens ECE-1 gene (exon 9)
5146	17718	30147	1.11	9.0E-88	AB026888.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8951	21489	34412	3.16	6.0E-88	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1868	14454		0.86	5.0E-88	7661887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2666	15224	27797	2.31	5.0E-88	N89399.1	EST_HUMAN	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
3031	15647	28125	0.77	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3044	15660	28140	0.81	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3044	15660	28141	0.91	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3436	16044		2.91	5.0E-88	AI693217.1	EST_HUMAN	wd68b08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2336799 3' similar to contains Alu repetitive element; contains element MER22 MER22 repetitive element ;
3588	16192	28676	0.76	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
4843	17421	29874	0.79	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
6868	18602	32434	2.99	5.0E-88	Y10932.1	EST_HUMAN	ym06b10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:47129 5'
7870	20412	33318	1.73	5.0E-88	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9236	21762	34708	0.54	5.0E-88	BF680206.1	EST_HUMAN	602154958F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295775 5'
11942	14454		1.37	5.0E-88	7661887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
1374	13968	26495	1.93	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
1374	13968	26496	1.93	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
7292	19820	32879	2.25	4.0E-88	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
10789	23312	36320	1.93	4.0E-88	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
11362	23814	36874	2.42	4.0E-88	7661847	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
11362	23814	36875	2.42	4.0E-88	7661847	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
761	13380	25877	0.96	3.0E-88	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1848	14438		2.59	3.0E-88	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
2874	15590	28073	4.76	3.0E-88	N66951.1	EST_HUMAN	za48f12.61 Soares fetal liver spleen 1N1S Homo sapiens cDNA clone IMAGE:295823 3'
4325	16911	29352	0.64	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4325	16911	29353	0.64	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4576	17159		4.33	3.0E-88	11429300	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
5502	18136	30546	2.95	3.0E-88	11429567	NT	Homo sapiens valcain-containing protein (VCP), mRNA
5773	18398	31112	4.24	3.0E-88	5965888	NT	Homo sapiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA
5882	18504	31230	3.86	3.0E-88	11420697	NT	Homo sapiens v-ral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6309	18918	31690	1.3	3.0E-88	11417370	NT	Homo sapiens interleukin 13 (IL13), mRNA
6545	24764	31938	0.99	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6545	24764	31939	0.99	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7125	19465	32283	15.2	3.0E-88	AF279265.1	NT	Homo sapiens putative anion transporter 1 mRNA, complete cds
7548	20068	32940	5.75	3.0E-88	11436400	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
7861	20403	33310	9.25	3.0E-88	11421728	NT	Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA
8137	20678	33589	1.57	3.0E-88	AF034374.1	NT	Homo sapiens myoblast fusion factor 1 (myoblast fusion factor 1) (MFBF1), mRNA
9355	20294	33183	2.09	3.0E-88	11526262	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
8941	22339	35320	0.87	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
9841	22339	35321	0.87	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
9867	22364	35343	0.89	3.0E-88	11439085	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
11928	24263	30828	5.36	3.0E-88	11417974	NT	Homo sapiens transcobalamin II, macrocytic anemia (TCN2), mRNA
11944	24954	30828	1.26	3.0E-88	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12889	24738	30828	1.41	3.0E-88	11528140	NT	Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA
1074	13679	26168	1.87	2.0E-88	7305198	NT	Homo sapiens Caldesin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1665	14258	28792	1.57	2.0E-88	AF248219.1	NT	Homo sapiens SNARE protein kinase SNARE mRNA, complete cds
1786	14376	28820	4.58	2.0E-88	AF248219.1	NT	Homo sapiens SNARE protein kinase SNARE mRNA, complete cds
4518	17100	28547	2.07	2.0E-88	5031666	NT	Homo sapiens dynein, axonemal, light polypeptide 4 (DNAL4), mRNA
6070	18687	31430	5.11	1.0E-88	AW139565.1	EST_HUMAN	U1-H-B11-aaa-d-04-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
6070	18687	31431	5.11	1.0E-88	AW139565.1	EST_HUMAN	U1-H-B11-aaa-d-04-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
6753	19346	32153	22.7	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
6753	19346	32154	22.7	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
7176	19708	32556	1.3	1.0E-88	AB09034.1	EST_HUMAN	wg70a12.x1 NCI_CGAP_GCB Homo sapiens cDNA clone IMAGE:824732 3' similar to WP.B0272.2
7238	19768	32822	4.05	1.0E-88	AA488981.1	EST_HUMAN	aa54a11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP.B0272.2
9168	21743	34886	0.9	1.0E-88	AA180388.1	EST_HUMAN	CE00851 ;
9499	21999	34956	3.09	1.0E-88	AL043314.2	EST_HUMAN	zp87c02.r1 Stratiagene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:827170 5' similar to SW:POL1_HUMAN P10268 RETROVIRUS-RELATED POL POLYPROTEIN ;
11319	23017	36028	6.14	1.0E-88	AA891479.1	EST_HUMAN	DKFZp434N0323.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
12160	24400		5.36	1.0E-88	AL163246.2	NT	os91g03.s1 NCI_CGAP_GCB3 Homo sapiens cDNA clone IMAGE:1612758 3' similar to gb.M16342
10830	23351	36366	3.58	9.0E-89	11421238	NT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);
							Homo sapiens chromosome 21 segment HS21C048
							Homo sapiens transgelin 2 (TAGLN2), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2763	16317	27684	1.05	8.0E-89	BE311557.1	EST_HUMAN	601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506186 5'
7012	19510	32331	1.07	8.0E-89	11421514	NT	Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
458	13092	25585	1.26	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
458	13092	25586	1.26	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
5012	17588	30028	2.51	7.0E-89	4557390	NT	Homo sapiens complement component 8, beta polypeptide (C8B), mRNA
5064	17637	30060	6.15	7.0E-89	AL045748.1	EST_HUMAN	DKFZp434E246_r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434E246 5'
5623	18252	30720	1.26	7.0E-89	X99832.1	NT	H. sapiens CLN3 gene, complete CDS
5623	18252	30721	1.26	7.0E-89	X99832.1	NT	H. sapiens CLN3 gene, complete CDS
6483	19084	31865	1.06	7.0E-89	7549808	NT	Homo sapiens plasmin 3 (T1 isoform) (PLS3), mRNA
6483	19084	31866	1.06	7.0E-89	7549808	NT	Homo sapiens plasmin 3 (T1 isoform) (PLS3), mRNA
7510	20031	32866	1.86	7.0E-89	11420754	NT	Homo sapiens actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1A), mRNA
7620	20362	33269	0.51	7.0E-89	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
7820	20362	33270	0.51	7.0E-89	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8415	20955	33872	0.83	7.0E-89	J02923.1	NT	Human 65-kilodalton phosphoprotein (p65) mRNA, complete cds
10423	22917	35917	1.3	7.0E-89	X62048.1	NT	H. sapiens Wee1 hu gene
10423	22917	35918	1.3	7.0E-89	X62048.1	NT	H. sapiens Wee1 hu gene
10440	22934	35942	0.97	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
10440	22934	35943	0.97	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
12604	24905		1.86	7.0E-89	J05235.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
1061	13668	26177	1.41	6.0E-89	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (IMMT), mRNA
2254	14828	27404	1.24	6.0E-89	4506124	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA
2477	15044	27611	1.37	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
2477	15044	27612	1.37	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
3577	16181	28663	0.91	6.0E-89	7661817	NT	Homo sapiens HSPC159 protein (HSPC159), mRNA
4743	17324	29765	3	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4743	17324	29766	3	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
5366	17628	30340	0.62	6.0E-89	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5366	17926	30341	0.62	6.0E-89	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5234	17768	30216	2.68	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylar-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
5234	17768	30217	2.68	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylar-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
7587	20102	32977	0.91	4.0E-89	BE762749.1	EST_HUMAN	QV3-NT0022-080600-219-g03 NT0022 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11020	23534	36570	1.69	4.0E-89	AI798872.1	EST_HUMAN	we01c03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348452 3'
2801	15518	27888	2.21	3.0E-89	AW976181.1	EST_HUMAN	EST388290 IMAGE ressequences, MAGN Homo sapiens cDNA
7194	18725	32575	1.5	3.0E-89	AI217359.1	EST_HUMAN	qh17b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844915 3'
10878	23210	36221	2.24	3.0E-89	N57357.1	EST_HUMAN	yw88e11.r1 Soares_placenta_8to9weeks_2NbpHP8c9W Homo sapiens cDNA clone IMAGE:259148 5'
12270	24840	30799	2.82	3.0E-89	AV708431.1	EST_HUMAN	similar to SW:P14K_HUMAN P42356 PHOSPHATIDYLINOSITOL 4-KINASE ALPHA ;
12364	24537	30902	1.32	3.0E-89	AV705749.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
132	13066	25561	0.74	2.0E-89	7706670	NT	AV705749 ADB Homo sapiens cDNA clone ADBBGA01 5'
132	13066	25562	0.74	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
433	13066	25561	0.65	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
433	13066	25562	0.65	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
1828	14415	26862	1.71	2.0E-89	AJ238277.1	NT	Homo sapiens mRNA for cancer-testis-associated protein (CTP11 gene)
2805	15522	27992	1.84	2.0E-89	AI222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131
3608	16212	28691	0.67	2.0E-89	AA759149.1	EST_HUMAN	GAMMA-GLUTAMYLTRANSEPTIDASE 1 PRECURSOR (HUMAN)/contains Alu repetitive element;
3608	16212	28692	0.67	2.0E-89	AA759149.1	EST_HUMAN	ah70e03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320988 3'
4226	16814	29261	1.18	2.0E-89	AF080997.1	NT	ah70e03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320988 3'
4233	16821	29271	5.23	2.0E-89	X58742.1	NT	Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds
4233	16821	29272	5.23	2.0E-89	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4441	17027	29487	0.7	2.0E-89	AL163203.2	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4596	17178	29628	1.52	2.0E-89	AJ007378.1	NT	Homo sapiens chromosome 21 segment HS21C003
5546	18178	30780	1.07	2.0E-89	BE541744.1	EST_HUMAN	Homo sapiens GGT gene, exon 5
5672	18299	30780	3.13	2.0E-89	AB007546.1	NT	601065996F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452423 5'
5960	18582	31316	1.44	2.0E-89	U03985.1	NT	Homo sapiens gene for LECT2, complete cds
6358	18962	31739	0.7	2.0E-89	AL163285.2	NT	Human N-ethylmaleimide-sensitive factor mRNA, partial cds
7694	20176	33063	4.46	2.0E-89	U81004.1	NT	Homo sapiens chromosome 21 segment HS21C085
7875	20417	33325	3.22	2.0E-89	1142880.1	NT	Human GT24 (GT24) mRNA, partial cds
8356	20898	33816	1	2.0E-89	AJ245503.1	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
9177	21754	34701	0.69	2.0E-89	AB037754.1	NT	Homo sapiens partial mRNA for PEX5-related protein
9724	22222	35197	0.65	2.0E-89	AF170814.1	NT	Homo sapiens mRNA for KIAA1333 protein, partial cds
9724	22222	35198	0.65	2.0E-89	AF170814.1	NT	Homo sapiens CaBP5 (CABP5) gene, exon 5

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11252	23782	36838	2.58	2.0E-89	11434411	NT	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
11444	23894	36959	5.1	2.0E-99	11433673	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
11584	24011	37081	2.25	2.0E-89	U10892.1	NT	Human MAGE-7 antigen (MAGE7) pseudogene, complete cds
11449	23899	36965	6.8	1.0E-89	BF196052.1	EST_HUMAN	h181d09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778
11449	23899	36966	6.8	1.0E-89	BF196052.1	EST_HUMAN	SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN ;
8169	20710	33026	1.59	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8169	20710	33027	1.59	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1101	13706	28214	1.9	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1102	13706	28214	2.3	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1375	15439	28497	4.58	8.0E-90	BE670581.1	EST_HUMAN	7a36f08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1375	15439	28498	4.58	8.0E-90	BE670581.1	EST_HUMAN	7a36f08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
8495	21034	33955	0.88	8.0E-90	BE177830.1	EST_HUMAN	RC1-HT0598-120400-022-b08 HT0598 Homo sapiens cDNA
10579	23114	36127	1.61	8.0E-90	AI222085.1	EST_HUMAN	q99608.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
10579	23114	36128	1.61	8.0E-90	AI222085.1	EST_HUMAN	q99608.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
869	13484		4.46	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8363	20903		1.73	7.0E-90	AA782877.1	EST_HUMAN	ai63d08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375503 3'
8896	21434	34357	1.47	7.0E-90	BE982525.2	EST_HUMAN	601655837R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3855824 3'
8896	21434	34358	1.47	7.0E-90	BE982525.2	EST_HUMAN	601655837R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3855824 3'
10042	22537	35533	2.15	7.0E-90	H68849.1	EST_HUMAN	y86604.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
10042	22537	35534	2.15	7.0E-90	H68849.1	EST_HUMAN	y86604.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
10352	22846	35840	0.89	7.0E-90	BF526089.1	EST_HUMAN	602071208F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214257 5'
3104	15719	28189	1.18	6.0E-90	X91928.1	NT	H. sapiens ECE-1 gene (exon 6)
3104	15719	28190	1.18	6.0E-90	X91928.1	NT	H. sapiens ECE-1 gene (exon 6)

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4311	16897	29341	8.88	6.0E-90	89223398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4311	16897	29342	8.68	6.0E-90	89223398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
6137	18751	31508	3.08	6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
6137	18751	31509	3.08	6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
8269	20810	33730	3.18	6.0E-90	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
8269	20810	33731	3.18	6.0E-90	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
168	12829		24.29	5.0E-90	AB035344.1	NT	Homo sapiens TCL6 gene, exon 1-10b
1234	13833	26347	2.39	5.0E-90	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1858	14446	27002	2.57	5.0E-90	A1222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPETIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
1858	14446	27003	2.57	5.0E-90	A1222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPETIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
2591	15153	27720	4.06	5.0E-90	AF114487.1	NT	Homo sapiens intersecin long isoform (ITSN) mRNA, complete cds
4838	17220	29874	10.01	5.0E-90	4508354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4660	17242	29698	0.64	5.0E-90	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5777	18402	31118	2.63	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
5871	18493	31220	1.13	5.0E-90	AB015617.1	NT	Homo sapiens ELKS mRNA, complete cds
5939	18402	31118	2.21	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
7267	19795	32651	2.58	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7267	19795	32652	2.58	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7564	20881	32957	13.89	5.0E-90	4557258	NT	Homo sapiens adenylate cyclase 9 (ADCY9) mRNA
8234	20775	33597	4.57	5.0E-90	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
9598	22098	35081	1.24	5.0E-90	11419428	NT	Homo sapiens similar to actonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
10181	22876	35669	0.71	5.0E-90	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10311	22805	35797	0.53	5.0E-90	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10311	22805	35798	0.53	5.0E-90	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10343	22837	35832	8.78	5.0E-90	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
10399	22893	35887	0.51	5.0E-90	7682051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10399	22893	35888	0.51	5.0E-90	7682051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10795	23318	36328	3.38	5.0E-90	D49387.1	NT	Human mRNA for NADP dependent leukotriene b4 12-hydroxydehydrogenase, partial cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12421	24607		1.6	5.0E-90	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12471	24598		5.4	5.0E-90	AI523368.1	EST_HUMAN	ai78h05.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2128761 3'
324	12978	25468	1.61	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
324	12978	25467	1.61	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1125	13728	26239	4.34	4.0E-90	4505316	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1727	14318	28861	8.55	4.0E-90	X98033.1	NT	H. sapiens gene encoding discoidin receptor tyrosine kinase, exon 16
3024	15640	28117	0.97	4.0E-90	AF007544.1	NT	Homo sapiens prolactin-specific membrane antigen (PSM) gene, complete cds
4781	17342	29790	3.77	4.0E-90	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4915	17490	29944	2.2	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4943	17518	29860	1.62	4.0E-90	M85967.1	NT	Human prothormone converting enzyme (NEC2) gene, exon 8
5098	17669		0.7	3.0E-90	AI370786.1	EST_HUMAN	qz89d08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2041743 3' similar to gb:M31470 RAS-LIKE PROTEIN TC10 (HUMAN);
7794	20337	33244	1.07	3.0E-90	BF516168.1	EST_HUMAN	UI-H-BW1-amy-b-04-0-UI.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
7794	20337	33245	1.07	3.0E-90	BF516168.1	EST_HUMAN	UI-H-BW1-amy-b-04-0-UI.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
11481	23940	37011	33.84	3.0E-90	BE563833.1	EST_HUMAN	601335244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689147 5'
230	12890	25378	4.32	2.0E-90	BE537913.1	EST_HUMAN	601067378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1215	13815	26329	16.29	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1215	13815	26330	16.29	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
2420	14988		1.78	2.0E-90	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
3912	16510	28972	2.37	2.0E-90	AI138213.1	EST_HUMAN	qc54c02.x1 Soares_placenta_8tc9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:1713410 3'
4798	17378	29827	1.16	2.0E-90	AB006627.1	NT	similar to SW:OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3 ;
5035	17609	30053	10.95	2.0E-90	5729855	NT	Homo sapiens mRNA for KIAA0289 gene, partial cds
5948	18569	31300	0.72	2.0E-90	11525901	NT	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
5948	18569	31301	0.72	2.0E-90	11525901	NT	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
5955	18577	31311	4.78	2.0E-90	AW672686.1	EST_HUMAN	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
9705	22204	35176	8.36	2.0E-90	11427320	NT	be49d05.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2898881 5' similar to TR:O75208 O75208 HYPOTHETICAL 35.5 KD PROTEIN ;
9705	22204	35177	8.36	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
9870	22367	35344	0.92	2.0E-90	AU118985.1	EST_HUMAN	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
9870	22367	35345	0.92	2.0E-90	AU118985.1	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
11345	23043	36053	4.12	2.0E-90	11024711	NT	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
							Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
298	12954	25443	3.2	1.0E-90	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
397	15386	25533	2.02	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
398	15386	25533	1.38	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
724	13344	25835	1.49	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
724	13344	25836	1.49	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
759	13378	25874	13.32	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
759	13378	25875	13.32	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1149	13752		3.05	1.0E-90	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1349	13944	26487	2.46	1.0E-90	AF086154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1349	13944	26488	2.46	1.0E-90	AF086154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1707	14300		1.38	1.0E-90	BE378884.1	EST_HUMAN	601159563F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511118 5'
1948	14530	27088	2.82	1.0E-90	11420514	NT	Homo sapiens similar to SALL1 (sal) (Drosophila)-like (LOC57167), mRNA
2878	15496	27967	7.6	1.0E-90	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (ORF2), mRNA
3918	16516	28980	0.98	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3918	16516	28981	0.98	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
4514	17098	29545	1.84	1.0E-90	AF187340.1	NT	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
5855	18478	31201	1.98	1.0E-90	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
6002	18622	31357	0.95	1.0E-90	11428910	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7133	19473	32293	0.68	1.0E-90	U91834.1	NT	Human retina-derived POU-domain factor-1 mRNA, complete cds
							Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
7665	20177	33064	2.52	1.0E-90	11428758	NT	
8755	21284	34214	4.17	1.0E-90	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
9217	21734		0.97	1.0E-90	AF163884.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
9239	21785	34712	1.33	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
9239	21765	34713	1.33	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
4274	18660	28309	6.54	8.0E-91	D12234.1	EST_HUMAN	HUM000381 Liver HepG2 cell line. Homo sapiens cDNA clone s381 3'
8248	20789	33708	2.74	7.0E-91	11419234	NT	Homo sapiens makrin, ring finger protein, 1 (MKRN1), mRNA
10201	22698	33690	0.74	7.0E-91	AB04151.1	EST_HUMAN	CM-BT043-090259-075 BT043 Homo sapiens cDNA
3521	16128	28608	1.52	5.0E-91	AA702784.1	EST_HUMAN	z90b04.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4814	17197	29843	1.21	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4814	17197	29844	1.21	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4831	17506	29952	0.86	5.0E-91	7110834	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4931	17508	29953	0.86	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
6729	19323	32128	1.08	5.0E-91	AI879995.1	EST_HUMAN	au49f09.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518121 3' similar to SW:ASPG FLAME Q47898 N4-(BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR ;
8147	20688	33601	1.52	5.0E-91	BF314882.1	EST_HUMAN	601801624F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130933 5'
8695	21234	34155	1.4	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'
8695	21234	34158	1.4	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'
12443	24579		1.78	5.0E-91	AI193566.1	EST_HUMAN	qe70f11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:174365 3' similar to contains MIR.b2 MIR MIR repetitive element ;
3236	15848	28328	1.25	4.0E-91	AF156778.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3236	15848	28329	1.25	4.0E-91	AF156778.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
10810	23333	36346	3.96	4.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
11882	24229	31001	3.09	4.0E-91	M77994.1	EST_HUMAN	EST01578 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
11882	24229	31047	3.09	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
12181	24417	30947	1.36	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
12181	24417	30948	1.36	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
1660	14253	26787	4.64	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1660	14253	26788	4.64	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
3383	15992	28470	1.4	3.0E-91	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3509	16114	28592	3.17	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3509	16114	28593	3.17	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3558	16454	28918	1.2	3.0E-91	AF084530.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4693	17275	29722	4.36	3.0E-91	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5115	17687	30124	1.19	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5115	17687	30125	1.19	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5885	18487	31211	1.5	3.0E-91	11434964	NT	Homo sapiens epididymal secretory protein (19:5kD) (HE1), mRNA
6446	19048		2.85	3.0E-91	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6897	19293	32097	4.48	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6697	19293	32098	4.48	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
7634	20146	33028	4.04	3.0E-91	U66959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
7634	20146	33029	4.04	3.0E-91	U66959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
7887	20429	33338	0.46	3.0E-91	6601589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8708	21245	34168	2.6	3.0E-91	D16494.1	NT	Human mRNA for very low density lipoprotein receptor, complete cds
9212	21729	34672	0.8	3.0E-91	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
12504	18025	30406	9.31	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
12504	18025	30407	9.31	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
52	12732	25199	2.37	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1288	13883	26408	6.6	1.0E-91	AW449746.1	EST_HUMAN	UI-H-B3-aks-d-01-Q-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'
5608	18237	30687	0.84	1.0E-91	11434402	NT	Homo sapiens hypothetical protein PRO1855 (PRO1855), mRNA
6930	19589	32419	1.76	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157804 5'
6930	19589	32420	1.76	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157804 5'
1284	13880	26402	9.55	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
1284	13880	26403	9.55	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
5369	17947	30359	0.59	9.0E-92	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
5654	18281	30760	4.15	9.0E-92	J03007.1	NT	Human Nar.K+ ATPase alpha-subunit mRNA, partial cds
5790	18416	31131	2.63	9.0E-92	11427149	NT	Homo sapiens NALP1 mRNA, complete cds
6581	19178	31978	4	9.0E-92	AF310105.1	NT	Homo sapiens partial TMSF2 gene for tetraspanin protein, exon 5
7798	20341	33249	0.75	9.0E-92	AJ250566.1	NT	Homo sapiens partial TMSF2 gene for tetraspanin protein, exon 5
7798	20341	33250	0.75	9.0E-92	AJ250566.1	NT	Homo sapiens partial TMSF2 gene for tetraspanin protein, exon 5
8315	20856	33781	1.11	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
8315	20856	33782	1.11	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
9198	21715	34659	1.84	9.0E-92	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
96	12772	25254	11	8.0E-92	W26387.1	EST_HUMAN	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
307	12962	25451	6.03	8.0E-92	BF386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
1860	14448	27005	1.03	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG), mRNA
1860	14448	27006	1.03	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG), mRNA
4306	18992	29335	0.98	8.0E-92	AA809157.1	EST_HUMAN	om13e02.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1540922 3' similar to contains L1.52 L1 repetitive element;
5265	17827	30251	2.02	8.0E-92	AW157571.1	EST_HUMAN	au8308.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to TR:O60302 O60302 KIAA0555 PROTEIN ; contains element MER22 repetitive element ;
5591	18222	30871	0.78	8.0E-92	AB046820.1	NT	Homo sapiens mRNA for KIAA1600 protein, partial cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST'E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5690	18316	30815	0.96	8.0E-92	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6668	19282	32066	1.25	8.0E-92	AJ000979.1	NT	Homo sapiens MCP-4 gene
6669	19265	32069	0.72	8.0E-92	AF179428.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit variant 1 (REV3L) mRNA, complete cds
7747	20255	33149	5.06	8.0E-92	X69536.1	NT	H. sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exons 7-8
7747	20255	33150	5.06	8.0E-92	X69536.1	NT	H. sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exons 7-8
8035	20577		0.68	8.0E-92	11416961	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
8364	20804	33822	4.96	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8364	20804	33823	4.96	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8461	21001	33918	0.67	8.0E-92	11426569	NT	Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA
8992	21530	34459	2.47	8.0E-92	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
9939	22434	35410	1.76	8.0E-92	Y13829.1	NT	Homo sapiens mRNA for MBNL protein
10683	23214	36226	5.17	8.0E-92	AF074393.1	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
11239	23770	36828	2.58	8.0E-92	4503340	NT	Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
257	15411	25402	1.61	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
257	15411	25403	1.61	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
617	13244	26439	1.09	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Seprase truncated isoform mRNA, complete cds
1323	13917	27728	3.02	7.0E-92	4502364	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2229	14904	27375	1.25	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2229	14904	27376	1.25	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2599	15161	27728	1.45	7.0E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2751	15306	27870	2.14	7.0E-92	6005738	NT	Homo sapiens NRAS-related gene (D1S155E), mRNA
2781	15334	27904	1.03	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3389	18003	28474	0.65	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3389	18003	28475	0.65	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4887	17269	28718	1.08	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2980 nt]
4887	17269	28719	1.08	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2980 nt]
5147	17717	30148	1.15	7.0E-92	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5350	17910	30325	1.12	7.0E-92	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
5468	18101	30419	4.93	7.0E-92	AA446206.1	EST_HUMAN	zw68d12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781175 5'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1831	14223		1.18	5.0E-92	BE360882.1	EST_HUMAN	601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605018 5'
2793	15346	27815	2.12	3.0E-92	BE909714.1	EST_HUMAN	601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902939 5'
6036	18656	31397	7.84	3.0E-92	AA378338.1	EST_HUMAN	EST91020 Synovial sarcoma Homo sapiens cDNA 5' end similar to similar to ribosomal protein S13
10845	23177	36189	2.86	3.0E-92	X15904.1	NT	Human mRNA for alpha-actinin
10845	23177	36190	2.86	3.0E-92	X15904.1	NT	Human mRNA for alpha-actinin
12358	25103		1.76	3.0E-92	BF367138.1	EST_HUMAN	RC1-GN0021-240800-012-e11 GN0021 Homo sapiens cDNA
28	12707	25164	1.57	2.0E-92	4501898	NT	Homo sapiens actin A receptor, type IIB (ACVR2B) mRNA
153	12816	25304	29.76	2.0E-92	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
191	12851	25334	3.47	2.0E-92	11422846	NT	Homo sapiens hypothetical protein dJ462023.2 (DJ462023.2), mRNA
191	12851	25335	3.47	2.0E-92	11422846	NT	Homo sapiens hypothetical protein dJ462023.2 (DJ462023.2), mRNA
778	13398	25900	12.47	2.0E-92	BE299190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
779	13398	25901	12.47	2.0E-92	BE299190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1752	14342		1.42	2.0E-92	S78653.1	NT	img=mas-related [human, Genomic, 2416 nt]
1980	14563	27122	4.27	2.0E-92	AB181119.1	EST_HUMAN	wk27607.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
1980	14563	27123	4.27	2.0E-92	AB181119.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2092	14672	27242	4.82	2.0E-92	4506860	NT	wk27607.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
2883	15241	27809	21.03	2.0E-92	5912457	NT	Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4) mRNA
2857	14287	26923	1.16	2.0E-92	11418424	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2857	14287	26824	1.16	2.0E-92	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
3673	16274	28740	1.13	2.0E-92	AF231919.1	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
3673	16274	28741	1.13	2.0E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3749	16350	28818	6.13	2.0E-92	5803180	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
4376	16963	29409	1.46	2.0E-92	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
4868	17444	29895	0.75	2.0E-92	AF136523.1	NT	Homo sapiens bile salt export pump (BSEP) mRNA, complete cds
5133	17705		4.94	2.0E-92	AL040437.1	EST_HUMAN	DKFZp434C0414_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C0414 5'
6444	19046		0.68	2.0E-92	4504756	NT	Homo sapiens integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL) mRNA
6727	19321	32126	2.75	2.0E-92	AB028691.1	NT	Homo sapiens mRNA for KIAA1068 protein, partial cds
7469	20005		0.75	2.0E-92	U67780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
8789	21328	34253	1.78	2.0E-92	AW340174.1	EST_HUMAN	hd02102.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:O02711
							O02711 PRO-POL-DUTPASE POLYPROTEIN ;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10639	23171	36182	0.98	2.0E-92	11434900	NT	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA
10628	23444	36465	1.92	2.0E-92	5803103	NT	Homo sapiens male-specific lethal-3 (Drosophila)-like 1 (MSL3L1), mRNA
11022	23536	36571	1.64	2.0E-92	AW838290.1	EST_HUMAN	CM4-LT0026-181299-082-g08.LT0026 Homo sapiens cDNA
11022	23536	36572	1.64	2.0E-92	AW838290.1	EST_HUMAN	CM4-LT0026-181299-082-g08.LT0026 Homo sapiens cDNA
12248	24459	30960	2.99	2.0E-92	AB029016.1	NT	Homo sapiens mRNA for KIAA1083 protein, partial cds
12533	15241	27809	98.37	2.0E-92	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1890	14475	27034	1.6	1.0E-92	R78078.1	EST_HUMAN	y80e08.r1 Soares placenta N52HP Homo sapiens cDNA clone IMAGE:145574 5'
1890	14475	27035	1.6	1.0E-92	R78078.1	EST_HUMAN	y80e08.r1 Soares placenta N52HP Homo sapiens cDNA clone IMAGE:145574 5'
2118	14698	27265	10.49	1.0E-92	4506668	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
8189	20730	33642	1.01	1.0E-92	BE439625.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
9091	21627	34563	4.16	1.0E-92	AI380356.1	EST_HUMAN	ig01b02.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107487 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element;contains element MER17 repetitive element ;
9091	21627	34564	4.16	1.0E-92	AI380356.1	EST_HUMAN	ig01b02.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107487 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element;contains element MER17 repetitive element ;
2076	14858	27228	3.52	9.0E-93	AU121681.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
2088	14867		10.76	9.0E-93	AA316723.1	EST_HUMAN	EST189414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2873	15231		1.18	9.0E-93	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3674	16275	28742	1.02	9.0E-93	BE388571.1	EST_HUMAN	601281867F1NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5'
11501	23950		18.44	9.0E-93	11418526	NT	Homo sapiens ribosomal protein L10a (RPL10A), mRNA
6705	19300	32104	4.23	8.0E-93	BF030384.1	EST_HUMAN	601460521F1NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3663908 5'
287	12924	25410	8.56	7.0E-93	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3111	15726	28197	0.59	6.0E-93	11626176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6782	19373	32189	1.17	6.0E-93	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6998	19494	32315	1.37	6.0E-93	AF095771.1	NT	Homo sapiens PTH-responsive osteosarcoma B1 protein (B1) mRNA, complete cds
1423	14016	26545	1.92	5.0E-93	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
1453	14045	26574	6.35	5.0E-93	AB074184.1	EST_HUMAN	wc09c08.x1 NCL CGAP_Pz28 Homo sapiens cDNA clone IMAGE:2314670 3'
1453	14045	26575	6.35	5.0E-93	AB074184.1	EST_HUMAN	wc09c08.x1 NCL CGAP_Pz28 Homo sapiens cDNA clone IMAGE:2314670 3'
1523	14116		0.97	5.0E-93	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
1882	15452	27008	0.9	5.0E-93	AJ297710.1	NT	Homo sapiens mRNA for CDC2L5 protein kinase, (CDC2L5 gene), isoform 2
3270	15882	28384	2.6	5.0E-93	X04201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5967	18568	31323	0.93	5.0E-93	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
6257	18668		1.49	5.0E-93	AF045555.1	NT	Homo sapiens wbscr1 (WBSOCR1) and wbscr5 (WBSOCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7700	20209	33096	3.68	5.0E-93	AF067136.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
8541	21080	34000	0.68	5.0E-93	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
8541	21080	34001	0.68	5.0E-93	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9541	22041	35002	2.28	5.0E-93	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9721	22219	35184	2.87	5.0E-93	5032156	NT	Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA
9882	22477	35459	1.58	5.0E-93	AF069313.2	NT	Homo sapiens WSB1 protein (WSB1) mRNA, complete cds
10705	23234	36247	2.14	5.0E-93	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12145	24731	30856	2.11	5.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
91	12767		6.55	4.0E-93	AA459933.1	EST_HUMAN	z50509.g1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:785688 3' similar to SW:CLPA_RAT
470	13103	25595	1.56	4.0E-93	4557878	NT	P37397 CALPONIN, ACIDIC ISOFORM;
470	13103	25596	1.56	4.0E-93	4557878	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
804	13421	25926	2.39	4.0E-93	7657454	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
804	13421	25927	2.39	4.0E-93	7657454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
1225	13824	26336	1.5	4.0E-93	8923650	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
2020	14602	27167	5.25	4.0E-93	AF047677.1	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
2638	15197	27771	1.41	4.0E-93	7656972	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
3624	16227	28705	0.8	4.0E-93	7703396	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
4122	16715	28171	2.14	4.0E-93	4504654	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
5171	16227	28705	0.86	4.0E-93	7703396	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
5825	18449	31172	5.27	4.0E-93	T46884.1	EST_HUMAN	y694c12.11 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:78838 5' similar to similar to SP:A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN,
11013	23527	36563	14.54	4.0E-93	AV692051.1	EST_HUMAN	AV692051 GK6 Homo sapiens cDNA clone GKDRF07 5'
3713	16314	28781	8.68	3.0E-93	BF690630.1	EST_HUMAN	602248554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
3713	16314	28782	8.68	3.0E-93	BF690630.1	EST_HUMAN	602248554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
4319	16905		5.51	3.0E-93	AF225886.1	NT	Homo sapiens tensin mRNA, complete cds
6679	19275	32079	1.28	3.0E-93	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10680	23212	38223	4.85	3.0E-93	AB24829.1	EST_HUMAN	wb2d05.x1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:2304489 3'
204	12865	25349	28.58	2.0E-93	AB015810.1	NT	Chloroebus aethiops mRNA for ribosomal protein S4X, complete cds
204	12866	28350	28.58	2.0E-93	AB015810.1	NT	Chloroebus aethiops mRNA for ribosomal protein S4X, complete cds
345	12897	25483	10.28	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
346	12897	25483	6.68	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1657	14250	26784	7.56	2.0E-93	AF225896.1	NT	Homo sapiens tensin mRNA, complete cds
2527	15091	27664	1.01	2.0E-93	BE252982.1	EST_HUMAN	601117586F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5'
5611	18240	30889	6.13	2.0E-93	AW864385.1	EST_HUMAN	EST378458 MAGe resequences, MAGe Homo sapiens cDNA
5818	18442	31164	1.06	2.0E-93	U74313.1	EST_HUMAN	Homo sapiens hypothetical protein (LOC51318), mRNA
5832	18456	31177	0.76	2.0E-93	U74313.1	EST_HUMAN	HSU74313 Human chromosome 14 Homo sapiens cDNA clone 1-36
6785	19378		1.21	2.0E-93	AW502002.1	EST_HUMAN	U1HF-BNO-aka-g-09-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078329 5'
12032	24322		2.49	2.0E-93	AA126735.1	EST_HUMAN	z29c10.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503346 3'
12119	24378		2.91	2.0E-93	L41826.1	NT	Homo sapiens CYP17 gene, 5' end
12404	24582		5.66	2.0E-93	BF035327.1	EST_HUMAN	601458831F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
107	12783	25265	33.31	1.0E-93	AF238967.1	NT	Homo sapiens CTR1 pseudogene
107	12783	25266	33.31	1.0E-93	AF238967.1	NT	Homo sapiens CTR1 pseudogene
544	13175	25655	7.63	1.0E-93	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
626	13253	25727	3.51	1.0E-93	AI146755.1	EST_HUMAN	9y84b08.x1 NCL CGAP_CELL1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q62384 Q62384
805	13519	26037	5.19	1.0E-93	D87675.1	NT	ZINC FINGER PROTEIN. ;
1280	13875	26395	6.4	1.0E-93	8923270	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1280	13875	26396	6.4	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1389	13983	26509	1.09	1.0E-93	AB046783.1	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
2375	14945	27518	1.57	1.0E-93	AF231981.1	NT	Homo sapiens mRNA for KIAA1563 protein, partial cds
2503	15067	27941	2.87	1.0E-93	AF055086.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2849	13933	28453	1.93	1.0E-93	BE297389.1	EST_HUMAN	Homo sapiens MHC class 1 region
2849	13933	28454	1.93	1.0E-93	BE297389.1	EST_HUMAN	60117686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2860	15576	28055	1.99	1.0E-93	D87675.1	NT	60117686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
3252	15864		1.51	1.0E-93	AF231981.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4520	17104	29550	1.82	1.0E-93	AL163284.2	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
5755	18381	31082	1.36	1.0E-93	U78509.1	NT	Homo sapiens chromosome 21 segment HS21C084
5755	18381	31093	1.36	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5938	18559	31288	0.99	1.0E-93	AF227138.1	NT	Homo sapiens candidate taste receptor T2R14 gene, complete cds
6074	18691	31437	9.26	1.0E-93	4557782	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA
6344	18950	31728	1.02	1.0E-93	7692241	NT	Homo sapiens KIAA0872 gene product (KIAA0872), mRNA
6888	18921	32455	2.16	1.0E-93	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7297	19825	32884	5.6	1.0E-93	D42072.1	NT	Human mRNA for NF1 N-isoform-exon11, complete cds
8203	20744	33857	2.4	1.0E-93	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
8480	21018	33934	1.1	1.0E-93	Y10183.1	NT	H sapiens mRNA for MEMD protein
8583	21122	34042	1.26	1.0E-93	AF182032.1	NT	Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds
9373	20312	33214	1.64	1.0E-93	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
9377	20318	33218	1.26	1.0E-93	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9507	22007	34963	4.34	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9507	22007	34964	4.34	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9641	22141	35108	0.59	1.0E-93	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10050	22545	35540	0.51	1.0E-93	11433848	NT	Homo sapiens ryanodine receptor 3 (RYR3), mRNA
11686	24822	30763	1.37	1.0E-93	AI268282.1	EST_HUMAN	q103c12.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880758 3' similar to WP.T19B4.4 CE13742 ;
12301	24498		2.08	1.0E-93	AJ230125.1	NT	Homo sapiens GGT1 gene, exon 1
12397	24557		5.43	1.0E-93	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12568	24887	30874	1.72	1.0E-93	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12584	25080		2.21	1.0E-93	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
10484	22878		1.17	8.0E-94	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4034	16932	29101	2.19	6.0E-94	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
12524	24840		1.31	6.0E-94	11418351	NT	Homo sapiens mitogen-activated protein kinase 12 (MAPK12), mRNA
5570	18201	30650	3.71	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0812 protein, partial cds
5570	18201	30651	3.71	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0812 protein, partial cds
6199	18608	31578	6.6	5.0E-94	AA722434.1	EST_HUMAN	z87g06.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409594 3'
7081	19653	32481	1.45	5.0E-94	AI015900.1	EST_HUMAN	cf83d05.s1 Soares_fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623369 3'
8573	21112	34031	0.78	5.0E-94	BF529116.1	EST_HUMAN	602042163F1 NCI_CGAP_Bn87 Homo sapiens cDNA clone IMAGE:4180023 5'
10852	23373	36391	1.97	5.0E-94	11423982	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
10852	23373	36392	1.97	5.0E-94	11423982	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
12010	25083	30517	4.36	5.0E-94	T69398.1	EST_HUMAN	y08804.s1 Soares_fetal_liver_spleen_1NfLS Homo sapiens cDNA clone IMAGE:116239 3'
1682	14468		9.28	4.0E-94	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4827	17405	29859	3.19	4.0E-94	AI591312.1	EST_HUMAN	hw11f10.x1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TRQ16265 Q16265 PROTEIN TYROSINE PHOSPHATASE;
6594	19191	31965	2.35	4.0E-94	11440870	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6594	19191	31966	2.35	4.0E-94	11440870	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6992	19490		0.89	4.0E-94	L27386.1	NT	Homo sapiens huntingtin (HD) gene, exon 37
11328	23028	36035	1.8	4.0E-94	11545792	NT	Homo sapiens hypothetical protein FLJ12455 (FLJ12455), mRNA
11568	24041	37110	4	4.0E-94	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
639	13262	25738	3.74	3.0E-94	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
750	13370	25864	9.81	3.0E-94	4502508	NT	Homo sapiens complement component 5 (C5) mRNA
1776	14368	26910	1.19	3.0E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1776	14368	26911	1.19	3.0E-94	AF167706.1	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1809	14398	26944	5.11	3.0E-94	4557556	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
5951	18463	31207	4.01	3.0E-94	11496268	NT	Homo sapiens mRNA for MEGF2, partial cds
6299	18907	31878	1.07	3.0E-94	AB011536.1	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
6579	19177	31977	5.19	3.0E-94	11526228	NT	Homo sapiens protocadherin alpha 13 (PCDH-alpha13) mRNA, complete cds
8140	20681	33593	0.89	3.0E-94	AF152309.1	NT	Homo sapiens mRNA for KIAA0679 protein, partial cds
8523	21062	33984	3.81	3.0E-94	AB014579.1	NT	Homo sapiens glycogenin-1L mRNA, complete cds
9511	22011	34970	7.24	3.0E-94	AF087942.1	NT	Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA
10979	23493	36523	1.84	3.0E-94	4757821	NT	Human cbl-b truncated form 1 lacking leucine zipper mRNA, complete cds
11527	23975	37045	1.82	3.0E-94	U26711.1	NT	Human cbl-b truncated form 1 lacking leucine zipper mRNA, complete cds
9667	22166	35140	0.51	2.0E-94	AI010393.1	EST_HUMAN	w30h11.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2391813 3'
9667	22166	35141	0.51	2.0E-94	AI010393.1	EST_HUMAN	w30h11.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2391813 3'
160	12623	25311	2.34	1.0E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3125	15739	28207	1.98	1.0E-94	BE293433.1	EST_HUMAN	60111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3125	15739	28208	1.98	1.0E-94	BE293433.1	EST_HUMAN	60111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4450	17036	29480	1.14	1.0E-94	9506692	NT	Homo sapiens hypothetical protein (FLJ20746), mRNA
6223	18832	31608	1.21	1.0E-94	AE000289.1	NT	Escherichia coli K-12 MG1655 section 159 of 400 of the complete genome
6412	18015	31797	1.32	1.0E-94	AL040518.1	EST_HUMAN	DKFZp434G0314_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G0314 5'
6421	19024	31808	0.79	1.0E-94	H08270.1	EST_HUMAN	y8762.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:45053 5'
8057	20599	33507	0.56	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8057	20599	33508	0.56	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9180	21757	34703	2.29	1.0E-94	11428710	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9702	22201	35173	1.8	1.0E-04	BE780478.1	EST_HUMAN	601468748F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872099 5'
10945	23461	36483	3.48	1.0E-04	U66590.1	NT	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds
11197	23702	36753	2.05	1.0E-04	A1272244.1	EST_HUMAN	ap22602.x1 Schiller oligodendrogloma Homo sapiens cDNA clone IMAGE:1956122 3' similar to TR:Q62845
11592	24035	37104	2.28	1.0E-04	11418871	NT	Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR. ; Homo sapiens KIAA0184 gene product (KIAA0184), mRNA
12133	12823	25311	1.34	1.0E-04	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
1525	14117	26654	2.12	9.0E-05	AF027302.1	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3191	15803	28275	1.15	9.0E-05	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3191	15803	28278	1.15	9.0E-05	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5601	18230	30679	1.59	9.0E-05	X82569.1	NT	M.musculus glyt1 gene (exons 1c and 2)
5601	18230	30680	1.59	9.0E-05	X82569.1	NT	M.musculus glyt1 gene (exons 1c and 2)
8194	20735	33645	1.89	9.0E-05	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
155	12818	25306	10.05	8.0E-05	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
4634	17217	29669	1.92	8.0E-05	A1700988.1	EST_HUMAN	we09e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340806 3' similar to gb:K00558
4634	17217	29870	1.92	8.0E-05	A1700988.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN); we09e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340806 3' similar to gb:K00558
7028	19562	32389	0.7	8.0E-05	11418376	NT	TUBULIN ALPHA-1 CHAIN (HUMAN); Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
7290	19818	32677	1.44	8.0E-05	11426529	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
7290	19818	32678	1.44	8.0E-05	11426529	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
8138	20679	33590	1.93	8.0E-05	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
9287	21887	34832	1.98	8.0E-05	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
9287	21887	34833	1.98	8.0E-05	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
9762	22260	35243	3.42	8.0E-05	5174844	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
9763	22291	35291	3.07	8.0E-05	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
10134	22629	35617	0.75	8.0E-05	9845523	NT	Homo sapiens early growth response 2 (Krox-20 (Drosophila) homolog) (EGR2), mRNA
10592	23127	36141	1.76	8.0E-05	AF112152.1	NT	Homo sapiens developmental arteries and neural crest EGF-like protein mRNA, complete cds
11357	23811	36871	2.34	8.0E-05	10864024	NT	Homo sapiens HCF-binding transcription factor Zhangfei (ZF), mRNA
12365	24538		25.75	8.0E-05	AA928056.1	EST_HUMAN	zu84b01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1.11 L1 repetitive element ;
297	12953	25441	6.43	7.0E-05	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
297	12953	25442	6.43	7.0E-05	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4456	17042	29486	5.04	7.0E-05	M95708.1	NT	Homo sapiens Ly-6-like protein (CD58) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4505	17089		1.35	7.0E-95	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C048
9144	21679	34623	0.92	4.0E-95	BE439825.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
11548	23988	37068	1.69	4.0E-95	AW950834.1	EST_HUMAN	EST362704 MAGE resequences, MAGE Homo sapiens cDNA
11548	23988	37068	1.69	4.0E-95	AW950834.1	EST_HUMAN	EST362704 MAGE resequences, MAGE Homo sapiens cDNA
224	12885	25370	8.53	3.0E-95	AV648361.1	EST_HUMAN	AV648361 GLC Homo sapiens cDNA clone GLCBIF01 3'
5634	18263	30735	1.75	3.0E-95	BF526041.1	EST_HUMAN	602071146F1 NCI CGAP Brn64 Homo sapiens cDNA clone IMAGE:4214147 5'
5854	24750	31200	0.72	3.0E-95	4503354	NT	Homo sapiens dedicator of cyto-kinesis 1 (DOCK1) mRNA
7404	19829	32792	1.38	3.0E-95	AW958121.1	EST_HUMAN	EST370191 MAGE resequences, MAGE Homo sapiens cDNA
7404	19829	32793	1.38	3.0E-95	AW958121.1	EST_HUMAN	EST370191 MAGE resequences, MAGE Homo sapiens cDNA
9277	21803	34753	1.71	3.0E-95	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9277	21803	34754	1.71	3.0E-95	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9962	22161	35134	0.87	3.0E-95	BF213446.1	EST_HUMAN	601845212F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4070451 5'
10759	23283	36298	2.2	3.0E-95	R83190.1	EST_HUMAN	yp87g1.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194468 5'
973	13585	26099	2.57	2.0E-95	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
1886	14278	26811	1.55	2.0E-95	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1886	14278	26812	1.55	2.0E-95	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
							Homo sapiens tissue inhibitor of metalloproteinase 3 (Sersby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
1884	14568	27127	3.25	2.0E-95	4507512	NT	
1987	14569	27131	1.57	2.0E-95	BE393873.1	EST_HUMAN	601312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658862 5'
2470	15037	27604	1.23	2.0E-95	5453885	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2470	15037	27605	1.23	2.0E-95	5453885	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2505	15069	27642	4.2	2.0E-95	AF240786.1	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
2554	15118	27688	1.05	2.0E-95	4758423	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2844	13584	26098	8.06	2.0E-95	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
3193	15805	28278	2.54	2.0E-95	AF015452.1	NT	Homo sapiens Usurpin-gamma mRNA, complete cds
3621	16224	28701	2.98	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3621	16224	28702	2.98	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3677	16278	28745	0.72	2.0E-95	AB037807.1	NT	Homo sapiens mRNA for KIAA1388 protein, partial cds
							qm01c02.xt Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:1880548 3' similar to WP:T23G7.4
3813	16413	28877	0.64	2.0E-95	AI290264.1	EST_HUMAN	CE03705 ;
4452	17038	29481	1.42	2.0E-95	7657185	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
5048	17621	30086	3.24	2.0E-95	AF105087.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
5191	17756	30185	3.19	2.0E-95	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

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5251	17814	30237	1.69	2.0E-05	AA447931.1	EST_HUMAN	z11d07.r1 Soares_totat_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5'
5251	17814	30238	1.69	2.0E-05	AA447931.1	EST_HUMAN	z11d07.r1 Soares_totat_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5'
5671	18298	30778	5.36	2.0E-05	7705764	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA
5671	18298	30779	5.36	2.0E-05	7705764	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA
5876	18488	31223	1.21	2.0E-05	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5876	18488	31224	1.21	2.0E-05	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
6291	18899	31670	3.33	2.0E-05	M59724.1	NT	Human muscle-type phosphofructokinase (PFK-M) gene, exon 7
6577	19175	31974	1.08	2.0E-05	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6577	19175	31975	1.08	2.0E-05	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6685	19281	32084	2.42	2.0E-05	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6861	19595	32426	1.6	2.0E-05	11435773	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
9069	21606	34537	1.85	2.0E-05	11421795	NT	Homo sapiens ribophorin II (RPN2), mRNA
10263	22778	35769	0.49	2.0E-05	11434330	NT	Homo sapiens KIAA1065 protein (KIAA1065), mRNA
10602	23136	36150	2.21	2.0E-05	4757853	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRIA) mRNA
11546	23894	37065	1.74	2.0E-05	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11546	23894	37066	1.74	2.0E-05	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12103	24385	30971	2.55	2.0E-05	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12220	24442		1.41	2.0E-05	11417860	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
12534	24646	30869	8.02	2.0E-05	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
5798	18424	31140	7.86	1.0E-05	AA284651.1	EST_HUMAN	z23h04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1067084 G1067084 F55H2.6;
5798	18424	31141	7.86	1.0E-05	AA284651.1	EST_HUMAN	z23h04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1067084 G1067084 F55H2.6;
7523	20043	32912	4.16	1.0E-05	BF370000.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
7523	20043	32913	4.16	1.0E-05	BF370000.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
8135	20676	33588	1.51	9.0E-06	BE897259.1	EST_HUMAN	601437232F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922423 5'
487	15415	25592	1.19	8.0E-06	BE907607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
487	15415	25593	1.19	8.0E-06	BE907607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
5702	18328		2.71	8.0E-06	AW835047.1	EST_HUMAN	PMO-LT0019-080300-002-d09 LT0019 Homo sapiens cDNA
3980	16578	28048	0.99	7.0E-08	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
3360	15988	28445	1.65	6.0E-06	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3528	16134	28614	11.83	6.0E-06	M28873.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3'end

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5820	18444	31166	0.95	6.0E-96	11422842	NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminidase alpha 2,3-sialyltransferase) (SIAT6), mRNA
11420	23871	36832	2.52	6.0E-98	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11420	23871	36833	2.52	6.0E-98	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11461	23911	36978	1.96	6.0E-96	8923839	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
342	12894	26479	2.95	5.0E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
875	13489	26005	3.61	5.0E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
875	13489	26006	3.61	5.0E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2650	15209		0.91	5.0E-96	11418767	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
3061	15677	28151	0.99	5.0E-96	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
5030	17604		1.6	5.0E-96	X60812.1	NT	H. sapiens DNA for monoamine oxidase type A (7) (partial)
6758	19351	32160	1.1	5.0E-96	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
8878	19812	32445	4.05	5.0E-98	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
8878	19812	32446	4.05	5.0E-98	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
7080	19861	32501	0.76	5.0E-96	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7524	20044	32914	1.7	5.0E-96	AB024334.1	NT	Homo sapiens mRNA for 14-3-3gamma, complete cds
8050	20592	33499	1.62	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
8050	20592	33500	1.62	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
11618	24060	37124	1.68	5.0E-96	7681973	NT	Homo sapiens KIAA0175 gene product (KIAA0175), mRNA
4269	18855		8.01	3.0E-96	H88656.1	EST_HUMAN	yr87h12.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:212327 5'
440	13073		3.88	2.0E-96	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
777	13396	25897	1.52	2.0E-96	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4871	17447	29898	1.56	2.0E-96	BE148074.1	EST_HUMAN	RC3-PT0230-040500-110-g02 HT0230 Homo sapiens cDNA
8911	21449		5.45	2.0E-96	AV689461.1	EST_HUMAN	AV689461 GK Homo sapiens cDNA clone GKCFMD07 5'
11795	24176		1.71	2.0E-96	AW249440.1	EST_HUMAN	2819351.5prime NIH_MGC.7 Homo sapiens cDNA clone IMAGE:2819351 5'
699	13321	25808	2.62	1.0E-96	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1817	14407	26951	3.32	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGC resequences, MAGC Homo sapiens cDNA
1817	14407	26952	3.32	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGC resequences, MAGC Homo sapiens cDNA
2272	14846	27421	1.3	1.0E-96	M75967.1	NT	Human hepatocyte growth factor gene, exon 1
2272	14846	27422	1.3	1.0E-96	M75967.1	NT	Human hepatocyte growth factor gene, exon 1
2308	15398	27455	1.1	1.0E-96	U51472.2	NT	Felis catus superfast myosin heavy chain (sMyHC) mRNA, complete cds
7045	18065	30455	1.06	1.0E-96	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
8154	20695	33608	0.9	1.0E-96	7681803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8154	20695	33609	0.9	1.0E-96	7681803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8650	21189	34107	22.03	1.0E-96	11419428	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
8784	21323	34247	2.21	1.0E-96	AF274883.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10064	22559	35553	0.87	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
10064	22559	35554	0.87	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
11781	18023	30404	2.56	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
11781	18023	30405	2.56	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
3370	15978	28455	0.82	6.0E-97	BF245240.1	EST_HUMAN	601863712F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4081202 5'
7558	20078		2.76	6.0E-97	BE141849.1	EST_HUMAN	IL5-HT0117-011099-004-D07 HT0117 Homo sapiens cDNA
8864	21403	34327	0.74	6.0E-97	BE888012.1	EST_HUMAN	601440317F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3925133 5'
8864	21403	34328	0.74	6.0E-97	BE888012.1	EST_HUMAN	601440317F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3925133 5'
10486	22980	35987	0.52	6.0E-97	AA320332.1	EST_HUMAN	EST22872 Adipose tissue, white II Homo sapiens cDNA 5' end
10486	22980	35988	0.52	6.0E-97	AA320332.1	EST_HUMAN	EST22872 Adipose tissue, white II Homo sapiens cDNA 5' end
11284	23737	38783	1.8	6.0E-97	X15904.1	NT	Human mRNA for alpha-actinin
7957	20499	33409	2.45	5.0E-97	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
8085	20628	33540	12.84	5.0E-97	AA416026.1	EST_HUMAN	z07e12.e1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:767758 3' similar to TR:G1304125
8593	22093	35057	2.87	5.0E-97	BF154912.1	EST_HUMAN	G1304125 PMS4 MRNA
11421	23872	36934	1.96	5.0E-97	BE148597.1	EST_HUMAN	RCO-BT0812-250900-032-e09 BT0812 Homo sapiens cDNA
11421	23872	36935	1.99	5.0E-97	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-502 HT0241 Homo sapiens cDNA
975	13587	26102	6.69	4.0E-97	BE004436.1	EST_HUMAN	MRO-HT0241-150500-010-502 HT0241 Homo sapiens cDNA
1953	14537	27093	0.97	4.0E-97	5453572	NT	CMO-BN0106-170300-293-e06 BN0106 Homo sapiens cDNA
5754	19380	31091	17.27	4.0E-97	4557326	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
6912	19571	32399	6.05	4.0E-97	Y11339.2	NT	Homo sapiens apolipoprotein H (beta-2-glycoprotein I) (APOH) mRNA
6912	19571	32400	6.05	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase I, long form
7088	19659	32498	1.01	4.0E-97	7710125	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase I, long form
7128	19488	32286	1.01	4.0E-97	11422155	NT	Homo sapiens ligase III, DNA, ATP-dependent (LIG3), transcript variant alpha, mRNA
7778	20288	33186	0.74	4.0E-97	10947053	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
7778	20288	33187	0.74	4.0E-97	10947053	NT	Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA
8078	20620	33533	0.84	4.0E-97	4557708	NT	Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA
8299	20940	33761	1.57	4.0E-97	11421793	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2) mRNA
8555	21094	34014	0.73	4.0E-97	11423233	NT	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA
							Homo sapiens cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1), mRNA

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9172	21749	34892	1.23	4.0E-97	AB011186.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9172	21749	34893	1.23	4.0E-97	AB011186.1	NT	Homo sapiens mRNA for KIAA0584 protein, partial cds
10333	22827	35822	0.75	4.0E-97	11431060	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
11042	23558	36591	1.85	4.0E-97	11883122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11042	23558	36592	1.85	4.0E-97	11883122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11977	24288		4.75	4.0E-97	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
284	12922	25408	2.37	3.0E-97	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
907	13521	26039	8.51	3.0E-97	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
907	13521	26040	8.51	3.0E-97	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1480	15443	26623	2.15	3.0E-97	4758813	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
2483	15400	27618	1.36	3.0E-97	U36255.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 7
3205	15817	28263	37.82	3.0E-97	K02212.1	NT	Human alpha-1-antitrypsin gene (S variant), complete cds
3289	15910	28389	1.48	3.0E-97	5174478	NT	Homo sapiens pericentriem (PCNT) mRNA
3893	16492	28952	1.04	3.0E-97	AF136523.1	NT	Homo sapiens bile salt export pump (BSEP) mRNA, complete cds
4894	17469	29925	28.9	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
6558	19158	31952	2.38	1.0E-97	BE566486.1	EST_HUMAN	601339620F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681821 5'
9365	20304	33208	0.6	1.0E-97	AW379976.1	EST_HUMAN	RCO-HT0258-211199-011-q05 HT0258 Homo sapiens cDNA
9365	20304	33207	0.6	1.0E-97	AW379976.1	EST_HUMAN	RCO-HT0258-211199-011-q05 HT0258 Homo sapiens cDNA
9679	22178	35153	1.21	1.0E-97	R10887.1	EST_HUMAN	yf38c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134 3'
10584	23119	36134	4.07	1.0E-97	11427757	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
10584	23119	36135	4.07	1.0E-97	11427757	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
11189	23694	36743	3.53	1.0E-97	AA553761.1	EST_HUMAN	nk29g02.s1 NCI CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014982 3'
11343	23041	36050	18.96	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
11343	23041	36051	18.96	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
934	13547	26064	5.55	9.0E-98	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
1319	13913	28434	1.41	9.0E-98	8393082	NT	Homo sapiens cal eye syndrome critical region gene 1 (CECR1), mRNA
6445	18047		0.67	9.0E-98	AJ250713.1	NT	Homo sapiens CLDN12 gene for claudin-12
7865	20407	33314	7.35	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
7865	20407	33315	7.35	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
9044	21581	34510	2	9.0E-98	X06989.1	NT	Human mRNA for amyloid A4(751) protein
9151	21888	34629	1.94	9.0E-98	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
9216	21733	34876	1.46	9.0E-98	AB037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9262	21788		1.25	9.0E-98	AF057728.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 8
9289	21889	34835	1.15	9.0E-98	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
9289	21889	34836	1.15	9.0E-98	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
10161	22856	35651	0.54	9.0E-98	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
10268	22763	35750	0.5	9.0E-98	11431544	NT	Homo sapiens protease-activated receptor 3 (PAR3), mRNA
10883	23404	36422	2.37	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
10883	23404	36423	2.37	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11994	13547	26084	4.29	9.0E-98	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
27	12708		0.92	8.0E-98	AJ251158.1	NT	Homo sapiens partial MICB gene for MHC class I chain-related protein B, exons 2-3 and joined CDS
1607	14199	26732	1.04	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1607	14199	26733	1.04	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1784	14354	26900	1.64	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1784	14354	26901	1.64	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3893	18461	28925	7.16	8.0E-98	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
5276	17838		1.43	8.0E-98	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
6233	18842	31614	1.18	5.0E-98	BE895873.1	EST_HUMAN	601507503F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909097 5'
12398	24558	30808	1.68	4.0E-98	BE348727.1	EST_HUMAN	h68f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151899 3'
2222	14797	27370	1.15	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124.3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
2639	15198	27772	1.67	3.0E-98	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2777	15330		1.97	3.0E-98	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
7026	19560	32388	1.66	3.0E-98	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7026	19560	32387	1.66	3.0E-98	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
8686	21225	34145	3.05	3.0E-98	H46698.1	EST_HUMAN	yo17g09.r1 Soares adult brain N2b51HB55Y Homo sapiens cDNA clone IMAGE:178240 5'
9221	21737	34679	0.77	3.0E-98	8922066	NT	Homo sapiens uncharacterized bone marrow protein BM039 (BM039), mRNA
9798	22296	35279	1.8	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124.3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
9798	22296	35280	1.8	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124.3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
10369	22863	35858	0.86	3.0E-98	BE090454.1	EST_HUMAN	601873886F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956517 5'
10831	23352	36367	3.79	3.0E-98	U59309.1	NT	Human fumarate precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
12598	24685		5.13	3.0E-98	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
705	13384	25883	0.81	2.0E-98	BE261694.1	EST_HUMAN	601149486F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502245 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2124	14702	27272	3.36	2.0E-08	BE264281.1	EST_HUMAN	601172658F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
2279	14853	27431	1.37	2.0E-08	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4384	16971	29419	0.74	2.0E-08	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4432	17018	29458	4.65	2.0E-08	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4953	17528	29968	0.96	2.0E-08	AF218802.1	NT	Homo sapiens attractin precursor (ATRn) gene, exon 16
4953	17528	29969	0.86	2.0E-08	AF218802.1	NT	Homo sapiens attractin precursor (ATRn) gene, exon 16
5579	18210	30660	4.63	2.0E-08	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
5761	19354	32163	1.03	2.0E-08	4505798	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
7619	20132	33008	1.13	2.0E-08	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
7619	20132	33009	1.13	2.0E-08	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
8544	21083	34004	3.84	2.0E-08	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8544	21083	34005	3.84	2.0E-08	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8825	21164	34078	0.62	2.0E-08	L76666.1	NT	Homo sapiens NKAT4b mRNA, complete cds
8825	21164	34079	0.62	2.0E-08	L76666.1	NT	Homo sapiens NKAT4b mRNA, complete cds
9456	21892	34934	3.9	2.0E-08	X12684.1	NT	H. sapiens arginase gene exon 3 (EC 3.5.3.1)
10312	22806		1.31	2.0E-08	7705868	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
11078	23590	36628	1.6	2.0E-08	U22028.1	NT	Human cytochrome P450 (CYP2A13) gene, complete cds
11989	24305	30989	1.62	2.0E-08	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
430	13063	25558	57.28	1.0E-08	A1862007.1	EST_HUMAN	hw36b04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW:RL2B_HUMAN
480	13113	25603	2.16	1.0E-08	AW988611.1	EST_HUMAN	P29316 60S RIBOSOMAL PROTEIN L23A. ;
1832	14420	28970	13.48	1.0E-08	N49818.1	EST_HUMAN	PMO-BN0085-100300-001-c06 BN0065 Homo sapiens cDNA
5520	18152	30568	3.14	1.0E-08	AA195854.1	EST_HUMAN	Y23f05.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:243585 5' similar to
5758	18384	31097	1.12	1.0E-08	BE390827.1	EST_HUMAN	PIR:S54204 S54204 ribosomal protein L29 - human ;
5758	18384	31098	1.12	1.0E-08	BE390827.1	EST_HUMAN	z986c09.r1 Stratagene muscle 837209 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:G805562
8928	21466	34383	8.27	1.0E-08	AF141349.1	NT	G806562 NEBULIN. ;
8928	21466	34384	8.27	1.0E-08	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
5984	18604	31338	0.93	9.0E-09	A1805004.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
5984	18604	31339	0.93	9.0E-09	A1805004.1	EST_HUMAN	QV-B1073-191298-012 B1073 Homo sapiens cDNA
6191	18801	31571	4.33	9.0E-09	AW968635.1	EST_HUMAN	QV-B1073-191298-012 B1073 Homo sapiens cDNA
11001	23515	36549	3.39	9.0E-09	A1479829.1	EST_HUMAN	EST380711 IMAGE:2163421 3' similar to SW:RID_HUMAN

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11001	23515	36550	3.39	9.0E-99	AI479829.1	EST_HUMAN	tm6h07.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BD_HUMAN
11282	23744	36801	1.97	9.0E-99	AA134604.1	EST_HUMAN	P55957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
11627	24089	37133	2.11	9.0E-99	AJ271736.1	NT	Z190d02.11 Stragene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565443 5' similar to
8661	21200	34118	1.59	8.0E-99	8635487	NT	TR:G662994 G662994 GPI-ANCHORED PROTEIN P137. ;
5989	18819	31355	10.3	7.0E-99	AF035808.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
11477	23927	36998	2.52	7.0E-99	AF001888.1	NT	Human endogenous retrovirus, complete genome
497	13129	25618	0.57	6.0E-99	U10991.1	NT	Homo sapiens osicillin (hLn) gene, exon 5
4859	17437	29887	1.3	6.0E-99	4502660	NT	Homo sapiens NK-receptor (KIR-G2) gene, linker region exon
5382	17941	30355	1.01	6.0E-99	8923244	NT	Human G2 protein mRNA, partial cds
8711	19305	32109	1	6.0E-99	7706136	NT	Homo sapiens CD34 antigen (CD34) mRNA
6780	19371	32188	1.39	6.0E-99	L43610.1	NT	Homo sapiens hypothetical protein FLJ20272 (FLJ20272), mRNA
6780	19371	32187	1.39	6.0E-99	L43610.1	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
8048	20590	33497	1.11	6.0E-99	X99101.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8700	21239	34162	1.88	6.0E-99	AB036429.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8797	21336	34261	4.03	6.0E-99	AF080255.1	NT	H. sapiens mRNA for estrogen receptor
8797	21336	34262	4.03	6.0E-99	AF080255.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/sulfotransferase 4, complete cds
8854	21393	34315	0.62	6.0E-99	11431994	NT	Homo sapiens lodestar protein mRNA, complete cds
8854	21393	34316	0.62	6.0E-99	11431994	NT	Homo sapiens lodestar protein mRNA, complete cds
10598	23132	36146	4.18	6.0E-99	11526299	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
953	13565	26077	9.63	5.0E-99	U35464.1	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
953	13565	26078	9.63	5.0E-99	U35464.1	NT	Homo sapiens BH3 interacting domain death agonist (BID), mRNA
2007	14589	27149	1.33	5.0E-99	Y11365.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
4663	17245	28698	1.44	5.0E-99	AF009660.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
12009	24311		2.1	5.0E-99	BE890177.1	EST_HUMAN	H. sapiens IMPA gene, exon 8
8263	20804		5.49	3.0E-99	M95586.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
1282	13878		15.39	2.0E-99	AW274782.1	EST_HUMAN	601513157F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914391 5'
3297	15908	28388	1.27	2.0E-99	M30938.1	NT	Human E2AHLA fusion protein (E2AHLF) mRNA, complete cds
4841	17223	29877	1.67	2.0E-99	AF095703.1	NT	Human E2AHLA fusion protein (E2AHLF) mRNA, complete cds
7667	20179	33066	1.28	2.0E-99	AF257737.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
							Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene
							encoding mitochondrial protein, complete cds
							Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds

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8641	21180	34100	9.63	2.0E-99	W23507.1	EST_HUMAN	zb4d06.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306335 5' similar to
8078	21615	34550	0.83	2.0E-99	R78254.1	EST_HUMAN	gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
10984	23498	36528	3.8	2.0E-98	AF247457.2	NT	y81D09.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145625 5'
11617	24059	37123	1.61	2.0E-98	10863960	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
337	12989	25476	1.46	1.0E-99	AF114487.1	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
402	13046	25537	1.21	1.0E-99	11528150	NT	Homo sapiens Intersectin long isoform (ITSN) mRNA, complete cds
1466	14058	26592	2.52	1.0E-99	M30938.1	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
1603	14185	26726	2.14	1.0E-99	AF192523.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1603	14195	26727	2.14	1.0E-98	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1971	14555	27111	0.81	1.0E-99	4503730	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1971	14555	27112	0.81	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (35kD) (FKBP6) mRNA, and translated products
3121	15735	28204	0.9	1.0E-98	J03171.1	NT	Homo sapiens FK506-binding protein 6 (39kD) (FKBP6) mRNA, and translated products
4469	17055	29499	2.98	1.0E-99	AF098018.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
4469	17055	29499	2.98	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
5896	19630	32487	2.18	1.0E-99	11421007	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
5896	19630	32468	2.18	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7193	24778	32574	0.8	1.0E-99	X98022.1	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
9127	21682		1.04	1.0E-99	11419721	NT	H. sapiens EB-AP gene exon 2
9439	21985	34914	1.81	1.0E-99	AW340174.1	EST_HUMAN	Homo sapiens ALEX1 protein (LOC51309), mRNA
11064	23576	36814	1.82	1.0E-99	5901979	NT	h02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:O02711
11255	23785	36841	2.94	1.0E-98	AB023222.1	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
11557	24005	37077	1.8	1.0E-99	AF223391.1	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
11637	24078	37136	1.57	1.0E-99	AF223391.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11764	24155		9.05	1.0E-99	AF240786.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1	12682	26138	1.19	1.0E-100	AL163247.2	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2	12682	25138	1.73	1.0E-100	AL163247.2	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
72	12750	25227	1.35	1.0E-100	11418230	NT	Homo sapiens chromosome 21 segment HS21C047 ;
72	12750	25228	1.35	1.0E-100	11418230	NT	Homo sapiens chromosome 21 segment HS21C047
80	12766	25250	0.79	1.0E-100	AW275237.1	EST_HUMAN	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
							Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
							xx78b11.x1 NCL_CGAP_Brm53 Homo sapiens cDNA clone IMAGE:2824805 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
180	12842	25328	1.18	1.0E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
339	12991	25478	1.76	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
365	13014	25497	2.06	1.0E-100	T05087.1	EST_HUMAN	EST02875 Fetal brain, Stralagene (cat#336206) Homo sapiens cDNA clone HFBOR32
482	13096		1.84	1.0E-100	AF003628.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
515	13148		8.1	1.0E-100	X99831.1	NT	G.gorilla DNA for ZNF80 gene homolog
535	13168	25847	1.78	1.0E-100	BE180609.1	EST_HUMAN	RC3-H10625-040500-022-b09 HT0625 Homo sapiens cDNA
1057	13682	26172	3.18	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1057	13682	26173	3.18	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1483	14076	26614	0.93	1.0E-100	BF530735.1	EST_HUMAN	602072064F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215039 5'
1594	14187		2.49	1.0E-100	AW207555.1	EST_HUMAN	U1-H-B11-afk-c-07-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
1598	14190	26721	1.32	1.0E-100	AI200857.1	EST_HUMAN	qf62f09.X1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA
2284	14858		2.78	1.0E-100	D83349.1	NT	P81081 CYSTATIN 1
2482	15048	27617	0.87	1.0E-100	X62468.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2731	15286	27853	2.8	1.0E-100	11418976	NT	H. sapiens mRNA for IFN-gamma (pKC-0)
3053	15689		3.92	1.0E-100	D11078.1	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
4289	18875	29224	1.93	1.0E-100	AF037354.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4320	18906	29348	2.66	1.0E-100	4503792	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
5253	17818	30239	3.18	1.0E-100	5032104	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5253	17818	30240	3.18	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5493	18127	30535	1.55	1.0E-100	BF244218.1	EST_HUMAN	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5699	18325	30828	0.87	1.0E-100	AW075983.1	EST_HUMAN	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5979	18501	31227	1.93	1.0E-100	AU118182.1	EST_HUMAN	601863164F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080999 5'
5920	18542	31268	1.36	1.0E-100	AF135116.1	NT	xa8201.X1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2573305 3' similar to gb:X12433
6003	18623	31358	10.01	1.0E-100	X14690.1	NT	PROTEIN PHPS1-2 (HUMAN);
6311	18918	31892	1.06	1.0E-100	4557568	NT	AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5'
6311	18918	31893	1.06	1.0E-100	4557568	NT	Homo sapiens NF-E2-related factor 3 gene, complete cds
6566	19164		1.29	1.0E-100	5729887	NT	Homo sapiens NF-E2-related factor 3 gene, complete cds
6623	19220	32025	5.02	1.0E-100	AU140214.1	EST_HUMAN	Human mRNA for plasma inter-alpha-trypsin inhibitor heavy chain H(3)
6787	19378	32193	1.46	1.0E-100	R10987.1	EST_HUMAN	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6868	19600	32431	2.42	1.0E-100	7382479	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
							Homo sapiens hct domain and RLD 2 (HERC2), mRNA
							AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5'
							Y38c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134 3'
							Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA

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6929	19588	32417	1.2	1.0E-100	AA496841.1	EST_HUMAN	ee33b08.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418
6929	19588	32418	1.2	1.0E-100	AA496841.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN ;
6968	19543	32368	1.25	1.0E-100	BF376478.1	EST_HUMAN	ee33b08.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418
6968	19543	32367	1.25	1.0E-100	BF376478.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN ;
6974	19550	32375	8.47	1.0E-100	X04571.1	NT	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
8469	21009	33826	12.09	1.0E-100	BF103853.1	EST_HUMAN	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
8503	21042		4.81	1.0E-100	AL163203.2	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
8944	21482	34404	0.87	1.0E-100	AL163203.2	EST_HUMAN	601647357F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3931310 5'
8944	21482	34405	0.87	1.0E-100	AL163203.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
9159	21694	34638	3.35	1.0E-100	AB040918.1	NT	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9234	21956		1.06	1.0E-100	AI972388.1	EST_HUMAN	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9354	20263	33192	1.65	1.0E-100	AW998611.1	EST_HUMAN	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9407	21916		1.74	1.0E-100	AU127720.1	EST_HUMAN	Homo sapiens mRNA for KIAA1626 protein, partial cds
9504	22004	34961	2.84	1.0E-100	AB046846.1	NT	PMO-BN0085-100300-001-c06 BN0085 Homo sapiens cDNA
9504	22004	34962	2.84	1.0E-100	AB046846.1	NT	AU127720 NT2RP2 Homo sapiens cDNA clone NT2RP2001918 5'
9757	22255	35237	1.81	1.0E-100	AW630487.1	EST_HUMAN	Homo sapiens mRNA for KIAA1626 protein, partial cds
9757	22255	35238	1.81	1.0E-100	AW630487.1	EST_HUMAN	h83c11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969396 5'
9917	22413	35388	0.5	1.0E-100	AV732101.1	EST_HUMAN	h83c11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969396 5'
10366	22680	35853	1.46	1.0E-100	BF347519.1	EST_HUMAN	AV732101 HTF Homo sapiens cDNA clone HTF9IG01 5'
10452	22946		1.38	1.0E-100	Y10391.1	NT	602020554F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4156165 5'
10638	23170	36181	7.35	1.0E-100	BF327292.1	EST_HUMAN	Human endogenous retrovirus HERV-K, pol gene
11166	23673	36719	2.59	1.0E-100	X94633.1	NT	MRO-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA
11166	23673	36720	2.59	1.0E-100	X94633.1	NT	H.sapiens CD97 gene exon 4
11232	23763	36818	4.28	1.0E-100	AF111170.3	NT	H.sapiens CD97 gene exon 4
11232	23763	36819	4.28	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11261	12682	25138	2.14	1.0E-100	AL163247.2	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11529	23977		1.65	1.0E-100	AF266285.1	NT	Homo sapiens chromosome 21 segment HS21C047
11683	24100	37150	9.41	1.0E-100	AF240786.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
12000	24306	30960	2.92	1.0E-100	11545732	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12842	24717	30868	3.53	1.0E-100	11417974	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
							Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA

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Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
81	12758	25240	2.04	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
81	12758	25241	2.04	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
715	13336	25822	1.77	1.0E-101	AB007815.2	NT	Homo sapiens mRNA for KIAA0446 protein, partial cds
733	13353	25848	5.29	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
733	13353	25849	5.29	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
803	13420	25925	3.37	1.0E-101	7657454	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
886	13500	26018	1.96	1.0E-101	4503914	NT	Homo sapiens phosphoribosylcycloheximide formyltransferase, phosphoribosylcycloheximide synthetase,
881	13572	26088	0.88	1.0E-101	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
1022	13632	26149	24.99	1.0E-101	BF681218.1	EST_HUMAN	602156474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287281 5'
1080	13695	26204	1.58	1.0E-101	AJ221878.1	EST_HUMAN	q99809.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
1782	14372	26917	0.9	1.0E-101	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1782	14372	26918	0.9	1.0E-101	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1888	14570	27132	1.54	1.0E-101	4502866	NT	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1), mRNA
2101	14680	27248	1.93	1.0E-101	BE843070.1	EST_HUMAN	RC3-ST0281-160600-018-h09 ST0281 Homo sapiens cDNA
2388	15465	27528	1.24	1.0E-101	5728892	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2848	15205	27778	10.93	1.0E-101	X72893.1	NT	H. sapiens EWS gene, exon 5
2771	15324	27891	2.71	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
2771	15324	27892	2.71	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
2882	15598		10.39	1.0E-101	AJ252312.1	NT	Homo sapiens genomic downstream Rhesus box
3237	15849	28330	2.92	1.0E-101	4885270	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3278	15889		2.37	1.0E-101	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3862086 5'
3427	16035	28515	1.94	1.0E-101	AW865556.1	EST_HUMAN	EST377629 MAGI resequences, MAGI Homo sapiens cDNA
3447	15324	27891	2.93	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
3447	15324	27892	2.93	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
3945	18543	28010	4.28	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
5185	17750	30180	1.38	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5185	17750	30181	1.38	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5521	18153	30587	1.28	1.0E-101	AW965139.1	EST_HUMAN	EST377212 MAGI resequences, MAGI Homo sapiens cDNA
6154	18767	31530	3.48	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6154	18767	31531	3.48	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6798	19387	32203	1.06	1.0E-101	11430734	NT	Homo sapiens carbonic anhydrase VII (CA7), mRNA
7317	19844		1.18	1.0E-101	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7361	19887	32749	4.87	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7361	19887	32750	4.87	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
7491	20014	32860	11.99	1.0E-101	AW008475.1	EST_HUMAN	w55f12.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2533487 3'
7576	20092		1.88	1.0E-101	BE257384.1	EST_HUMAN	601108217F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349901 5'
7707	20216	33104	7.87	1.0E-101	BF33759.1	EST_HUMAN	RC1-BT0313-220700-018-f12 BT0313 Homo sapiens cDNA
7854	20398	33301	0.98	1.0E-101	BE275821.1	EST_HUMAN	601121621F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345889 5'
7854	20398	33302	0.98	1.0E-101	BE275821.1	EST_HUMAN	601121621F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345889 5'
7899	20541	33443	6.69	1.0E-101	BF029174.1	EST_HUMAN	601784886F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996837 5'
8264	20805	33722	0.66	1.0E-101	AW630070.1	EST_HUMAN	hh74g10.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
8264	20805	33723	0.66	1.0E-101	AW630070.1	EST_HUMAN	hh74g10.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
8940	21478	34389	1.55	1.0E-101	AA036800.1	EST_HUMAN	2K29q08.r1 Soares pregnant uterus NBHPU Homo sapiens cDNA clone IMAGE:471998 5' similar to PIR:S54840 S54840 YD9335.03c protein - yeast;
9253	21779	34730	0.8	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9253	21779	34731	0.8	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9383	20321	33225	17.2	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9383	20321	33226	17.2	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9398	21819	34769	18.05	1.0E-101	9845492	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
9672	22171	35146	12.54	1.0E-101	BE619667.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
9672	22171	35147	12.54	1.0E-101	BE619667.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
9808	22308	35280	0.85	1.0E-101	10863960	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
10308	22802	35764	1.71	1.0E-101	11428127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10337	22831	35825	5.16	1.0E-101	AI570293.1	EST_HUMAN	to77d11.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10337	22831	35826	5.16	1.0E-101	AI570293.1	EST_HUMAN	to77d11.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10442	22938	35945	0.85	1.0E-101	BE973648.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
10442	22938	35946	0.85	1.0E-101	BE973648.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
10757	23281	36295	1.63	1.0E-101	S39327.1	NT	branched-chain alpha-keto acid dehydrogenase complex E1 alpha subunit (human, Genomic, 195 nt, segment 8 of 9)
10988	23502	36932	1.68	1.0E-101	AB020626.1	NT	Homo sapiens mRNA for KIAA0819 protein, partial cds
11620	24062	37128	18.03	1.0E-101	AA321316.1	EST_HUMAN	EST23783 Bone marrow Homo sapiens cDNA 5' end similar to defensin 1
12274	24478		15.99	1.0E-101	AW639051.1	EST_HUMAN	QV1-DT0088-240200-085-a01 DT0088 Homo sapiens cDNA
43	12722	25183	0.8	1.0E-102	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
363	13012	25494	4.36	1.0E-102	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
848	13271	25749	1.2	1.0E-102	BE252470.1	EST_HUMAN	601108292F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344328 5'
807	13424	25930	1.24	1.0E-102	4557534	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1156	13759	26269	5.76	1.0E-102	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1311	13905	26424	3.09	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1311	13905	26425	3.09	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1327	13921	26442	1.92	1.0E-102	4826977	NT	Homo sapiens reelin (RELN) mRNA
1484	14056	26589	104.12	1.0E-102	BE408447.1	EST_HUMAN	601269982F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629901 5'
2348	14919	27493	1.34	1.0E-102	AI124669.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95 ;
2348	14919	27494	1.34	1.0E-102	AI124669.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95 ;
3101	15718	28187	1.58	1.0E-102	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
3167	15781	28251	4.07	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
3167	15781	28252	4.07	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4316	16902	29346	1.84	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4503	17087	29535	2.55	1.0E-102	BE251310.1	EST_HUMAN	601107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343882 5'
5287	17849	30275	1.19	1.0E-102	R66488.1	EST_HUMAN	y32c04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140934 5'
5574	18205	30656	1.66	1.0E-102	AF067133.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
5923	18545		4.52	1.0E-102	AB034951.1	NT	Homo sapiens HSC54 mRNA for heat shock cognate protein 54, complete cds
5957	18578	31313	2.43	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5957	18578	31314	2.43	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5962	18584	31318	0.75	1.0E-102	11433048	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
8435	19038	31825	2.89	1.0E-102	AI459825.1	EST_HUMAN	ar6209.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137 Q13137 NDP52 ;
7190	19722	32570	0.67	1.0E-102	BE729323.1	EST_HUMAN	601561505F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3631241 5'
7217	19748	32604	0.83	1.0E-102	BE386106.1	EST_HUMAN	601277215F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618243 5'
7392	19917	32781	7.37	1.0E-102	AJ238994.1	NT	Homo sapiens mRNA for Centaurin-alpha2 protein
7620	20133	33010	2.75	1.0E-102	AV710738.1	EST_HUMAN	AV710738 Cu Homo sapiens cDNA clone CUAARD03 5'
8185	20708	33622	3.41	1.0E-102	BE763051.1	EST_HUMAN	QV3-NT0026-210600-236-h08 NT0025 Homo sapiens cDNA
8244	20785	33704	1.5	1.0E-102	BE910555.1	EST_HUMAN	601501107F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903145 5'
8431	20971	33893	1.65	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKGC Homo sapiens cDNA clone GKCEEE11 5'
8431	20971	33894	1.65	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKGC Homo sapiens cDNA clone GKCEEE11 5'
8539	21078	33997	0.52	1.0E-102	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8861	21400	34324	0.75	1.0E-102	BE388083.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
8861	21400	34325	0.75	1.0E-102	BE388083.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
9175	21752	34868	0.57	1.0E-102	AI762859.1	EST_HUMAN	wi63b06.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2397971 3' similar to contains MER4.11 MER4 MER4 repetitive element:
9205	21722	34868	0.76	1.0E-102	AV755842.1	EST_HUMAN	AV755842 BM Homo sapiens cDNA clone BMFAUD06 5'
9245	21771	34719	2.15	1.0E-102	T70393.1	EST_HUMAN	yd13d07.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'
9245	21771	34720	2.15	1.0E-102	T70393.1	EST_HUMAN	yd13d07.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'
9332	21848	34786	3.3	1.0E-102	AU124629.1	EST_HUMAN	AU124629 NT2RM4 Homo sapiens cDNA clone NT2RM4000309 5'
10284	22779		0.54	1.0E-102	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
10365	22859	35851	3.54	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-260489-014 BT074 Homo sapiens cDNA
10365	22859	35852	3.54	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-260489-014 BT074 Homo sapiens cDNA
10422	22918	35916	1.58	1.0E-102	AA970786.1	EST_HUMAN	on57h04.s1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:1560823 3' similar to SW/CAV2_HUMAN P51636 CAVEOLIN-2. [1].
10949	23464	36486	1.83	1.0E-102	BE897468.1	EST_HUMAN	60143992F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924166 5'
10952	23467	36490	6.26	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
10952	23467	36491	6.26	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11200	23705	36756	1.54	1.0E-102	AA868675.1	EST_HUMAN	ak49h10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1409347 3'
11282	23735	36780	3.6	1.0E-102	BF359243.1	EST_HUMAN	RC6-ET0072-150600-011-F01 ET0072 Homo sapiens cDNA
11555	24003	37076	3.66	1.0E-102	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
11689	24105		8.01	1.0E-102	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
12261	24471	30931	6.87	1.0E-102	AW300862.1	EST_HUMAN	xk07c12.x1 NCI_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2666038 3'
12588	24681		1.79	1.0E-102	J05235.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
73	12751	25229	2.49	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
73	12751	25230	2.49	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
104	12780	25282	8.29	1.0E-103	D87078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
222	12883	25368	2.74	1.0E-103	5453793	NT	Homo sapiens nuclear protein (KKE/D repeat) (NOP56) mRNA
1017	13627	26140	0.82	1.0E-103	AJ278348.1	NT	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1286	13881	26408	10.5	1.0E-103	BE877541.1	EST_HUMAN	601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5'
1640	14232	26768	2.26	1.0E-103	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2018	14600	27163	1.43	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2018	14600	27164	1.43	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2343	14914	27488	1	1.0E-103	AU134991.1	EST_HUMAN	AU134891 PLACE1 Homo sapiens cDNA clone PLACE1000965 5'
2494	15058	27632	1.88	1.0E-103	AF060588.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2631	15192	27762	1.54	1.0E-103	BF520378.1	EST_HUMAN	602041882F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179429 5'
2631	15192	27763	1.54	1.0E-103	BF529379.1	EST_HUMAN	602041882F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179429 5'
3105	15192		2.9	1.0E-103	BE744722.1	EST_HUMAN	601573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'
3428	16034	28514	3.71	1.0E-103	AW288245.1	EST_HUMAN	UI-H-BWO-qj-h-11-Q-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733165 3'
3487	16092	28564	1.19	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3818	16418		6.77	1.0E-103	AF023881.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3861	16459	28923	1.17	1.0E-103	AA485663.1	EST_HUMAN	ab10d12.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element ;
4075	16671	29132	3.62	1.0E-103	T23883.1	EST_HUMAN	seq340 b4HB3MA-Cot109+10-Bio Homo sapiens cDNA clone b4HB3MA-Cot109+10-Bio-7 3'
4946	17521	29883	0.88	1.0E-103	BE900203.1	EST_HUMAN	601873135F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955953 5'
6091	18707	31455	0.73	1.0E-103	BF569527.1	EST_HUMAN	602186023F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310573 5'
6097	18713	31463	1.8	1.0E-103	AF178995.1	NT	Homo sapiens septin 2 (SEP2) mRNA, partial cds
6413	19016	31788	0.71	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6413	19016	31789	0.71	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6587	19184	31985	0.78	1.0E-103	AW954568.1	EST_HUMAN	EST366836 MAGC resequences, MAGC Homo sapiens cDNA
6587	19184	31986	0.76	1.0E-103	AW954566.1	EST_HUMAN	EST366836 MAGC resequences, MAGC Homo sapiens cDNA
6707	24787	32108	1.16	1.0E-103	AA781442.1	EST_HUMAN	aj26603.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391452 3'
6743	19337	32142	0.88	1.0E-103	AF053490.1	NT	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4
6819	19409	32227	1.69	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS ;
6819	19409	32228	1.69	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS ;
6933	18041	30484	1.87	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
6933	18041	30485	1.87	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
7047	18067	30457	1.07	1.0E-103	11431100	NT	Homo sapiens ribosomal protein L3-like (RPL3L), mRNA
7101	19671	32510	1.13	1.0E-103	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
7278	19808	32665	1.34	1.0E-103	AW965778.1	EST_HUMAN	EST377849 MAGC resequences, MAGI Homo sapiens cDNA
7372	19898	32759	3.38	1.0E-103	BE748158.1	EST_HUMAN	601571537F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838545 5'
7749	20257	33152	4.44	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS ;

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7749	20257	33153	4.44	1.0E-103	AI590071.1	EST_HUMAN	in58b05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS ;
8556	21095	34015	1.14	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8556	21095	34016	1.14	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8637	21176	34095	1.13	1.0E-103	BF109244.1	EST_HUMAN	7160603.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525964 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;
9036	21573	34502	2.82	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9036	21573	34503	2.82	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9075	21612	34544	1.06	1.0E-103	AA581086.1	EST_HUMAN	nd13c02.s1 NCI_CGAP_OV1 Homo sapiens cDNA clone IMAGE:800162 3' similar to gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
9117	21653	34594	1.29	1.0E-103	AA774980.1	EST_HUMAN	ae84d12.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:970871 3' similar to gb:X03747_cds1 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-1 (HUMAN);
9870	22465	35449	1.55	1.0E-103	Z37976.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
10011	22506	35497	1.64	1.0E-103	AW963676.1	EST_HUMAN	EST375749 MAGE resequences, MACH Homo sapiens cDNA
10137	22632	35821	9.06	1.0E-103	AI878956.1	EST_HUMAN	au51g04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518326 5' similar to TR:Q15046 O15046 KIAA0338 ;
10521	23059	36069	2.78	1.0E-103	BE549706.1	EST_HUMAN	7b41f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230813 3' similar to gb:M69043 MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN (HUMAN);
10612	23145	36156	3.46	1.0E-103	AI782759.1	EST_HUMAN	c102d06.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1522283 5' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
10713	23241	36257	2.21	1.0E-103	11424061	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
10713	23241	36258	2.21	1.0E-103	11424061	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
10724	23251	36266	3.66	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
10724	23251	36267	3.66	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
11253	23783	36839	2.51	1.0E-103	AU136283.1	EST_HUMAN	AU136283 PLACE1 Homo sapiens cDNA clone PLACE1003923 5'
11320	23018	36027	5.36	1.0E-103	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
11590	24033	37103	4.36	1.0E-103	BE844611.1	EST_HUMAN	7e68a10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER29.3 MER29 repetitive element ;
11684	24101		2.23	1.0E-103	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
11717	24126		1.91	1.0E-103	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
11816	24254	31010	2.99	1.0E-103	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
254	12914	25398	4.81	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 564 (synonym: hfbt2) Homo sapiens cDNA clone DKFZp564H1072 5'
254	12914	25399	4.81	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 564 (synonym: hfbt2) Homo sapiens cDNA clone DKFZp564H1072 5'

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1932	14518	27072	2.06	1.0E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2235	14810	27382	2.22	1.0E-104	AA132975.1	EST_HUMAN	z022c06.s1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:587626 3' similar to
2245	14819	27394	1.47	1.0E-104	BE744628.1	EST_HUMAN	gbZ14116.na1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2407	14875	27548	0.89	1.0E-104	BF334221.1	EST_HUMAN	601577460F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926438 5'
2407	14875	27549	0.89	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-112 CT0249 Homo sapiens cDNA
2481	15047	27616	1.28	1.0E-104	5031570	NT	RC1-CT0249-110900-214-112 CT0249 Homo sapiens cDNA
2898	15513	27883	8.17	1.0E-104	M34871.1	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2941	15557		3.21	1.0E-104	Y11151.1	NT	Human lymphocytic antigen CD59/MEM43 mRNA, complete cds
3438	16048		1.77	1.0E-104	AA319436.1	EST_HUMAN	H sapiens gene encoding phenylpyruvate tautomerase II
3661	16263	28735	0.63	1.0E-104	AB033102.1	NT	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end
3661	16263	28736	0.63	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
4015	16813	29086	1.2	1.0E-104	AB032988.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
4210	16769	29248	0.82	1.0E-104	F11745.1	EST_HUMAN	Homo sapiens mRNA for KIAA1172 protein, partial cds
4468	17052	28496	6.67	1.0E-104	X02761.1	NT	HSC31A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07
4715	17298	29740	1.26	1.0E-104	AF231920.1	NT	Human mRNA for fibronectin (FN precursor)
4715	17298	29741	1.28	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
5330	17891	30305	1.84	1.0E-104	U43379.1	4502152	Homo sapiens chromosome 21 unknown mRNA
6095	18711	31459	1.18	1.0E-104	U43379.1	NT	Homo sapiens apolipoprotein B (including Ag(x) antigen) (APOB) mRNA
6095	18711	31460	1.18	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6139	18753	31511	0.98	1.0E-104	AB017332.1	NT	Human Down Syndrome region of chromosome 21 DNA
6593	19180	31883	8.25	1.0E-104	A1768797.1	EST_HUMAN	Homo sapiens alk3 mRNA for Aurora/pi1-related kinase 3, complete cds
6593	19180	31894	8.25	1.0E-104	A1768797.1	EST_HUMAN	w03b12.x1 NCI_CGAP_K12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145
6756	19349	32158	1.07	1.0E-104	7706512	NT	KIAA0132 PROTEIN; contains element LTR7 repetitive element;
6895	19828	32465	1.48	1.0E-104	BE314182.1	EST_HUMAN	KIAA0132 PROTEIN; contains element LTR7 repetitive element;
6895	19828	32466	1.48	1.0E-104	BE314182.1	EST_HUMAN	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
7276	19804	32863	2.22	1.0E-104	11425572	NT	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
8533	21072	33992	0.71	1.0E-104	BF509244.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
9094	21830	34588	2.59	1.0E-104	BF448230.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
9187	21704	34646	0.6	1.0E-104	AA682308.1	EST_HUMAN	UI-H-B14-acw-b-09-Q-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086176 3'
9208	21725		1.62	1.0E-104	IT74219.1	EST_HUMAN	z098b05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:3365948 3'
9238	21784	34710	4.74	1.0E-104	AF091395.1	NT	yc83f02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22440 5'

Table 4

Single Exon Probes Expressed in Fetal Liver.

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9238	21784	34711	4.74	1.0E-104	AF091395.1	NT	Homo sapiens Tio isoform mRNA, complete cds
9362	20301	33201	4.6	1.0E-104	BF332841.1	EST_HUMAN	IL3-HT0819-080900-249-F07 HT0819 Homo sapiens cDNA
9362	20301	33202	4.6	1.0E-104	BF332841.1	EST_HUMAN	IL3-HT0819-080900-249-F07 HT0819 Homo sapiens cDNA
9668	22167	35142	0.69	1.0E-104	AW103848.1	EST_HUMAN	xd76d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116
9668	22167	35143	0.69	1.0E-104	AW103848.1	EST_HUMAN	xd76d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116
9858	22355	35336	0.54	1.0E-104	AF113514.1	NT	Homo sapiens histone acetyltransferase MORF mRNA, complete cds
10005	22500	35490	3.86	1.0E-104	BE791713.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10005	22500	35491	3.86	1.0E-104	BE791713.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10269	22763	36783	1.05	1.0E-104	AV728070.1	EST_HUMAN	AV728070 HTC Homo sapiens cDNA clone HTCBYA07 5'
10338	22832	35827	4.98	1.0E-104	AU130765.1	EST_HUMAN	AU130765 NT2RP3 Homo sapiens cDNA clone NT2RP3001398 5'
10445	22839	35949	3.94	1.0E-104	U68535.1	NT	Human beta4-integrin (ITGB4) gene, exons 19,20,21,22,23,24 and 25
10457	22951		1.04	1.0E-104	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
11178	23683	36728	2.44	1.0E-104	BE720191.1	EST_HUMAN	RCO-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
11178	23683	36729	2.44	1.0E-104	BE720191.1	EST_HUMAN	RCO-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
11208	23712	36766	5.34	1.0E-104	BF684288.1	EST_HUMAN	602141215F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302507 5'
12538	24848		2.96	1.0E-104	BE393892.1	EST_HUMAN	601312181F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658876 5'
300	15384	25445	2.78	1.0E-105	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
450	12679	25135	15.84	1.0E-105	4505150	NT	Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA
620	13247	25720	5.78	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
620	13247	25721	5.78	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1719	14311		1.84	1.0E-105	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
1859	14447	27004	1.35	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1870	14554	27110	1.24	1.0E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2231	14908	27379	1.36	1.0E-105	AA318369.1	EST_HUMAN	EST20609 Spleen 1 Homo sapiens cDNA 5' end similar to autoimmune antigen Ku, p70/p80 subunit
2747	15302		1.43	1.0E-105	AA584808.1	EST_HUMAN	no10d05.x1 NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100265 3'
3039	15655		3.35	1.0E-105	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3394	16002	28482	0.72	1.0E-105		NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
3394	16002	28483	0.72	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4173	16764	29212	2.65	1.0E-105	AW061688.1	EST_HUMAN	EST373761 MAGG resequences, MAGG Homo sapiens cDNA
4853	17431	29881	0.65	1.0E-105	BE868881.1	EST_HUMAN	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'
4853	17431	29882	0.65	1.0E-105	BE868881.1	EST_HUMAN	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4874	17449	29600	1.06	1.0E-105	AA69835.1	EST_HUMAN	z144g02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:433682 3'
5073	17848			1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5533	18165	30578	0.97	1.0E-105	AF016704.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 2
5594	18224		1.12	1.0E-105	11420134	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
6985	19483	32303	1.68	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
6985	19483	32304	1.68	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
7058	18077	30430	3.65	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7058	18077	30431	3.65	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7328	19855	32718	1.09	1.0E-105	BE902816.1	EST_HUMAN	60167279F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960019 5'
7800	20343	33252	0.87	1.0E-105	X12556.1	NT	Human mRNA for dbi proto-oncogene
7971	20513	33420	5.86	1.0E-105	T05087.1	EST_HUMAN	EST02975 Fetal brain, Stratagene (cat#336206) Homo sapiens cDNA clone HFBOR32
8337	20878	33789	1.43	1.0E-105	AW007194.1	EST_HUMAN	ws50c10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2500626 3' similar to
8858	21397	34320	0.75	1.0E-105	AW840817.1	EST_HUMAN	SW:ACSA_PENCH P36333 ACETYL-COENZYME A SYNTHETASE ;
8980	21518	34444	2.92	1.0E-105	AW016879.1	EST_HUMAN	RC1-CN0008-070100-011-e05 CN0008 Homo sapiens cDNA
9131	21666	34608	0.87	1.0E-105	AW882372.1	EST_HUMAN	UIH-B10p-ab1-b-12-Q-UI.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711782 3'
9131	21666	34607	0.87	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0062-140300-083-d09 OT0062 Homo sapiens cDNA
9487	21944	34891	1.07	1.0E-105	BE867793.1	EST_HUMAN	QV2-OT0062-140300-083-d09 OT0062 Homo sapiens cDNA
9487	21944	34892	1.07	1.0E-105	BE867793.1	EST_HUMAN	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
10812	23334	36347	6.07	1.0E-105	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
11109	23819	36660	2.15	1.0E-105	D63548.1	NT	Homo sapiens COL4A6 gene for a6(V) collagen, exon 31
11161	23668	36713	2.07	1.0E-105	7705938	NT	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
11457	23907	36974	2.56	1.0E-105	AW027554.1	EST_HUMAN	ww74107.x1 Soares_thymus_NHFTf Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR:P87892
11524	23972	37042	1.82	1.0E-105	BF430921.1	EST_HUMAN	P87892 PROTEASE ;
13	12692	25148	2.28	1.0E-106	AI904463.1	EST_HUMAN	7o18c10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3574291 3' similar to TR:P97680 P97680
162	12825		1.55	1.0E-106	AW503208.1	EST_HUMAN	RIN1. ;
219	12880	25366	1.75	1.0E-106	AI66065.1	EST_HUMAN	IL-BT057-281198-001 BT057 Homo sapiens cDNA
567	13198	25678	1.82	1.0E-106	AW965556.1	EST_HUMAN	UIHF-BNO-akt-g-07-Q-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
633	13258	25733	2.3	1.0E-106	J00149.1	NT	qt79c01.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2215008 3'
634	13258	25733	3.03	1.0E-106	J00149.1	NT	EST377628 MAGE resequences, MAGI Homo sapiens cDNA
1572	14165	26696	1.57	1.0E-106	AF145712.1	NT	Human dihydrofolate reductase pseudogene (psi-hd1)
1739	14329	26873	4.72	1.0E-106	U48724.1	NT	Human dihydrofolate reductase pseudogene (psi-hd1)
							Human dihydrofolate reductase pseudogene (psi-hd1)
							Human dihydrofolate reductase pseudogene (psi-hd1)
							Homo sapiens soluble neuropilin-1 mRNA, complete cds
							Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1757	14347	26892	0.89	1.0E-106	U04510.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41
1839	14427	26878	5.32	1.0E-106	AA527446.1	EST_HUMAN	hg41c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element;
1839	14427	26878	5.32	1.0E-106	AA527446.1	EST_HUMAN	hg41c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element;
2167	14744	27313	2.48	1.0E-106	BE144286.1	EST_HUMAN	MRO-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
2358	14927	27501	3.35	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2638	15108	27769	1.49	1.0E-106	BE260201.1	EST_HUMAN	601149783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502481 5'
2788	15339	27810	6.69	1.0E-106	AI276528.1	EST_HUMAN	q176h10.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1878307 3'
2852	14071	26609	1.52	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2852	14071	26610	1.52	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2899	15516	27985	0.98	1.0E-106	BE394296.1	EST_HUMAN	601272675F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3613818 5'
2898	15583	28063	6.37	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
2968	15583	28064	6.37	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3214	15828	28303	2.04	1.0E-106	8922985	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3214	15828	28304	2.04	1.0E-106	8922985	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3420	16028	28509	0.72	1.0E-106	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3488	16093	28565	1.14	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3488	16093	28566	1.14	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4111	18705	29158	9.08	1.0E-106	AW974850.1	EST_HUMAN	EST386875 MAGC resequences, MAGN Homo sapiens cDNA
4111	18705	29159	9.08	1.0E-106	AW974850.1	EST_HUMAN	EST386875 MAGC resequences, MAGN Homo sapiens cDNA
4706	17288	29732	1.47	1.0E-106	BE144286.1	EST_HUMAN	MRO-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
5438	17993	30399	8.5	1.0E-106	SE7479.1	NT	(GC*IS)=vitamin D-binding protein/group specific component (human, peripheral blood leukocytes, Genomic, 2126 nt, segment 5 of 8)
5572	18203	30853	2.76	1.0E-106	AA781155.1	EST_HUMAN	g24609.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391225 3' similar to gb:X12433 PROTEIN PHS1-2 (HUMAN);
6017	18638	31375	0.67	1.0E-106	AU130113.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
6017	18638	31376	0.67	1.0E-106	AU130113.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
6145	18759	31517	0.82	1.0E-106	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6145	18759	31518	0.82	1.0E-106	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6250	18859	31631	13.05	1.0E-106	BF679574.1	EST_HUMAN	602154012F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295087 5'
6355	18960	31738	0.68	1.0E-106	BE897112.1	EST_HUMAN	601439870F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6551	19149	31945	19.14	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6551	19149	31946	19.14	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7406	19931	32795	5.83	1.0E-106	AA663778.1	EST_HUMAN	aa72e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969732 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
7453	19977	32842	4.92	1.0E-106	11429817	NT	Homo sapiens XPMC2 protein (LOC57109). mRNA
7514	20035	32901	1.23	1.0E-106	BE292722.1	EST_HUMAN	601105736F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988345 5'
7606	20119	32995	8.75	1.0E-106	11425503	NT	Homo sapiens sorting nexin 11 (SNX11). mRNA
7606	20119	32996	8.75	1.0E-106	11425503	NT	Homo sapiens sorting nexin 11 (SNX11). mRNA
7769	20277	33175	0.72	1.0E-106	AW163047.1	EST_HUMAN	au91f05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783649 5' similar to TR:O75834 O75834 CULLIN-4A;
7826	20468	33376	5.97	1.0E-106	BE741408.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
7826	20468	33377	5.97	1.0E-106	BE741408.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8115	20656	33565	13.65	1.0E-106	AI523086.1	EST_HUMAN	ar68a07.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2127732 3' similar to gb:X08233 CALGRANULIN B (HUMAN);
8564	21103	34022	0.74	1.0E-106	BE387950.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604483 5'
8564	21103	34023	0.74	1.0E-106	BE387950.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604483 5'
8640	21179	34089	3.9	1.0E-106	AI654123.1	EST_HUMAN	ly62a05.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN Q05084 69 KD ISLET CELL AUTOANTIGEN;
8845	21184	34103	0.54	1.0E-106	AI891109.1	EST_HUMAN	wu38c03.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522308 3' similar to TR:O70273 O70273 ETS HOMOLOGOUS FACTOR;
8982	21520	34448	0.56	1.0E-106	AW538831.1	EST_HUMAN	CM4-LT0059-150200-098-e08 LT0059 Homo sapiens cDNA
9074	21611	34542	2	1.0E-106	AA825307.1	EST_HUMAN	cc87e08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354780 3'
9074	21611	34543	2	1.0E-106	AA825307.1	EST_HUMAN	cc87e08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354780 3'
9210	21727	34670	2.03	1.0E-106	AI750447.1	EST_HUMAN	cn03a04.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn03a04 random
9350	21864	34814	1.46	1.0E-106	AI479569.1	EST_HUMAN	lm41f02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.13 TAR1 PTR5 repetitive element;
9350	21864	34815	1.46	1.0E-106	AI479569.1	EST_HUMAN	lm41f02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.13 TAR1 PTR5 repetitive element;
9913	22409	35385	1.35	1.0E-106	BE389234.1	EST_HUMAN	601282387F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604217 5'
9986	22491	35479	1.47	1.0E-106	BF027310.1	EST_HUMAN	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
9996	22491	35480	1.47	1.0E-106	BF027310.1	EST_HUMAN	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
10139	22634	35624	8.16	1.0E-106	AA604417.1	EST_HUMAN	np57b10.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
10139	22634	35625	8.16	1.0E-106	AA604417.1	EST_HUMAN	np57b10.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
10185	22680	35672	1.56	1.0E-106	AW363299.1	EST_HUMAN	RCC-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
10180	22685	35677	0.77	1.0E-106	11436432	NT	Homo sapiens multimarin (NMNRN). mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10190	22685	35678	0.77	1.0E-108	11438432	NT	Homo sapiens multimerin (MMRN), mRNA
10358	22852	35846	0.45	1.0E-108	AL039888.1	EST_HUMAN	DKFZp434F0712_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434F0712 5'
10472	22968	35976	3.31	1.0E-108	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10775	23299	36304	6.85	1.0E-106	BF032755.1	EST_HUMAN	601453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857368 5'
10775	23299	36305	6.85	1.0E-108	BF032755.1	EST_HUMAN	601453461F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857368 5'
10941	23457	36480	2.83	1.0E-106	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
10941	23457	36481	2.93	1.0E-106	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
11288	23739	36795	1.67	1.0E-108	BE257385.1	EST_HUMAN	601108219F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349997 5'
11418	23869	36928	1.83	1.0E-106	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
11418	23869	36930	1.83	1.0E-106	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
11782	24887	36887	5.89	1.0E-106	AW410405.1	EST_HUMAN	fr05h11.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861644 5'
11991	24301	30889	4.03	1.0E-106	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
11991	24301	30887	4.03	1.0E-106	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12216	24339		3.44	1.0E-106	BE695905.1	EST_HUMAN	RC1-CT0248-090800-024-d05 CT0248 Homo sapiens cDNA
255	12915		2.78	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
286	12942		1.25	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
658	13281	25761	1.82	1.0E-107	AF155103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
848	13462	25970	1.45	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
919	13532	26050	2.27	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
1004	13615	26129	8.14	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1321	13915	26437	1.33	1.0E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1615	14208	26741	2.61	1.0E-107	BF087405.1	EST_HUMAN	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA
1788	14378	26922	2.7	1.0E-107	AF138275.1	NT	Homo sapiens cathepsin Z precursor (CTS2) gene, exon 3
1880	14486	27023	0.89	1.0E-107	AB007822.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1880	14486	27024	0.89	1.0E-107	AB007822.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2249	14823	27399	1.17	1.0E-107	U13729.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2400	14968	27541	0.94	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2400	14968	27542	0.94	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2572	15135	27706	5.5	1.0E-107	BE732460.1	EST_HUMAN	601587619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2572	15135	27707	5.5	1.0E-107	BE732460.1	EST_HUMAN	601587619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
3040	15656	28135	3.03	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3040	15656	28136	3.03	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3134	15748	28217	3.02	1.0E-107	5902087	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3898	16497	28959	4.68	1.0E-107	AF020671.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
3972	16570	29039	1.69	1.0E-107	M19816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
3972	16570	29040	1.69	1.0E-107	M19816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
6026	18844	31388	4.74	1.0E-107	BE867469.1	EST_HUMAN	601442558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846494 5'
7399	18924	32788	1.4	1.0E-107	AW503913.1	EST_HUMAN	UI-HF-BNO-alf-c-08-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078310 5'
7399	18924	32789	1.4	1.0E-107	AW503913.1	EST_HUMAN	UI-HF-BNO-alf-c-08-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078310 5'
7536	20056	32930	1.28	1.0E-107	AI765078.1	EST_HUMAN	wt56h04.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384791 3'
9309	21909	34858	0.88	1.0E-107	AU122469.1	EST_HUMAN	AU122469 MAMMA1 Homo sapiens cDNA clone MAMMA1002433 5'
10533	23070	36083	2.05	1.0E-107	BE168726.1	EST_HUMAN	QY1-HT0518-140300-107-c10 HT0518 Homo sapiens cDNA
10583	23118	36133	3.35	1.0E-107	AI392850.1	EST_HUMAN	tg10d08.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICD1
10825	23346	36362	2.18	1.0E-107	L49141.1	NT	P05095 ALPHA-ACTININ 3, NON MUSCULAR
10839	23360	36375	2.39	1.0E-107	BF666511.1	EST_HUMAN	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
11203	23708	36760	4.35	1.0E-107	BE540550.1	EST_HUMAN	602123963F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281039 5'
11271	23009	36016	4.67	1.0E-107	11419701	NT	601066681F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452828 5'
11271	23009	36017	4.67	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
11677	24023	37082	3.77	1.0E-107	4507822	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
11830	25014		7.41	1.0E-107	AA001415.1	EST_HUMAN	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
189	12850		1.3	1.0E-108	AA341934.1	EST_HUMAN	2a45e01.s1 Soares retina NZB4HR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b1
890	13602	28116	1.64	1.0E-108	BE286042.1	EST_HUMAN	THR repetitive element
1308	13902	28421	4.66	1.0E-108	Y18000.1	NT	EST47363 Fetal muscle Homo sapiens cDNA 5' end
2123	14701	27271	0.95	1.0E-108	BF026728.1	EST_HUMAN	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
2368	14939	27511	1.91	1.0E-108	AI686040.1	EST_HUMAN	Homo sapiens NF2 gene
2368	14939	27512	1.91	1.0E-108	AI686040.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
							tb91e10.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
							tb91e10.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
2472	15039	27607	7.53	1.0E-108	BE206694.1	EST_HUMAN	bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963889 3' similar to gb:X53777 60S
3392	16000	28478	0.73	1.0E-108	AF032897.1	NT	RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
3392	16000	28479	0.73	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
							Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4237	16825	29275	1.43	1.0E-108	AW684438.1	EST_HUMAN	H12a11.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE
							P55194 SH3-BINDING PROTEIN 3BP-1.;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4624	17207	29556	1.92	1.0E-108	U72961.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4624	17207	29557	1.92	1.0E-108	U72961.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4926	17501	29549	2.66	1.0E-108	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5044	17617	30062	0.93	1.0E-108	AW504789.1	EST_HUMAN	UI-HF-BNO-ah-e-04-U1.r1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3080166 5'
5084	17657	30098	2.16	1.0E-108	AJ008005.1	NT	Homo sapiens PSN1 gene, alternative transcript
5318	17880	30289	0.81	1.0E-108	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
5670	18297	30777	1.2	1.0E-108	AW384094.1	EST_HUMAN	RCO-HT0372-241199-Q31-Q03 HT0372 Homo sapiens cDNA
5718	18344	30851	2.96	1.0E-108	BE869016.1	EST_HUMAN	601444922F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3848980 5'
5718	18344	30852	2.96	1.0E-108	BE869016.1	EST_HUMAN	601444922F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3848980 5'
6084	18701		0.83	1.0E-108	AF012823.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 20
6153	18766	31529	0.88	1.0E-108	BF334851.1	EST_HUMAN	PM4-CT0403-240700-Q01-c10 CT0403 Homo sapiens cDNA
6288	18896	31667	5.83	1.0E-108	AF284717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6288	18896	31667	5.83	1.0E-108	AF284717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6409	18012	31785	1.16	1.0E-108	AJ133269.1	NT	Homo sapiens cavedin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6409	18768	31529	1.01	1.0E-108	BF334851.1	EST_HUMAN	PM4-CT0403-240700-Q01-c10 CT0403 Homo sapiens cDNA
6732	19326	32130	0.85	1.0E-108	AF016706.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
6732	19326	32131	0.85	1.0E-108	AF016706.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7211	19742	32596	5.04	1.0E-108	11431857	NT	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPRC5B), mRNA
7465	19987	32852	3.44	1.0E-108	4758333	NT	Homo sapiens delta-6 fatty acid desaturase (FADS6) mRNA
7492	20015	32881	1.67	1.0E-108	BE252607.1	EST_HUMAN	601113747F1 NIH_MGC 16 Homo sapiens cDNA clone IMAGE:3354064 5'
7516	20036	32903	1.06	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181037 5'
7516	20036	32904	1.06	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181037 5'
8008	20550		1.77	1.0E-108	AF083500.1	NT	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
8058	20600	33509	1.47	1.0E-108	AW408694.1	EST_HUMAN	UI-HF-BMO-ads-e-12-0-U1.r1 NIH_MGC 38 Homo sapiens cDNA clone IMAGE:3062878 5'
8058	20600	33510	1.47	1.0E-108	AW408694.1	EST_HUMAN	UI-HF-BMO-ads-e-12-0-U1.r1 NIH_MGC 38 Homo sapiens cDNA clone IMAGE:3062878 5'
8977	21515	34439	1.08	1.0E-108	AF203977.1	NT	Homo sapiens ETS-family transcription factor EHF (EHF) mRNA, complete cds
9015	21552	34480	0.52	1.0E-108	N44974.1	EST_HUMAN	y35h10.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIR:A45773
10501	22995	36004	0.49	1.0E-108		NT	A45773 kelch protein, long form - fruit fly;
10547	20278	33176	1.87	1.0E-108	BE535227.1	EST_HUMAN	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10707	18037	30487	2.06	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)
11151	23659	36703	4.23	1.0E-108	AW669185.1	EST_HUMAN	EST378258 MAGI resequences, MAGI Homo sapiens cDNA
11204	23709	36761	1.81	1.0E-108	AV708790.1	EST_HUMAN	AV708790 ADC Homo sapiens cDNA clone ADCAEE03 5'
11204	23709	36762	1.81	1.0E-108	AV708790.1	EST_HUMAN	AV708790 ADC Homo sapiens cDNA clone ADCAEE03 5'
11249	23779		2.91	1.0E-108	11441465	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
11305	23798	36857	1.72	1.0E-108	D63539.1	NT	Homo sapiens COL4A6 gene for $\alpha 1(V)$ collagen, exon 23
12005	24308	30991	5.17	1.0E-108	AK024447.1	NT	Homo sapiens mRNA for FLJ00037 protein, partial cds
12414	24567		7.56	1.0E-108	BF346358.1	EST_HUMAN	602018571F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154297 5'
46	12725	25186	2.13	1.0E-109	AW803116.1	EST_HUMAN	IL2-UJ0077-260400-079-D08 UM0077 Homo sapiens cDNA
69	12747	25225	3.04	1.0E-109	D86974.1	NT	Human mRNA for KIAA0220 gene, partial cds
235	12895	25378	4.41	1.0E-109	11422488	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
246	12805	25386	2.89	1.0E-109	11438391	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
492	13125	25310	4.89	1.0E-109	4507712	NT	Homo sapiens tetrahydrocortisol repeat domain 2 (TTC2) mRNA
624	13251	25725	19.67	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
624	13251	25726	19.67	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1050	13657	26168	0.72	1.0E-109	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1244	13842	26359	24.19	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1245	13842	26359	15.92	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1589	14182	26714	0.98	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959836 5'
1589	14182	26715	0.98	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959836 5'
1915	14500	27055	3.28	1.0E-109	D13643.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2283	14857	27434	1.19	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2292	14868	27441	2.08	1.0E-109	V17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
2652	15211	27783	2.86	1.0E-109	AI023228.1	EST_HUMAN	aw95a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:O02197 O02197 CIRCULATING CATHODIC ANTIGEN. ;
2652	15211	27784	2.86	1.0E-109	AI023228.1	EST_HUMAN	aw95a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:O02197 O02197 CIRCULATING CATHODIC ANTIGEN. ;
2653	15212	27785	2.01	1.0E-109	4504208	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
3094	15709	28180	1.68	1.0E-108	N85190.1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3435	16043	28524	1.34	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-110 NN0009 Homo sapiens cDNA
3435	16043	28525	1.34	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-110 NN0009 Homo sapiens cDNA
3569	16173	28655	0.9	1.0E-109	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3909	16508		0.93	1.0E-109	BE146144.1	EST_HUMAN	MRO-HT0209-110400-108-a04 HT0209 Homo sapiens cDNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4228	18816	28264	4.43	1.0E-109	AI655417.1	EST_HUMAN	ts98g06.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP.F53A2.8
4493	17078	29528	2.7	1.0E-109	4504206	NT	CE16100 ;
4705	17287	29731	1.18	1.0E-109	7662083	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
5051	17824	30069	1.14	1.0E-109	R15400.1	EST_HUMAN	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
5465	18100	30418	0.78	1.0E-109	BF673718.1	EST_HUMAN	ye48e06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53057 5'
5516	18148	30560	2.6	1.0E-109	5174822	NT	802136440F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272922 5'
5792	18417	31448	1.24	1.0E-109	BE179356.1	EST_HUMAN	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA
6085	24758	31448	1.02	1.0E-109	BF378888.1	EST_HUMAN	RC1-HT0815-200400-022-d04 HT0815 Homo sapiens cDNA
8147	18417	31875	1.3	1.0E-109	BE179356.1	EST_HUMAN	CM1-UJ0038-060900-399-h07 UT0038 Homo sapiens cDNA
8491	18092	31875	0.8	1.0E-109	M23442.1	NT	RC1-HT0815-200400-022-d04 HT0815 Homo sapiens cDNA
8491	18092	31876	0.8	1.0E-109	M23442.1	NT	Human interleukin 4 (IL-4) gene, complete cds
7289	18817	32678	0.95	1.0E-109	AB046811.1	NT	Human interleukin 4 (IL-4) gene, complete cds
7566	20083	32659	4.08	1.0E-109	11432574	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
7568	20085	32861	5.94	1.0E-109	BF182707.1	EST_HUMAN	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7568	20085	32862	5.94	1.0E-109	BF182707.1	EST_HUMAN	601809485F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
8114	20655	33584	1.17	1.0E-109	AL049784.1	NT	601809485F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
8227	20788	33887	1.27	1.0E-109	AW749130.1	EST_HUMAN	Novel human gene mapping to chromosome 13
8591	21130	34125	2.55	1.0E-109	AA077498.1	EST_HUMAN	PMO-BT0340-091299-002-e05 BT0340 Homo sapiens cDNA
8669	21208	34126	14.1	1.0E-109	BE787540.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
8669	21208	34126	14.1	1.0E-109	BE787540.1	EST_HUMAN	601478417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
8808	21446	34368	0.57	1.0E-109	BE145672.1	EST_HUMAN	601478417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
9163	21698	34642	1.82	1.0E-109	H84860.1	EST_HUMAN	ILC-HT0205-071199-142-g01 HT0205 Homo sapiens cDNA
9272	21798	34747	0.54	1.0E-109	BE397088.1	EST_HUMAN	ye90g08.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222110 5' similar to SP:A53491
9272	21798	34748	0.54	1.0E-109	BE397088.1	EST_HUMAN	A53491 BUMETANIDE-SENSITIVE NA-K-Cl COTRANSPORTER - SPINY ;
9405	21914	34863	3.55	1.0E-109	F06604.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
10653	23185	36200	2.73	1.0E-109	BE540909.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
10653	23185	36201	2.73	1.0E-109	BE540909.1	EST_HUMAN	HSC1EC121 normalized infant brain cDNA Homo sapiens cDNA clone c-1ec12
10687	23217	36229	35.59	1.0E-109	BF694831.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
10847	23368	36386	2	1.0E-108	7662278	NT	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
10847	23368	36387	2	1.0E-109	7662278	NT	602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5'
11004	23518	36553	1.95	1.0E-109	AU121370.1	EST_HUMAN	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
11248	23778	36835	2.84	1.0E-109	4502838	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
							AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002690 5'
							Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11285	23738	36794	6.81	1.0E-109	W16510.1	EST_HUMAN	zb08b12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to
12131	14866	27441	1.6	1.0E-109	Y17123.1	NT	PIR:S43969 p54-beta stress-activated protein kinases - rat ;
12252	24463	30961	15.45	1.0E-109	AB011398.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
3	12683	25139	1.19	1.0E-110	7548804	NT	Homo sapiens gene for AF-6, complete cds
40	12719	25179	4.61	1.0E-110	5803073	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
40	12719	25179	4.61	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
114	12683	25139	0.83	1.0E-110	7548804	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
316	12970	25459	1	1.0E-110	D67291.1	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
553	13184	25662	0.93	1.0E-110	U84550.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
1222	13822	26337	0.97	1.0E-110	5031820	NT	Human dystrobrevin (DTN) gene, exon 20
1322	13916	26438	1.28	1.0E-110	AB032253.1	NT	Homo sapiens calcitonin receptor-like (CALCRL) mRNA
1985	14549	27105	1.48	1.0E-110	BE379477.1	EST_HUMAN	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
2103	14682		1.65	1.0E-110	BF508896.1	EST_HUMAN	601237645f1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609683 5'
2666	15484		0.95	1.0E-110	4503098	NT	UI-H-BI4-acs-b-05-U1.s1 NC1_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
3065	13916	26438	0.85	1.0E-110	AB032253.1	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
3123	15737		1.2	1.0E-110	U78027.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
3228	15940	28319	8.37	1.0E-110	11436041	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein
3228	15940	28320	8.37	1.0E-110	11436041	NT	(L44L) and FTP3 (FTP3) genes, complete cds
4128	16720	28175	0.92	1.0E-110	BE018556.1	EST_HUMAN	Homo sapiens pregnancy-zone protein (PZP), mRNA
4281	16867	28314	1.06	1.0E-110	M15918.1	NT	bb82a05.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048848 5' similar to TR.O80312 O80312 KIAA0566 PROTEIN ;
4740	17321	29761	2.32	1.0E-110	A017213.1	EST_HUMAN	Human autoimmune antigen small nuclear ribonucleoprotein E pseudogene
4758	17339	29785	3.26	1.0E-110	AU117812.1	EST_HUMAN	alpha32b10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627963 3' similar to
5109	17681		1.8	1.0E-110	7692441	NT	SW.N121_RAT_P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
5498	18132	30540	2.16	1.0E-110	BE299406.1	EST_HUMAN	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
5800	18522	31247	0.7	1.0E-110	BE821089.1	EST_HUMAN	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
5917	18539	31264	6.81	1.0E-110	11419323	NT	601118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028538 5'
5917	18539	31265	6.81	1.0E-110	11419323	NT	601483677F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895795 5'
6818	24771	32226	3.2	1.0E-110	M55112.1	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
7159	19691	32536	0.83	1.0E-110	U08888.1	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
7159	19691	32537	0.83	1.0E-110	U08888.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
							Human GS2 gene, exon 2
							Human GS2 gene, exon 2

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7364	19890	32753	0.74	1.0E-110	AI560288.1	EST_HUMAN	Int12d08.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2187407 3' similar to SW:ETV1_HUMAN
7454	19878	32843	11.28	1.0E-110	AV714276.1	EST_HUMAN	P50549 ETS TRANSLOCATION VARIANT 1 ;
7454	19878	32844	11.28	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
7478	20000	32865	2.84	1.0E-110	AB020675.1	NT	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
7571	20088	32864	1.06	1.0E-110	AU137923.1	EST_HUMAN	Homo sapiens mRNA for KIAA0868 protein, partial cds
9258	21784	34737	0.54	1.0E-110	BE302594.1	EST_HUMAN	AU137823 PLACE1 Homo sapiens cDNA clone PLACE1007511 5'
9497	21897	34953	2.91	1.0E-110	AW838394.1	EST_HUMAN	ba6801.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905561 5' similar to TR:O77258 O77258
10226	22721	35712	3.91	1.0E-110	11432732	NT	EG:114D9.2 PROTEIN. ;
10626	23168	36171	3.89	1.0E-110	Y12337.1	NT	QV2-L T0053-020400-119-e04 LT0053 Homo sapiens cDNA
10848	23367	36384	3.87	1.0E-110	BE734357.1	EST_HUMAN	Homo sapiens galactokinase 2 (GALK2), mRNA
10846	23367	36385	3.87	1.0E-110	BE734357.1	EST_HUMAN	H. sapiens mRNA for myotonic dytroph protein kinase like protein
11317	23015	36024	3.28	1.0E-110	AA446529.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11719	24128		2.86	1.0E-110	BE897218.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11849	24209		11.86	1.0E-110	AW062258.1	EST_HUMAN	zw67g02.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781298 5' similar to TR:G1145816
12092	24360		2.73	1.0E-110	AB011396.1	NT	G1145816 FKBP54 ;
12239	25027		6.39	1.0E-110	BF304546.1	EST_HUMAN	601439784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924548 5'
12537	14682		1.43	1.0E-110	BF508896.1	EST_HUMAN	IL0-BT0183-040889-094-g10 BT0183 Homo sapiens cDNA
186	12847		28.49	1.0E-111	U43701.1	NT	Homo sapiens gene for AF-6, complete cds
210	12871	25357	0.94	1.0E-111	4758907	NT	PM3-NN1082-140900-008-112 NN1082 Homo sapiens cDNA
764	13383		1.64	1.0E-111	BF035327.1	EST_HUMAN	UI-H-B14-aos-b-05-0-UI.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
773	13392	25892	5.46	1.0E-111	8393092	NT	Human ribosomal protein L23a mRNA, complete cds
962	13573	26089	2.34	1.0E-111	M25142.1	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
1670	14263	26797	2.34	1.0E-111		EST_HUMAN	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
4250	16838	29288	1.25	1.0E-111		NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
4423	17008	29451	4.84	1.0E-111	K02888.1	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
5814	18438	31160	0.81	1.0E-111	BE867609.1	EST_HUMAN	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
6183	18793	31562	1.58	1.0E-111	A1344679.1	EST_HUMAN	Human enkephalin B (enkb) gene, exon 4 and 3' flank and complete cds
6781	19372	32188	1	1.0E-111	AL040762.1	EST_HUMAN	601443690F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847665 5'
6868	19632	32470	1.3	1.0E-111	AW284648.1	EST_HUMAN	qp09g12.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917574 3' similar to gb:M28893 RAS-
7471	19893	32856	2.68	1.0E-111	BF366228.1	EST_HUMAN	RELATD PROTEIN RAL-A (HUMAN);
						EST_HUMAN	DKFZp434C1815.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1815 5'
						EST_HUMAN	UI-H-BW0-ail-d-03-0-UI.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2729625 3'
						EST_HUMAN	IL2-NT0101-280700-114-E03 NT101 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7540	20060	32934	3.47	1.0E-111	A1761228.1	EST_HUMAN	w168d01.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398465 3' similar to gb:J04813 CYTOCHROME P450 IIAS (HUMAN);
7610	20123	33000	1.1	1.0E-111	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8038	20580	33486	0.77	1.0E-111	AA278888.1	EST_HUMAN	zs79g03.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410 G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR.;
8038	20580	33487	0.77	1.0E-111	AA278888.1	EST_HUMAN	zs79g03.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410 G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR.;
8129	20670	33580	0.89	1.0E-111	11431896	NT	Homo sapiens protein x0001 (LOC51185), mRNA
8183	20724	33638	5.9	1.0E-111	U68533.1	NT	Human beta4-integrin (ITGB4) gene, exon 13
8613	21152	34066	0.82	1.0E-111	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
8710	21249	34172	0.89	1.0E-111	AK024453.1	NT	Homo sapiens mRNA for FLJ00045 protein, partial cds
8743	21282	34280	23.24	1.0E-111	BF214802.1	EST_HUMAN	601847132f1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078303 5'
8817	21358	34281	12.59	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
8817	21358	34281	12.59	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
8917	21554	34482	3.03	1.0E-111	AF081395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9241	21767	34718	0.58	1.0E-111	BF333210.1	EST_HUMAN	QV2-BT0817-270900-398-e08 BT0817 Homo sapiens cDNA
10056	22551	35546	2.03	1.0E-111	AA504160.1	EST_HUMAN	aa58g02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825170 3' similar to gb:U09235 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
10082	22577		1.53	1.0E-111	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
10173	22668	35663	5.78	1.0E-111	AA131248.1	EST_HUMAN	z131f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10922	23441	36462	4.93	1.0E-111	U68159.1	NT	Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6
11674	24083	37146	4.3	1.0E-111	11417901	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
12234	24450	30954	2.23	1.0E-111	AV708482.1	EST_HUMAN	AV708482 ADC Homo sapiens cDNA clone ADCACB08 5'
12360	24816	30781	6.35	1.0E-111	W22562.1	EST_HUMAN	72C9 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
12507	18039	30498	1.31	1.0E-111	AB035356.1	NT	Homo sapiens mRNA for neurexin I-alpha protein, complete cds
636	13259	25734	1.69	1.0E-112	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
638	13281	25738	5.94	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
638	13281	25737	5.94	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
660	13283	25763	1.42	1.0E-112	BF509039.1	EST_HUMAN	UI-H-B14-eot-g-04-0-J1.st NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
660	13283	25764	1.42	1.0E-112	BF509039.1	EST_HUMAN	UI-H-B14-eot-g-04-0-J1.st NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1039	13649	26161	3.88	1.0E-112	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1100	13705	26213	2	1.0E-112	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
1722	14313	26853	4.44	1.0E-112	7882125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1722	14313	26854	4.44	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1858	14444	27000	1.58	1.0E-112	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
2550	15114	27684	1.81	1.0E-112	BE66859.1	EST_HUMAN	601442674F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846858 5'
3114	15728		0.59	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3953	16551	29020	0.74	1.0E-112	BE076073.1	EST_HUMAN	MR2-BT0560-090300-113-109 BT0560 Homo sapiens cDNA
4709	17291	29735	0.65	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4864	17441	29891	5.1	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
4884	17441	29892	5.1	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5948	18472	31198	38.42	1.0E-112	N46046.1	EST_HUMAN	Y35d07.r1 Soares melanocyte 2Nbl-HM Homo sapiens cDNA clone IMAGE:273229 5'
6227	18838	31609	1.38	1.0E-112	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6294	18902	31672	0.85	1.0E-112	AW502437.1	EST_HUMAN	UI-HF-BR0p-ajs-g-06-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075658 5'
6294	18902	31673	0.85	1.0E-112	AW502437.1	EST_HUMAN	UI-HF-BR0p-ajs-g-06-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075658 5'
6397	19000	31778	1.2	1.0E-112	BE741668.1	EST_HUMAN	601594717F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948557 5'
6747	19340	32148	0.68	1.0E-112	BE73103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'
6747	19340	32147	0.68	1.0E-112	BE73103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'
6928	19587	32416	1.36	1.0E-112	BF574235.1	EST_HUMAN	602131405F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270921 5'
7375	19901	32784	1.57	1.0E-112	11418777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7375	19901	32785	1.57	1.0E-112	11418777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
8134	20875	33587	1.93	1.0E-112	AU118051.1	EST_HUMAN	AU118051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5'
8887	21425	34350	2.49	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
8887	21425	34351	2.49	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
9807	22305	35289	2.06	1.0E-112	BF111413.1	EST_HUMAN	7130g07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523020 3' similar to
10857	23189	36205	3.51	1.0E-112	AW863327.1	EST_HUMAN	TR-Q8VVW35 Q8VVW35 CG8743 PROTEIN ;
10743	23287	36283	1.85	1.0E-112	T83987.1	EST_HUMAN	MR3-SN0009-100400-106-b12 SN0009 Homo sapiens cDNA
10743	23287	36284	1.85	1.0E-112	T83987.1	EST_HUMAN	Yd56d10.st Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to
10827	23348	36384	4.28	1.0E-112	AJ248900.1	NT	SP-C40H1.1 CE00109 OVARIAN PROTEIN ;
10876	23491	36521	1.76	1.0E-112	BE280479.1	EST_HUMAN	Yd56d10.st Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to
11051	23584	36598	2.08	1.0E-112	AJ904584.1	EST_HUMAN	SP-C40H1.1 CE00109 OVARIAN PROTEIN ;
11052	23574	36611	4.71	1.0E-112	AW377670.1	EST_HUMAN	Yd56d10.st Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to
							SP-C40H1.1 CE00109 OVARIAN PROTEIN ;
							Yd56d10.st Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to
							SP-C40H1.1 CE00109 OVARIAN PROTEIN ;
							Yd56d10.st Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to
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							Yd56d10.st Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to
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							Yd56d10.st Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to
							SP-C40H1.1 CE00109 OVARIAN PROTEIN ;
							Yd56d10.st Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to
							SP-C40H1.1 CE00109 OVARIAN PROTEIN ;
							Yd56

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
772	13391	25890	5.13	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
772	13391	25891	5.13	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
978	13590	26105	6.33	1.0E-113	M11855.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1588	14181	26713	2.48	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
1983	15395	27126	0.92	1.0E-113	AF240775.1	NT	Homo sapiens eIF4E-transporter mRNA, complete cds
2142	14720	27281	1.02	1.0E-113	BF515218.1	EST_HUMAN	U1H-BW1-enf-f-03-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082876 3'
3164	15778	28249	2.08	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
5454	24852		3.07	1.0E-113	BE780858.1	EST_HUMAN	601469465F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872536 5'
5684	18311	30808	6	1.0E-113	AU127214.1	EST_HUMAN	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5'
6080	18697	31444	3.89	1.0E-113	AU140291.1	EST_HUMAN	AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5'
6106	18722	31475	1	1.0E-113	AF016535.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6220	18830	31604	2.43	1.0E-113	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
6304	18911	31684	0.88	1.0E-113	8961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6304	18911	31685	0.88	1.0E-113	8961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6458	18059	31844	0.71	1.0E-113	8006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
6458	18059	31845	0.71	1.0E-113	8006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7362	19888	32751	0.77	1.0E-113	BE282161.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508382 5'
7362	19888	32752	0.77	1.0E-113	BE282161.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508382 5'
9024	21561	34488	3	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
9024	21561	34489	3	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
9322	21836		0.72	1.0E-113	BE772967.1	EST_HUMAN	RC1-FT0134-280600-021-d02 F.T0134 Homo sapiens cDNA
9745	22243	35224	1.2	1.0E-113	11428367	NT	Homo sapiens transmembrane protein 2 (TMEM2), mRNA
9843	22341	35223	0.55	1.0E-113	M21535.1	NT	Human erg protein (ets-related gene) mRNA, complete cds
9963	22458	35441	0.81	1.0E-113	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
9963	22458	35442	0.81	1.0E-113	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
11002	23516	36551	1.71	1.0E-113	AW500519.1	EST_HUMAN	U1-HF-BN0-ekj-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077326 5'
11011	23525	38559	2.11	1.0E-113	AW630291.1	EST_HUMAN	hh81a09.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969176 5' similar to TR:O60327 O60327
11011	23525	38560	2.11	1.0E-113	AW630291.1	EST_HUMAN	hh81a09.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969176 5' similar to TR:O60327 O60327
11097	18059	31844	1.58	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11087	19069	31845	1.68	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
11141	23049	36891	3.51	1.0E-113	BE292988.1	EST_HUMAN	601105529F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2888386 5'
11370	23822	36884	2.53	1.0E-113	AA580720.1	EST_HUMAN	nc80b03.11 NCLCGAP_GC1 Homo sapiens cDNA clone IMAGE:797069 5' similar to SW:FEN1_HUMAN
11370	23822	36885	2.53	1.0E-113	AA580720.1	EST_HUMAN	nc80b03.11 NCLCGAP_GC1 Homo sapiens cDNA clone IMAGE:797069 5' similar to SW:FEN1_HUMAN
62	12741	25213	1.2	1.0E-114	Y17151.2	NT	P39748 FLAP ENDONUCLEASE-1;
62	12741	25214	1.2	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
62	12741	25215	1.2	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
673	13297	25779	22.22	1.0E-114	T70551.1	EST_HUMAN	yd15c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element;
1109	13713	26223	2.93	1.0E-114	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080) mRNA
1358	13950	26476	3.57	1.0E-114	7657529	NT	Homo sapiens rhadoid tumor deletion region protein 1 (RTDR1) mRNA
1894	14276	26909	1.26	1.0E-114	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3) mRNA
1711	14304	28841	7.13	1.0E-114	6879073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1) mRNA
2830	12727	25189	2.13	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
2830	12727	25190	2.13	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3165	15779	28250	2.36	1.0E-114	X04088.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3207	15919	28295	1.02	1.0E-114	BF206374.1	EST_HUMAN	601869932F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
4088	16684	29142	1.81	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4480	17065	29515	0.92	1.0E-114	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
5324	17888	30302	0.89	1.0E-114	BE275324.1	EST_HUMAN	601122173F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346089 5'
5360	17920	30334	0.93	1.0E-114	AA194488.1	EST_HUMAN	zq05e05.1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628832 5' similar to contains MER22 t3 MER22 repetitive element;
5597	18227	30874	1.36	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5597	18227	30875	1.36	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5781	18408	31122	1.35	1.0E-114	9257201	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1), transcript variant 2, mRNA
7137	19478	32674	1.13	1.0E-114	AB041533.1	NT	Homo sapiens HMGOGT-1 mRNA for sperm antigen, complete cds
7288	19816	32674	1.2	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7288	19816	32675	1.2	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7328	19853	32715	7.05	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7326	19853	32716	7.05	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
7632	20374	33280	1.88	1.0E-114	4557600	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA
8108	20849	33557	1.81	1.0E-114	A1363139.1	EST_HUMAN	q68406.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017163 3'
8108	20849	33558	1.81	1.0E-114	A1363139.1	EST_HUMAN	q68406.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017163 3'
8635	21174	34093	4.12	1.0E-114	U63041.1	NT	Human neural cell adhesion molecule CD56 mRNA, complete cds
8702	21241	34185	5.52	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
8702	21241	34186	5.52	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
9110	21848	34588	0.92	1.0E-114	BF109832.1	EST_HUMAN	7169g12.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3528847 3' similar to
9335	21849		18.44	1.0E-114	AW327455.1	EST_HUMAN	TR:Q9UHN8 Q9UHN8 TRANSMEMBRANE PROTEIN 2.;
9384	20322	33227	3.14	1.0E-114	AF07754.1	NT	dq03105.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846744 5'
9487	21982		6.13	1.0E-114	M13536.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
10045	22540	35537	0.94	1.0E-114	BE870004.1	EST_HUMAN	Human ceruloplasmin mRNA
10066	22561	35556	1.32	1.0E-114	AL163227.2	NT	601449752F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3653500 5'
10434	22928	35935	0.71	1.0E-114	BE171984.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
							MRO-HT0559-250200-002-407 HT0559 Homo sapiens cDNA
							ba73g12.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906086 5' similar to gb:X17206 40S
							RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20692 Mouse LLRep3 protein mRNA from a repetitive element,
10666	23198		13.82	1.0E-114	BE302666.1	EST_HUMAN	complete (MOUSE);
11070	23582	36622	3.31	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
11070	23582	36623	3.31	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
12137	25093		3.79	1.0E-114	11418041	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
12410	24565	30909	2.85	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
12410	24565	30910	2.85	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
25	12704	25182	6.12	1.0E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA
135	12800	25288	2.34	1.0E-115	4503938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
139	12804		8.73	1.0E-115	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
314	12968	25456	3.77	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA
561	13182	25670	0.85	1.0E-115	A1339206.1	EST_HUMAN	q06101.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536
561	13182	25671	0.95	1.0E-115	A1339206.1	EST_HUMAN	q06101.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536
819	13436	25942	1.29	1.0E-115	5174702	NT	TTF-1 INTERACTING PEPTIDE 5;
819	13436	25943	1.29	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
821	13438	25945	190.74	1.0E-115	4503794	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
							Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1606	14188	26730	1.2	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1606	14188	26731	1.2	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1881	14467	27025	1.19	1.0E-115	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2125	14703	27273	1.11	1.0E-115	BE745489.1	EST_HUMAN	601578338F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2125	14703	27274	1.11	1.0E-115	BE745489.1	EST_HUMAN	601578338F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
3149	15763	28230	2.81	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3149	15763	28231	2.81	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3519	16124	28904	2.12	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4115	16709	29184	4.23	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4353	16940	29382	1.31	1.0E-115	AL137163.1	NT	Novel human gene mapping to chromosome X
4490	17075	29525	2.96	1.0E-115	6912859	NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
4529	17113	29557	4.4	1.0E-115	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
4783	17363	29813	2.89	1.0E-115	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4783	17363	29814	2.89	1.0E-115	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
5032	17606	30050	3.79	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
5032	17606	30051	3.79	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
5550	18182	30597	2.42	1.0E-115	AW970335.1	EST_HUMAN	EST382416 IMAGE resequences, MAGK Homo sapiens cDNA
5617	18246	30697	1.07	1.0E-115	BF665387.1	EST_HUMAN	602118346F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276738 5'
5732	18358	31063	1.79	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5732	18358	31064	1.79	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5869	18491	31217	1.1	1.0E-115	AI928799.1	EST_HUMAN	au84g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb:L07807
5869	18491	31218	1.1	1.0E-115	AI928799.1	EST_HUMAN	DYNAMIN-1 (HUMAN);
6408	19011	31793	0.89	1.0E-115	11428786	NT	Homo sapiens sperm surface protein (HSS), mRNA
6408	19011	31794	0.89	1.0E-115	11428786	NT	Homo sapiens sperm surface protein (HSS), mRNA
6529	19129	31923	20.52	1.0E-115	11426038	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63436), mRNA
6649	19245	32047	1.74	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
6649	19245	32048	1.74	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
7014	19512	32333	0.89	1.0E-115	T86774.1	EST_HUMAN	y486x08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115095 5' similar to SP:DPOG_YEAST P15801 DNA POLYMERASE GAMMA ;
7322	19849	32709	1.16	1.0E-115	AI076598.1	EST_HUMAN	alpha31a08.x1 Soares total fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'
7322	19849	32710	1.16	1.0E-115	AI076598.1	EST_HUMAN	alpha31a08.x1 Soares total fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7438	19862	32828	6.85	1.0E-115	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
8101	20842	33553	12.93	1.0E-115	BE830187.1	EST_HUMAN	RC6-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
8101	20842	33554	12.93	1.0E-115	BE830187.1	EST_HUMAN	RC6-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
8747	21286	34207	4.14	1.0E-115	11434772	NT	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA
9690	22189	35162	0.56	1.0E-115	BF382029.1	EST_HUMAN	601816352F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050108 5'
9910	22407	35382	2.13	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
9910	22407	35383	2.13	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
10414	22908	35908	1.08	1.0E-115	AI221878.1	EST_HUMAN	q99609.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843338 3'
10414	22908	35907	1.08	1.0E-115	AI221878.1	EST_HUMAN	q99609.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843338 3'
10420	22914	35914	0.68	1.0E-115	AI524687.1	EST_HUMAN	th12a07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2118036 3' similar to TR:O16129 O16129
10448	22942	35952	0.79	1.0E-115	BE886295.1	EST_HUMAN	PHENYLALANYL TRNA SYNTHETASE ;
10596	23130	36144	3.79	1.0E-115	AW571544.1	EST_HUMAN	xx3208.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2639239 3' similar to SW:CAYP_CANFA
11140	23648	36889	1.94	1.0E-115	BE045890.1	EST_HUMAN	P10463 CALCYPHOSINE ;
11140	23648	36890	1.94	1.0E-115	BE045890.1	EST_HUMAN	hq54c10.x1 NCI_CGAP_Pan3 Homo sapiens cDNA clone IMAGE:3123186 3' similar to TR:O88378 O88378
11276	23729	36784	2.64	1.0E-115	4502528	NT	PRP4 PROTEIN KINASE HOMOLOG ;
11698	24111		1.46	1.0E-115	AF240786.1	NT	PRP4 PROTEIN KINASE HOMOLOG ;
598	13227	25701	2.19	1.0E-116	BE275502.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E) mRNA
833	13450	25957	1.23	1.0E-116	4507334	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
892	13506		0.9	1.0E-116	4507334	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2040	14922	27190	3.39	1.0E-116	5174478	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
2040	14922	27191	3.39	1.0E-116	5174478	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
2072	14652	27224	1.95	1.0E-116	AU133080.1	EST_HUMAN	Homo sapiens pericentrin (PCNT) mRNA
2145	15458	27283	2.87	1.0E-116	M19824.1	NT	Homo sapiens pericentrin (PCNT) mRNA
2145	15458	27284	2.87	1.0E-116	M19824.1	NT	Homo sapiens pericentrin (PCNT) mRNA
2346	14917	27491	1.87	1.0E-116	5453941	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2380	14948		0.87	1.0E-116	U78308.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2497	15061	27635	2.84	1.0E-116	AB018333.1	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA
2762	15404	27883	2.18	1.0E-116	BE889256.1	EST_HUMAN	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo_olfr17-01 (OR17-01) pseudogene, complete cds
							Homo sapiens mRNA for KIAA0790 protein, partial cds
							601513337F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914600 5'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3209	15821	28286	4.18	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
3209	15821	28287	4.18	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4467	17053	29497	2.11	1.0E-116	5031954	NT	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4981	17555	29967	1.88	1.0E-116	A1907096.1	EST_HUMAN	PM-BT135-070499-016 BT135 Homo sapiens cDNA
5383	17923	30337	0.88	1.0E-116	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
5483	18117	30525	0.82	1.0E-116	A1302062.1	EST_HUMAN	q18d04.x1 NCJ_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898695 3' similar to contains element MER25 repetitive element;
6132	18748	31502	2.1	1.0E-116	W42822.1	EST_HUMAN	zc24d07.r1 Soares, senescent, fibroblasts, NBHSF Homo sapiens cDNA clone IMAGE:323245 5' similar to SW:MDHM_MOUSE P08249 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR;
6359	18963	31740	1.81	1.0E-116	AB046856.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
6359	18963	31741	1.81	1.0E-116	AB046856.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
6423	19026	31809	1.14	1.0E-116	BE408097.1	EST_HUMAN	601302281F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636764 5'
6530	19130	31924	1.96	1.0E-116	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248087 5'
6637	19233	32382	1.82	1.0E-116	BE158133.1	EST_HUMAN	MR2-H10379-210200-102-504 HT0379 Homo sapiens cDNA
7023	19557	32382	2.08	1.0E-116	C02944.1	EST_HUMAN	C02944 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NH00567
7254	19782	32638	7.16	1.0E-116	AV716314	EST_HUMAN	AV716314 DCB Homo sapiens cDNA clone DCB8CG06 5'
8310	20851	33775	1.4	1.0E-116	AA354256.1	EST_HUMAN	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to keratin 2
8310	20851	33776	1.4	1.0E-116	AA354256.1	EST_HUMAN	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to keratin 2
8416	20858	33873	1.49	1.0E-116	A1804151.1	EST_HUMAN	CM-BT043-090269-075 BT043 Homo sapiens cDNA
8868	21407	34331	1.15	1.0E-116	BE555507.1	EST_HUMAN	601338268F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680680 5'
9028	21565	34494	2.75	1.0E-116	A1216352.1	EST_HUMAN	q109c05.x1 Soares, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:1844168 3' similar to gb:X53741_ma1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
9592	22092	35058	1.36	1.0E-116	11418646	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA
10171	22668	35661	0.87	1.0E-116	AJ277441.1	NT	Homo sapiens partial mRNA for xylosyltransferase I (XT-I) gene
10171	22668	35662	0.87	1.0E-116	AJ277441.1	NT	Homo sapiens partial mRNA for xylosyltransferase I (XT-I) gene
10250	22745	35733	0.82	1.0E-116	BE158913.1	EST_HUMAN	QV4-HT0401-281298-063-c09 HT0401 Homo sapiens cDNA
10587	23103	36117	3.89	1.0E-116	BF335849.1	EST_HUMAN	CM2-CT0482-300800-349-606 CT0482 Homo sapiens cDNA
11015	23529	36565	3.63	1.0E-116	A1367140.1	EST_HUMAN	q441e04.x1 Soares, NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1935102 3' similar to WP:B0495.7 CE01765;
12456	24948	37561	3.62	1.0E-116	AL134889.1	EST_HUMAN	DKFZp762L1110_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762L1110 5'
584	13214	25691	1.88	1.0E-117	4826636	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1116	15433	26231	1.46	1.0E-117	AF124393.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1) gene, exons 13a through 15
1288	13865	26382	0.81	1.0E-117	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1789	14379	26923	1.28	1.0E-117	AF123320.1	NT	Homo sapiens lymphocyte activation-associated protein mRNA, complete cds
1871	14457	27014	5.27	1.0E-117	M19816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
2252	14826	27402	1.15	1.0E-117	AW957699.1	EST_HUMAN	EST1369769 MAGE resequences, MAGE Homo sapiens cDNA
3306	15917	28394	1.53	1.0E-117	AA978114.1	EST_HUMAN	qp32c11.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3'
4062	16659	29122	8.83	1.0E-117	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
4438	17022	29482	2.27	1.0E-117	86589564	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4677	17259	29710	2.1	1.0E-117	AL042120.1	EST_HUMAN	DKFZp434C1120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1120 5'
4933	17508	29855	10.14	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4933	17508	29856	10.14	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
5074	17647	30088	3.26	1.0E-117	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
5551	18183	30598	3.8	1.0E-117	BE730508.1	EST_HUMAN	601562857F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832214 5'
7473	19995	32859	5.22	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
7473	19995	32860	5.22	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
7550	20069	32944	4.48	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
7550	20069	32945	4.48	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
7919	20461	33367	3.77	1.0E-117	AI950145.1	EST_HUMAN	wp86b07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468629 3' similar to TR:O75065
8253	20784	33711	1.07	1.0E-117	10834989	NT	O75065 KIAA0477 PROTEIN ;
8253	20784	33712	1.07	1.0E-117	10834989	NT	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
8350	20891	33811	1.32	1.0E-117	AI904151.1	EST_HUMAN	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
8350	20891	33812	1.32	1.0E-117	AI904151.1	EST_HUMAN	CM-BT043-090289-075 BT043 Homo sapiens cDNA
9223	21739	34682	1.73	1.0E-117	D16524.1	NT	CM-BT043-090289-075 BT043 Homo sapiens cDNA
9701	22700	35172	1.71	1.0E-117	BE733922.1	EST_HUMAN	Human gene for very low density lipoprotein receptor, exon 11
9857	24796	35335	0.83	1.0E-117	AF099033.1	NT	601569317F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843748 5'
10462	22856	35667	1.98	1.0E-117	11420222	NT	Homo sapiens gamma-aminobutyric acid type B receptor 2 (GABABR2) mRNA, complete cds
10737	23262	36277	1.89	1.0E-117	D83776.1	NT	Homo sapiens Drosophila Kelch like protein (DKELCHL), mRNA
10901	23421	36439	1.81	1.0E-117	W80605.1	EST_HUMAN	Human mRNA for KIAA0191 gene, partial cds
10917	23438	36458	1.65	1.0E-117	11424835	NT	z883b11.1 Soares_fetal_heart_NDHH19W Homo sapiens cDNA clone IMAGE:347229 5' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
10917	23438	36457	1.65	1.0E-117	11424835	NT	Homo sapiens protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA
11153	23660	36704	3.46	1.0E-117	AB011541.1	NT	Homo sapiens protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA
11153	23660	36705	3.46	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
11272	23725		31.65	1.0E-117	BE269856.1	EST_HUMAN	Homo sapiens mRNA for MEGF8, partial cds
							601186203F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544296 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11464	23914	36981	2.04	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
11464	23914	36982	2.04	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
11936	25028		1.7	1.0E-117	AF224689.1	NT	Homo sapiens mannose-6-phosphate isomerase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12682	15433	26231	1.81	1.0E-117	AF124983.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15
74	12752	25231	8.91	1.0E-118	AF161500.1	NT	Homo sapiens HSPC151 mRNA, complete cds
99	12775	25257	0.88	1.0E-118	AL045854.1	EST_HUMAN	DKFZp3401056_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp3401056 5'
543	13174	25654	5.79	1.0E-118	7657018	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
847	15429	26073	1.3	1.0E-118	5174880	NT	Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA
2275	14849	27425	1.93	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3604019 5'
2275	14849	27426	1.93	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3604019 5'
2275	14849	27427	1.93	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3604019 5'
2367	14938		0.98	1.0E-118	AW951729.1	EST_HUMAN	EST363799 IMAGE resequences, MAGB Homo sapiens cDNA
2768	15322	27688	2.82	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
2768	15322	27689	2.82	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3138	15752		4.01	1.0E-118	Y13932.1	NT	Homo sapiens PRKY exon 7
3229	15841	28321	6.49	1.0E-118	A1347694.1	EST_HUMAN	qp01f05.x1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
3229	15841	28322	6.49	1.0E-118	A1347694.1	EST_HUMAN	qp01f05.x1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
4162	16753	28204	9.69	1.0E-118	D23660.1	NT	Human mRNA for ribosomal protein, complete cds
4817	17395	29848	1.45	1.0E-118	11425793	NT	Homo sapiens KIAA0478 gene product (KIAA0478), mRNA
5616	18245	30695	1.89	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5616	18245	30696	1.89	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5813	18437	31158	1.01	1.0E-118	11422054	NT	Homo sapiens reelin (RELN), mRNA
5813	18437	31159	1.01	1.0E-118	11422054	NT	Homo sapiens reelin (RELN), mRNA
5890	18513	31239	0.77	1.0E-118	U08892.1	NT	Human GS2 gene, exon 6
5890	18513	31240	0.77	1.0E-118	U08892.1	NT	Human GS2 gene, exon 6
5944	18564	31284	0.92	1.0E-118	M55109.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 4
6023	18642	31383	1.2	1.0E-118	11425900	NT	Homo sapiens T-box 4 (TBX4), mRNA
6023	18642	31384	1.2	1.0E-118	11425900	NT	Homo sapiens T-box 4 (TBX4), mRNA
6098	18714	31484	1.4	1.0E-118	11420764	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6793	19384	32189	1.58	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
6793	19384	32200	1.58	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
7154	19686	32528	1.03	1.0E-118	AL043761.1	EST_HUMAN	DKFZp3400127_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp3400127 5'
7154	19686	32529	1.03	1.0E-118	AL043761.1	EST_HUMAN	DKFZp3400127_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp3400127 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7697	20111	32988	4.89	1.0E-118	11431050	NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA
7699	20122	32988	0.7	1.0E-118	L46590.1	NT	Homo sapiens very long chain acyl-CoA dehydrogenase gene, exons 1-20, complete cds
7913	20455	33361	2.75	1.0E-118	BE781223.1	EST_HUMAN	601469159F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872247 5'
8323	20864	33788	6.06	1.0E-118	BE092855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
8323	20864	33789	6.06	1.0E-118	BE092855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
8328	20869	33792	1.44	1.0E-118	AA443024.1	EST_HUMAN	z98d07.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8328	20869	33793	1.44	1.0E-118	AA443024.1	EST_HUMAN	z98d07.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8607	21148	34061	0.89	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8607	21148	34062	0.89	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8955	21194	34112	1.61	1.0E-118	4657732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8955	21194	34113	1.61	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8965	21503	34425	5.31	1.0E-118	BE263134.1	EST_HUMAN	601144863F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160502 5'
8996	21534	34464	0.52	1.0E-118	AL048474.2	EST_HUMAN	DKFZp586K1824_r1 588 (synonym: hute1) Homo sapiens cDNA clone DKFZp586K1824
9512	22012	34971	1.62	1.0E-118	7657016	EST_HUMAN	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
9597	22394	35370	0.62	1.0E-118	AL138321.1	EST_HUMAN	DKFZp5470017_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp5470017 5'
10237	22732	35723	0.98	1.0E-118	BE736213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603 5'
10237	22732	35724	0.98	1.0E-118	BE736213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603 5'
10277	22772	35761	1.6	1.0E-118	BF195407.1	EST_HUMAN	7n17e09.x1 NCI_CGAP_Brm23 Homo sapiens cDNA clone IMAGE:3964785 3' similar to SW_ZP3A_HUMAN
10425	22919	35921	0.52	1.0E-118	AW286351.1	EST_HUMAN	P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR ; UI-H-SW0-aic-a-07-0JLs1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729772 3'
11157	23664	36710	4.87	1.0E-118	AA315007.1	EST_HUMAN	EST186814 HCC cell line (matelasia to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light chain 1, cytoplasmic
11433	23883	36949	1.94	1.0E-118	BE908676.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11433	23883	36950	1.94	1.0E-118	BE908676.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11436	23886	36953	1.69	1.0E-118	BF093687.1	EST_HUMAN	QV0-UJ0091-120800-385-b12 UM0091 Homo sapiens cDNA
11436	23886	36954	1.69	1.0E-118	BF093687.1	EST_HUMAN	QV0-UJ0091-120800-385-b12 UM0091 Homo sapiens cDNA
11608	24049	37115	1.58	1.0E-118	BE218235.1	EST_HUMAN	h36a06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175474 3' similar to TR:Q9Z2H4
788	13408	25911	2.89	1.0E-119	AF170492.1	NT	Q9Z2H4 G PROTEIN-COUPLED RECEPTOR LGR4 ;
1075	15432	26189	1.82	1.0E-119	7705607	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
1977	14560	27118	2.24	1.0E-119	AB023147.1	NT	Homo sapiens CGI-105 protein (LOC51011), mRNA
3136	15750	28218	1.04	1.0E-119	8922205	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
3277	15888		0.79	1.0E-119	AA916780.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA on10b05.e1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1556241 3' similar to WP:E04F6.2 CE01214 ;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4026	16624	20096	1.09	1.0E-119	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5540	18172	30587	3.45	1.0E-119	AU133399.1	EST_HUMAN	AU133399 NT2RP4 Homo sapiens cDNA clone NT2RP4001991 5'
5553	18185	30600	15.55	1.0E-119	M89914.1	NT	Human neurofibromin (NF1) gene, complete cds
5557	18189	30605	3.01	1.0E-119	BE936121.1	EST_HUMAN	RC1-NN0073-250800-018-g06 NN0073 Homo sapiens cDNA
5625	18264	30723	1.52	1.0E-119	AV693731.1	EST_HUMAN	AV693731 GKC Homo sapiens cDNA clone GKCDH803 5'
6276	18884	31652	5.78	1.0E-119	AI150703.1	EST_HUMAN	q177c09.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10;
6429	19032	31815	0.68	1.0E-119	AF315683.1	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6429	19032	31816	0.68	1.0E-119	AF315683.1	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6473	19074	31857	1.08	1.0E-119	AI476732.1	EST_HUMAN	bm2310.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157451 3'
6588	19185	31987	2.82	1.0E-119	X06292.1	NT	Human c-fos/fps proto-oncogene
6598	19195	32000	4.9	1.0E-119	AW974193.1	EST_HUMAN	EST386298 IMAGE resequences, MAGM Homo sapiens cDNA
7440	19864	32830	1.27	1.0E-119	BE796814.1	EST_HUMAN	601592005F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946081 5'
8566	21135	34050	0.84	1.0E-119	BE615150.1	EST_HUMAN	601280564F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622526 5'
9870	22169	35145	0.55	1.0E-119	11545921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
9821	22319	35303	1.04	1.0E-119	11036843	NT	Homo sapiens KIAA0477 gene product (KIAA0477), mRNA
10145	22640	35630	2.78	1.0E-119	AA465124.1	EST_HUMAN	aa32705.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814977 5'
10398	22892	35888	0.92	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
10438	22932	35940	0.66	1.0E-119	11425837	NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
10502	22998	36005	3.99	1.0E-119	AB032281.1	NT	Homo sapiens Sod mRNA for stearyl-CoA desaturase, complete cds
11082	23594		10.54	1.0E-119	BF569571.1	EST_HUMAN	602186072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310633 5'
11997	25012		3.05	1.0E-119	AW847518.1	EST_HUMAN	RC3-CT0212-240999-011-f03 CT0212 Homo sapiens cDNA
258	12917	25404	0.65	1.0E-120	AB016301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
323	12977	25495	0.77	1.0E-120	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1079	13684	26195	2.82	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1079	13684	26196	2.82	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1471	14063	26598	3.24	1.0E-120	N44873.1	EST_HUMAN	Y40g12.1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:273766 5'
1845	14237	26772	2.49	1.0E-120	AF187708.1	NT	Homo sapiens cytosine-rich repeat-containing protein S82 precursor, mRNA, complete cds
1842	14430	26983	1.64	1.0E-120	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
3348	12977	25495	1.04	1.0E-120	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
4449	17035	29478	1.68	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4449	17035	29479	1.68	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4769	17350	29801	2.82	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4768	17350	29802	2.82	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
5150	17720	30151	1.11	1.0E-120	AF094821.1	NT	Homo sapiens cytochrome P-450 mRNA, complete cds
5442	17997		0.95	1.0E-120	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
5911	18533	31258	13.5	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
5911	18533	31259	13.5	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
7573	20089	32965	1.78	1.0E-120	D34619.1	NT	Human TBXAS1 gene for thromboxane synthase, exon 7
7835	20377	33282	1.81	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
7835	20377	33283	1.81	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8274	20815	33737	2.9	1.0E-120	BF337599.1	EST_HUMAN	602035352F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4183333 5'
8343	20884	33805	0.8	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8343	20884	33806	0.8	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8347	20888	33808	2.83	1.0E-120	AB007864.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8347	20888	33809	2.83	1.0E-120	AB007864.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8350	20930	33850	1.13	1.0E-120	AB007934.1	NT	Homo sapiens mRNA for KIAA0485 protein, partial cds
9421	21930	34877	4.6	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
9421	21930	34878	4.6	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
9660	22159	35131	3.07	1.0E-120	BF306541.1	EST_HUMAN	601888956F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122876 5'
9675	22174	35150	8.09	1.0E-120	AU133205.1	EST_HUMAN	AU133205 NT2RP4 Homo sapiens cDNA clone NT2RP4001541 5'
9692	22181	35165	0.69	1.0E-120	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
9988	22483	35469	2.88	1.0E-120	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
11008	23520	36555	14.73	1.0E-120	BE286387.1	EST_HUMAN	601178727F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532015 5'
11222	23753	36810	2.12	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
11222	23753	36811	2.12	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
11504	23953	37021	1.55	1.0E-120	U94774.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, 5'UTR and exon 1
12153	24395	30975	1.31	1.0E-120	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
77	12754	25235	0.92	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
401	13045	25536	1.68	1.0E-121	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
753	15423	25987	1.19	1.0E-121	5032182	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
2008	14590	27150	0.98	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2008	14590	27151	0.98	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2150	14727	27300	1.74	1.0E-121	L76631.1	NT	Homo sapiens melastatin-like receptor 1 beta (mGluR1beta) mRNA, complete cds
2998	15612	28092	1.03	1.0E-121	AF111188.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3117	15731	28201	3.63	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3117	15731	28202	3.63	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3589	16193	28977	0.94	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3589	16193	28978	0.94	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3741	16342	28810	8.78	1.0E-121	AF155156.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
4424	17009	29452	1.42	1.0E-121	AI283294.1	EST_HUMAN	qx57b01.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3'
5112	17684	30120	3.54	1.0E-121	X91637.1	NT	H.sapiens ECE-1 gene (exon 17)
5472	18106	30425	1.02	1.0E-121	BE222250.1	EST_HUMAN	hu09f08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166119 3'
5750	18376	31086	0.69	1.0E-121	BE271424.1	EST_HUMAN	601140485F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049820 5'
6968	19545		1.06	1.0E-121	AJ271736.1	NT	Homo sapiens Xq pseudocentromeric region, segment 2/2
7042	19662	30451	0.75	1.0E-121	AW898086.1	EST_HUMAN	RC3-NN0066-270400-011-f02 NN0066 Homo sapiens cDNA
7042	18062	30452	0.75	1.0E-121	AW898086.1	EST_HUMAN	RC3-NN0066-270400-011-f02 NN0066 Homo sapiens cDNA
7878	20420	33328	1.86	1.0E-121	11436217	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
7882	20424	33332	2.19	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
7882	20424	33333	2.19	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
9772	22270	35254	0.9	1.0E-121	AW593858.1	EST_HUMAN	ia05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:075457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.1
9772	22270	35255	0.9	1.0E-121	AW593858.1	EST_HUMAN	ia05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:075457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.1
10655	23187	36203	3.45	1.0E-121	11427788	NT	Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA
10662	23194	36209	4.2	1.0E-121	AF084200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele, complete cds
10848	23369	36388	3.51	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
10875	23396	36412	2.11	1.0E-121	N59924.1	EST_HUMAN	yv74c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248448 3'
289	12845	25430	1.68	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
358	13007	25490	3.01	1.0E-122	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
380	13027	25515	1.61	1.0E-122	11528178	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
915	13528	26047	5.28	1.0E-122	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
1282	13859	26376	4.63	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1731	14322	26864	1.06	1.0E-122	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1750	14340	26887	1.8	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1750	14340	26888	1.8	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1650	14438	26995	6.15	1.0E-122	BE906024.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899358 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2533	15097	27669	5.48	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2533	15097	27670	5.48	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2864	15483	27657	1.11	1.0E-122	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
4972	17546	29888	1.23	1.0E-122	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nepril, Alzheimer disease) (APP), mRNA
5127	17699		1.28	1.0E-122	AW504845.1	EST_HUMAN	U1-HF-BNO-ali-a-03-Q-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078948 5'
5752	18378	31089	1.38	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3354232 5'
6853	18378	31089	6.96	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3354232 5'
7266	19794	32650	0.68	1.0E-122	AA88671.1	EST_HUMAN	ak49h06.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1409339 3'
8731	21270	34189	0.55	1.0E-122	AJ276801.1	NT	Homo sapiens mRNA for doublesex and mab-3 related transcription factor 1 (DMRT1)
8958	21488	34418	1.37	1.0E-122	11424216	NT	Homo sapiens lethal giant larvae (Drosophila) homolog 2 (LLGL2), mRNA
9247	21773	34723	0.9	1.0E-122	AJ359618.1	EST_HUMAN	qy32h07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013737 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.1 ;
9247	21773	34724	0.9	1.0E-122	AJ359618.1	EST_HUMAN	qy32h07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013737 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.1 ;
10040	22535	35531	0.71	1.0E-122	AL117234.1	NT	Novel human gene mapping to chromosome X, isoform of dbi (proto-oncogene)
10868	23387	36402	1.55	1.0E-122	AW955634.1	EST_HUMAN	EST367904 MAGe resequences, MAGD Homo sapiens cDNA
11738	24141		3.99	1.0E-122	11418187	NT	Homo sapiens phosphoenolpyruvate carboxylase (PECK1), mRNA
202	12863	25347	19.89	1.0E-123	UJ31519.1	NT	Human phosphoenolpyruvate carboxylase (PECK1) gene, promoter region and partial cds
800	13417	25921	2.06	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
800	13417	25922	2.06	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
1051	13658	26169	5.07	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1060	13665	26176	5.53	1.0E-123	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1281	13876	26397	4.2	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1281	13876	26398	4.2	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
2147	14724	27298	3.41	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2147	14724	27297	3.41	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2147	14724	27288	3.41	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2354	14925		5.59	1.0E-123	7705962	NT	Homo sapiens RAB9-like protein (LOC51209), mRNA
3288	15699	28378	0.67	1.0E-123	6912817	NT	Homo sapiens glutamyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA
5638	18287	30739	1.6	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (RALBP) gene, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5638	18267	30740	1.6	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5769	18395	31109	1.33	1.0E-123	BE789746.1	EST_HUMAN	601591108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945433 5'
6595	19192	31997	2.14	1.0E-123	AU118435.1	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
7076	19648	32486	0.71	1.0E-123	HS3198.1	EST_HUMAN	y84603.1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:202444 5' similar to SP-YAK1_YEAST P14680 PROTEIN KINASE YAK1;
7084	19655	32494	1.22	1.0E-123	U42224.1	NT	Human growth hormone releasing hormone gene, exon 7
7245	19774	32631	0.68	1.0E-123	U55258.1	NT	Human hBRAVOIN/CAM precursor (hBRAVOIN/CAM) gene, complete cds
7433	19957	32822	0.73	1.0E-123	11525833	NT	Homo sapiens heparan sulfate (glucosaminide) 3-O-sulfotransferase 2 (HS3ST2), mRNA
7638	20150	33034	1.31	1.0E-123	11436439	NT	Homo sapiens 2'-5' oligoadenylate synthetase 2 (OAS2), mRNA
7647	20159	33046	1.79	1.0E-123	BE263001.1	EST_HUMAN	601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509182 5'
7764	20272	33170	0.8	1.0E-123	N35841.1	EST_HUMAN	y88411.1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49611 S49611 protein kinase PkpA - Phycomyces blakesleeanus;
7764	20272	33171	0.8	1.0E-123	N35841.1	EST_HUMAN	y88411.1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49611 S49611 protein kinase PkpA - Phycomyces blakesleeanus;
8472	21012		2.25	1.0E-123	AW371924.1	EST_HUMAN	RC4-BT0311-251199-012-407 BT0311 Homo sapiens cDNA
9291	21891	34838	2.04	1.0E-123	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9424	21933	34882	39.79	1.0E-123	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabelfaz) mRNA, complete cds
11567	24014	37083	5.42	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
11567	24014	37084	5.42	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
280	12946	25431	0.83	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
290	12946	25432	0.83	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
296	12952		1.2	1.0E-124	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
511	13144	25630	2.28	1.0E-124	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
720	13340	25829	4	1.0E-124	AA397551.1	EST_HUMAN	z81b04.1 Stratiene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
720	13340	25830	4	1.0E-124	AA397551.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
789	13407	25912	4.86	1.0E-124	AF155654.1	NT	z81b04.1 Stratiene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
841	13457	25968	1.18	1.0E-124	4507500	NT	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
937	13550	26008	5.09	1.0E-124	7705446	NT	Human putative ribosomal protein S1 mRNA
1358	13952	26479	0.62	1.0E-124	11419092	NT	Homo sapiens hypothetical protein (HSPC0068), mRNA
1391	13985	26511	6.15	1.0E-124	AF274892.1	NT	Homo sapiens ring finger protein (RNF), mRNA
1391	13985	26512	6.15	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1851	14439	26986	3.15	1.0E-124	AJ131712.1	NT	Homo sapiens mRNA for nucleolar RNA-helicase (noh61 gene)
2107	14885	27253	1.73	1.0E-124	BE879524.1	EST_HUMAN	601491715F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893954 5'
3537	16142	28824	0.72	1.0E-124	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3537	16142	28625	0.72	1.0E-124	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3967	16565	28034	0.66	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4150	16742	29196	0.8	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4855	17433	26884	2.18	1.0E-124	AB024068.1	NT	Homo sapiens gene for B120, exon 11
5068	17641		1.29	1.0E-124	M18178.1	NT	Human fibronectin gene extra type III repeat (EDII), exon x+1
5256	17819	30244	0.87	1.0E-124	AW963390.1	EST_HUMAN	EST375463 MAGE resequences, MAGH Homo sapiens cDNA
5501	18135	30545	10.59	1.0E-124	8922337	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5852	18476	31199	1.05	1.0E-124	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
6048	18667	31406	6.57	1.0E-124	BF696135.1	EST_HUMAN	602124844F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4281635 5'
6317	18824	31701	0.88	1.0E-124	AV711263.1	EST_HUMAN	AV711263 Cu Homo sapiens cDNA clone CUAADF07 5'
6563	19161	31959	0.9	1.0E-124	11420654	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
7083	18654	32493	3.45	1.0E-124	Y11717.1	NT	M.musculus mRNA for hoxa3 gene
7191	19723	32571	1.23	1.0E-124	BE271295.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2966585 5'
7191	19723	32572	1.23	1.0E-124	BE271295.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2966585 5'
7555	20074	32850	1.15	1.0E-124	AA630331.1	EST_HUMAN	ac08h05.s1 Strelagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:855897 3'
8201	20742	33655	18.99	1.0E-124	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
8399	20939	33861	1.45	1.0E-124	AW612106.1	EST_HUMAN	hg94409.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:095162
8399	20939	33862	1.45	1.0E-124	AW612106.1	EST_HUMAN	O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE.1
8399	20939	33862	1.45	1.0E-124	AW612106.1	EST_HUMAN	O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE.1
9089	21925	34590	1.42	1.0E-124	AI798864.1	EST_HUMAN	wc43g03.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2321428 3'
9089	21925	34591	1.42	1.0E-124	AI798864.1	EST_HUMAN	wc43g03.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2321428 3'
9411	21920	34868	2.52	1.0E-124	AV645633.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
9411	21920	34869	2.52	1.0E-124	AV645633.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
9498	21998	34954	1.14	1.0E-124	AF022655.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
9498	21998	34955	1.14	1.0E-124	AF022655.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
9526	22026	34984	8.22	1.0E-124	AI767133.1	EST_HUMAN	wf93f02.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
9526	22026	34985	8.22	1.0E-124	AI767133.1	EST_HUMAN	wf93f02.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
9785	22283	35269	1.66	1.0E-124	AW503755.1	EST_HUMAN	UI-HF-BN0-akz-b-04-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078846 5'
11213	23716	36770	3.81	1.0E-124	AW665663.1	EST_HUMAN	h05c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2980906 3'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11347	23045	36056	2.26	1.0E-124	A1446455.1	EST_HUMAN	U19603.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN ;
11347	23045	36057	2.26	1.0E-124	A1446455.1	EST_HUMAN	U19603.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN ;
11818	13340	25828	6.1	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
11818	13340	25830	6.1	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
12284	24474	30634	1.28	1.0E-124	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
12542	24960	30632	2.42	1.0E-124	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12542	24960	30633	2.42	1.0E-124	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
341	12893		8.05	1.0E-125	AB032898.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
451	12680	25136	3.95	1.0E-125	BE743922.1	EST_HUMAN	601577981.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926885 5'
672	13296	25777	23.21	1.0E-125	A1110856.1	EST_HUMAN	HA0088 Human fetal liver cDNA library Homo sapiens cDNA
672	13296	25778	23.21	1.0E-125	A1110856.1	EST_HUMAN	HA0088 Human fetal liver cDNA library Homo sapiens cDNA
757	13376	25871	1.7	1.0E-125	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
893	13507	26025	2.68	1.0E-125	AA042813.1	EST_HUMAN	z653c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
1036	13846	26158	2.18	1.0E-125	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1193	13794	26303	1.9	1.0E-125	7662279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
1712	15448	26842	1.65	1.0E-125	7661867	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
1836	14424	26975	0.96	1.0E-125	U78027.1	NT	Homo sapiens Brulon's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1847	14435	26981	2.28	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
1847	14435	26992	2.28	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
2397	14965	27536	1.03	1.0E-125	AA011278.1	EST_HUMAN	z01g09.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429588 5'
2632	15193	27764	1.06	1.0E-125	4504696	NT	Homo sapiens inhibitor, alpha (INH) mRNA
2632	15193	27765	1.06	1.0E-125	4504696	NT	Homo sapiens inhibitor, alpha (INH) mRNA
3925	16523	28991	1.59	1.0E-125	AA042813.1	EST_HUMAN	z653c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
4848	17230	29686	2.78	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4848	17230	29687	2.78	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4724	17305	29749	1.54	1.0E-125	BE315412.1	EST_HUMAN	601141152.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140796 5'
5932	18554	31281	0.69	1.0E-125	BF683645.1	EST_HUMAN	602139874.F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300770 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6033	18652	31394	1.55	1.0E-125	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
6052	18670	31409	1.18	1.0E-125	BE175169.1	EST_HUMAN	QV2-HT0577-010500-165-b06 HT0577 Homo sapiens cDNA
6089	18705	31453	3.2	1.0E-125	BE892680.1	EST_HUMAN	601433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5'
6128	18744	31497	0.75	1.0E-125	AI679904.1	EST_HUMAN	tu87c07.x1 NCI_CGAP_Gae4 Homo sapiens cDNA clone IMAGE:2256108 3' similar to WP:C45G9.2
6695	19291	32094	1.55	1.0E-125	BE562526.1	EST_HUMAN	CE01854 ;
6695	19291	32095	1.55	1.0E-125	BE562526.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
7121	19461	32277	65.83	1.0E-125	X03427.1	NT	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
7121	19461	32278	65.83	1.0E-125	X03427.1	NT	Homo sapiens IGF-II gene, exon 5
7538	20058	32932	0.75	1.0E-125	BE278823.1	EST_HUMAN	Homo sapiens IGF-II gene, exon 5
8483	21022	33938	1	1.0E-125	U90288.1	NT	601159076F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505603 5'
8483	21022	33939	1	1.0E-125	U90288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
9046	21583	34512	9.65	1.0E-125	BE181640.1	EST_HUMAN	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
9046	21583	34513	9.65	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
9303	21903	34852	1.05	1.0E-125	AI565998.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
10350	22844	35839	0.53	1.0E-125	BE784576.1	EST_HUMAN	tn52b03.x1 NCI_CGAP_Kld11 Homo sapiens cDNA clone IMAGE:2171981 3' similar to TR:Q14089 Q14089
10388	22882	35876	0.73	1.0E-125	AB002298.1	NT	HYPOTHETICAL PROTEIN ;
10562	23098	36112	3.76	1.0E-125	AF043458.1	NT	601590345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944531 5'
11016	23530	36566	4.05	1.0E-125	AB014587.1	NT	Human mRNA for KIAA0300 gene, partial cds
11169	23678	36722	1.56	1.0E-125	7669505	NT	Homo sapiens LREL gene, exon 5
11174	23681	36727	6.41	1.0E-125	AF026026.1	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
11278	23732	36787	2.99	1.0E-125	AW812899.1	EST_HUMAN	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
11375	23827	36888	6.08	1.0E-125	BE074287.1	EST_HUMAN	RC3-ST0186-250200-018-c11 ST0186 Homo sapiens cDNA
11375	23827	36889	6.08	1.0E-125	BE074287.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
806	13423	25929	3.44	1.0E-126	4758007	NT	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
809	13428	25932	1.92	1.0E-126	M61936.1	NT	Homo sapiens CDC-like kinase (CLK) mRNA
952	13564	26076	285	1.0E-126	X68735.1	NT	Human laminin B1 chain gene, exon 20
3108	15723	28194	9.08	1.0E-126	AA160709.1	EST_HUMAN	H.sapiens gene for alpha1-antitrypsin, exon 3
3108	15723	28195	9.08	1.0E-126	AA160709.1	EST_HUMAN	z072c03.11 Stralagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3891	16292	28781	0.88	1.0E-126	X53941.1	NT	z072c03.11 Stralagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3716	16317	28785	2.02	1.0E-126	7657038	NT	H.sapiens DNA for liver cytochrome b5 pseudogene
							Homo sapiens death receptor 6 (DR6), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4902	17477	29933	1.03	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4902	17477	29934	1.03	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4961	17538	29978	1.31	1.0E-126	N34078.1	EST_HUMAN	yk78c06.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:267850 5'
8380	18984	31784	3.46	1.0E-126	AA460075.1	EST_HUMAN	2x66e03.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796444 5' similar to TR:G1145880 G1145880 TITIN;
8432	19035	31820	4.2	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
8432	19035	31821	4.2	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
7511	20032	32897	0.85	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7511	20032	32898	0.85	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7819	20361	33267	0.92	1.0E-126	AB037715.1	NT	Homo sapiens mRNA for KIAA1234 protein, partial cds
7819	20361	33268	0.92	1.0E-126	AB037715.1	NT	Homo sapiens mRNA for KIAA1234 protein, partial cds
7929	20471	33360	5.76	1.0E-126	X18609.1	NT	Human mRNA for ankyrin (variant 2.1)
8124	20665	33575	0.85	1.0E-126	AA483368.1	EST_HUMAN	ne74b12.s1 NCI CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909983 similar to SW:TSG6_HUMAN
9711	22209	35181	0.52	1.0E-126	4505424	NT	P88066 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR;
10872	23204	36217	1.73	1.0E-126	M83198.1	NT	Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), splice variant 1, mRNA
10738	23263	36278	3.69	1.0E-126	BF683175.1	EST_HUMAN	Human macrophage mannose receptor (MRC1) gene, exon 5
11392	23844	36908	2.32	1.0E-126	BE261680.1	EST_HUMAN	602139138F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4298240 5'
11636	16292	28761	2.52	1.0E-126	X53841.1	NT	601149404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502129 5'
12304	18036	30496	6.76	1.0E-126	BE743922.1	EST_HUMAN	H. sapiens DNA for liver cytochrome b5 pseudogene
183	12845	25330	4.5	1.0E-127	AB024597.1	NT	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
183	12845	25331	4.5	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
184	12845	25330	2.76	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
184	12845	25331	2.76	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
295	12951	25439	1.3	1.0E-127	DB7875.1	NT	Homo sapiens DNA for casein kinase I epsilon, complete cds
295	12951	25440	1.3	1.0E-127	DB7875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
914	13527	26048	2.22	1.0E-127	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
949	13561	26075	1.37	1.0E-127	U72621.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1729	14320	26862	1.33	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2111	14689	27256	2.81	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2111	14689	27257	2.81	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2241	14816	27389	5.62	1.0E-127	4506620	NT	Homo sapiens ribosomal protein L26 (RPL26) mRNA
2381	14950	27523	3.29	1.0E-127	AF245505.1	NT	Homo sapiens adican mRNA, complete cds
2840	15199	27773	5.29	1.0E-127	X12881.1	NT	Human mRNA for cyokeratin 18
3753	16354	28822	1.02	1.0E-127	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3884	16482	28944	0.75	1.0E-127	AW161287.1	EST_HUMAN	au80e06.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ; contains element MER22 repetitive element ;
4194	16783	29232	0.66	1.0E-127	AF195188.1	NT	Homo sapiens delayed rectifier potassium channel subunit Isk mRNA, complete cds
4303	16889	29332	0.61	1.0E-127	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4340	16927	29387	21.24	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4340	16927	29388	21.24	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4595	17178	28625	0.68	1.0E-127	AF252297.1	NT	Homo sapiens cytochrome P450 retinoid metabolizing protein P450RAI-2 mRNA, complete cds
4708	17260	29734	5.02	1.0E-127	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4738	17319	29811	2.84	1.0E-127	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4780	17361	29811	1.04	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
5884	18508	31232	2.37	1.0E-127	W03547.1	EST_HUMAN	z001a10.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:291258 5' similar to SW:PIP6_RAT P10688 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 ;
5912	18534	31260	0.86	1.0E-127	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
5970	18591	31326	4.61	1.0E-127	X85764.1	NT	H. sapiens NOS2 gene, exon 6
6310	18917	31691	2.21	1.0E-127	X84060.1	NT	H. sapiens TCF11 gene, exon 3-6
6463	19064	31849	5.89	1.0E-127	4504778	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
6764	19357	32188	0.93	1.0E-127	11421595	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA
7122	19462	32279	0.85	1.0E-127	4826977	NT	Homo sapiens reelin (RELN) mRNA
7760	20268	33165	1.31	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7760	20268	33168	1.31	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7763	20271	33169	0.67	1.0E-127	BF671355.1	EST_HUMAN	602161232F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292575 5'
8820	21359	34285	0.7	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8820	21359	34288	0.7	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9558	22058	35018	4.96	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9558	22058	35020	4.96	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9767	22265	35270	0.66	1.0E-127	A1298932.1	EST_HUMAN	qm94h09.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896449 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10245	22740	35730	2.25	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
11037	23551	36585	6.54	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
11037	23551	36586	6.54	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
11490	23939	37009	1.9	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
11490	23939	37010	1.9	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
12046	12845	25330	1.43	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12046	12845	25331	1.43	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12253	24464	30862	1.7	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12620	24967		2.23	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
485	13118	25605	2.44	1.0E-128	BE385617.1	EST_HUMAN	601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618822 5'
1195	13766	26305	1	1.0E-128	4758081	NT	Homo sapiens chondroilin sulfate proteoglycan 2 (versican) (CSPG2), mRNA
1195	13766	26306	1	1.0E-128	4758081	NT	Homo sapiens chondroilin sulfate proteoglycan 2 (versican) (CSPG2), mRNA
2115	14883	27260	4.14	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, intron/exon repeat regions
2115	14883	27261	4.14	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, intron/exon repeat regions
2250	14824	27400	18.53	1.0E-128	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
3441	16049	28527	1.14	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4771	17352	29804	5.43	1.0E-128	11426673	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
5734	18360	31066	6.97	1.0E-128	X69539.1	NT	H. sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exon 12
6550	19148	31944	2.08	1.0E-128	11420985	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
7010	19508	32328	8.01	1.0E-128	BF224345.1	EST_HUMAN	7q66b10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3'
8206	20747	33659	0.75	1.0E-128	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
8206	20747	33660	0.75	1.0E-128	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
10043	22538	35535	1.62	1.0E-128	AA639198.1	EST_HUMAN	ns04a11.1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1182620 similar to TR:G951338 G951338
10598	23123	36137	5.48	1.0E-128	11425254	NT	CHROMOSOME SEGREGATION GENE HOMOLOG CAS. ;
10597	23131	36145	5.15	1.0E-128	AA926959.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA
11905	24244		4.37	1.0E-128	AW955290.1	EST_HUMAN	om88h08.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1552383 3' similar to gb:X54941 CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);
127	13071	25568	12.06	1.0E-129	S37722.1	NT	EST387360 MAGC resequences, MAGC Homo sapiens cDNA
438	13071	25568	14.64	1.0E-129	S37722.1	NT	insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1756	14346	26891	2.48	1.0E-129	AL068890.1	NT	insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1761	14351	26896	1.62	1.0E-129	AF240786.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1761	14351	26897	1.62	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1886	14471	27029	2.2	1.0E-129	11418522	NT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
3162	15776	28244	1.41	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3162	15776	28245	1.41	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3162	15776	28246	1.41	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4244	16832	29283	1.95	1.0E-129	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4367	16954	29394	2.57	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5
4367	16954	29395	2.57	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5
6241	18950	31620	4.78	1.0E-129	AJ006345.1	NT	Homo sapiens KVLQT1 gene
7181	19713	32561	4.38	1.0E-129	AJ006345.1	NT	Homo sapiens KVLQT1 gene
7241	19770	32826	14.44	1.0E-129	11420850	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63694), mRNA
7535	20055	32928	0.78	1.0E-129	AF041056.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
7535	20055	32929	0.78	1.0E-129	AF041056.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
8260	20901		3.93	1.0E-129	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
9991	22486	35473	1.16	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9991	22486	35474	1.16	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
11102	23612	36652	3.34	1.0E-129	AA625526.1	EST_HUMAN	at7207.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1047589 5'
11177	19770	32626	11.7	1.0E-129	11420850	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63694), mRNA
11892	24235		2.32	1.0E-129	H83155.1	EST_HUMAN	y49c05.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:199112 5' similar to
12297	24494		2.07	1.0E-129	AL120739.1	EST_HUMAN	SP-B48150 B48150 HP-25-HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS-ASIAN ;
80	12757	25239	1.85	1.0E-130	7705530	NT	DKFZp762K171_r1 762 (synonym: hmed2) Homo sapiens cDNA clone DKFZp762K171 5'
1212	13812	26326	1.23	1.0E-130	AB037835.1	NT	Homo sapiens hypothetical protein (HSPC242), mRNA
1706	14298	26836	8.52	1.0E-130	BE275192.1	EST_HUMAN	Homo sapiens mRNA for KIAA1414 protein, partial cds
1706	14298	26837	8.52	1.0E-130	BE275192.1	EST_HUMAN	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
2027	14609		4.6	1.0E-130	X04092.1	NT	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
2127	14705		1.69	1.0E-130	8394394	NT	Human gene for caldesmon (EC 1.1.1.1.6) exon 9 mapping to chromosome 11, band p13
2799	15351		7.47	1.0E-130	AJ010230.1	NT	Homo sapiens candidate taste receptor T2R16 (T2R16), mRNA
2903	15620	27899	1.17	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2903	15620	27899	1.17	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3637	16240	28716	0.98	1.0E-130	AF240898.1	NT	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
							Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3831	15520	27989	5.82	1.0E-130	BE584219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3831	15520	27989	5.82	1.0E-130	BE584219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
4010	16608	28081	1.56	1.0E-130	AW503580.1	EST_HUMAN	UI-HF-BN0-aky-g-06-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
4147	16739	29182	1.18	1.0E-130	M97710.1	NT	Human T-cell receptor (V alpha 22.1, J alpha 22.1, J alpha 22.1, J alpha 22.1) mRNA
4838	17219	29672	9	1.0E-130	AW843993.1	EST_HUMAN	CM4-CN0045-180200-511-02 CN0045 Homo sapiens cDNA
5258	17821	30246	1.11	1.0E-130	AW363299.1	EST_HUMAN	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
5258	17821	30247	1.11	1.0E-130	AW363299.1	EST_HUMAN	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
6910	19569	32398	0.74	1.0E-130	AW843875.1	EST_HUMAN	CM0-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6910	19569	32397	0.74	1.0E-130	AW843875.1	EST_HUMAN	CM0-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6923	19582	32411	0.7	1.0E-130	11425446	NT	Homo sapiens estrogen-responsive B box protein (EBBP), mRNA
7301	19828	32687	2.1	1.0E-130	11416777	NT	Homo sapiens solute carrier family 9 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
8616	21155		0.98	1.0E-130	AF008551.1	NT	Homo sapiens aurora-related kinase 1 (ARK1), mRNA, complete cds
8763	21292	34212	4.06	1.0E-130	AW968242.1	EST_HUMAN	EST368312 MAGE resequences, MAGD Homo sapiens cDNA
9141	21678	34618	1.97	1.0E-130	AB037756.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
9846	22344		0.78	1.0E-130	AW103454.1	EST_HUMAN	xd36606.x1 NCJ_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595874 3'
4	12684	25140	2.27	0.0E+00	AA228126.1	EST_HUMAN	z58c04.r1 Soares, NIHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
4	12684	25141	2.27	0.0E+00	AA228126.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
8	12687	25145	1.56	0.0E+00	4885136	NT	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA
17	12696	25152	2.85	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
17	12698	25153	2.85	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
24	12703	25160	4.29	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
24	12703	25161	4.29	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
29	12708	25165	30.44	0.0E+00	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
37	12716	25175	38.86	0.0E+00	5802897	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
39	12718	25178	23.21	0.0E+00	M56600.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
42	12721	25182	7.78	0.0E+00	M56600.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
44	12723	25184	4.41	0.0E+00	6857825	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
61	12740	25211	8.23	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
61	12740	25212	8.23	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
63	12742	25216	1	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN:516H08 5'
63	12742	25217	1	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN:516H08 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
64	12743	25218	28.22	0.0E+00	L16558.1	NT	Human ribosomal protein L7 (RPL7) mRNA, complete cds
66	12745	25221	11.83	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07.3'
66	12745	25222	11.83	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07.3'
70	12748	25226	0.9	0.0E+00	M60876.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
71	12749	25237	0.85	0.0E+00	M60876.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
78	12756	25237	3.66	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
78	12756	25238	3.66	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
82	12756	25237	1.9	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
82	12756	25238	1.9	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
85	12761	25244	0.85	0.0E+00	4501850	NT	Homo sapiens amiloride binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA
86	12762	25244	38.11	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
95	12771	25253	37.46	0.0E+00	5016088	NT	Homo sapiens actin, beta (ACTB) mRNA
98	12774	25256	28.23	0.0E+00	U99277.1	NT	Human polyhomeotic 1 homolog (HPH1) mRNA, partial cds
105	12781	25263	2.29	0.0E+00	A114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
106	12782	25264	2.19	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
112	12785	25268	0.64	0.0E+00	X91213.1	NT	H. sapiens ncx1 gene (exon 2)
121	12792	25274	1.98	0.0E+00	AB23701.1	EST_HUMAN	ts38b05.x1 NCL CGAP_U4 Homo sapiens cDNA clone IMAGE:2230833.3 similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
122	12792	25274	2.44	0.0E+00	AB23701.1	EST_HUMAN	ts38b05.x1 NCL CGAP_U4 Homo sapiens cDNA clone IMAGE:2230833.3 similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
123	15383	25275	2.64	0.0E+00	N36040.1	EST_HUMAN	Y01h09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270017.5'
123	15383	25276	2.64	0.0E+00	N36040.1	EST_HUMAN	Y01h09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270017.5'
126	12795	25281	1.12	0.0E+00	4505458	NT	Homo sapiens neuropilin 2 (NRP2) mRNA
136	12801	25289	3.85	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
136	12801	25290	3.85	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
144	13069	25552	0.8	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FCIGAMMA1BP) mRNA
146	12808	25297	0.85	0.0E+00	T56945.1	EST_HUMAN	ya83g04.r2 Stralagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310.5'
146	12808	25298	0.85	0.0E+00	T56945.1	EST_HUMAN	ya83g04.r2 Stralagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310.5'
164	12827		35.47	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
168	12831	25317	2.84	0.0E+00	BF038881.1	EST_HUMAN	601460375F NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803.5'
170	12833		82.51	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
173	12836	25320	0.75	0.0E+00	AF111168.2	NT	Homo sapiens betaine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
175	12838	25321	1.22	0.0E+00	BE295973.1	EST_HUMAN	60114270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864.5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
176	12838	25321	0.84	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
177	12839	25322	2.37	0.0E+00	W73973.1	EST_HUMAN	zb62b05.r1 Soares fetal heart NihH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to gb:X16282_cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);
178	12840	25323	0.77	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-004 HT0457 Homo sapiens cDNA
178	12840	25324	0.77	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-004 HT0457 Homo sapiens cDNA
179	12841	25325	1.97	0.0E+00	AF244088.1	NT	Homo sapiens zhc finger protein mRNA, complete cds
182	12844	25328	24.45	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
182	12844	25328	24.45	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
183	12853	25336	4.25	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863854 5' similar to WP:Y57A10A.Z
183	12853	25337	4.25	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863854 5' similar to WP:Y57A10A.Z
198	12858	25340	2.9	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
198	12858	25341	2.9	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
199	12859	25342	1.88	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
199	12859	25343	1.88	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
208	12869	25355	92.14	0.0E+00	D50659.1	NT	Human gamma-xyloplasmic actin (ACTGP9) pseudogene
213	12874	25360	4.7	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
213	12874	25361	4.7	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
215	12876	25363	8.92	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSI3-2 protein mRNA, complete cds
215	12876	25364	8.92	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSI3-2 protein mRNA, complete cds
225	15410	25371	33.35	0.0E+00	AI587308.1	EST_HUMAN	tq04f08.x1 NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:2207647 3' similar to gb:J03191 PROFILIN I (HUMAN);
225	15410	25372	33.35	0.0E+00	AI587308.1	EST_HUMAN	tq04f08.x1 NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:2207647 3' similar to gb:J03191 PROFILIN I (HUMAN);
227	12887	25374	1.91	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
231	12891		44.25	0.0E+00	4506632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
232	12892		8.89	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
239	12899	25382	2.84	0.0E+00	AB018284.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
240	12899	25382	1.89	0.0E+00	AB018284.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
241	12900	25383	3.13	0.0E+00	6878444	NT	Mus musculus testis-specific protein, Y-encoded-like (Tspy), mRNA
248	12908	25387	0.78	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466

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248	12908	25388	0.78	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4468 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4468
248	12908	25389	0.78	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4468 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4468
256	12916	25400	0.97	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
256	12916	25401	0.97	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
259	12918	25405	9.57	0.0E+00	5433805	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
261	12920		11.16	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
268	12925	25411	4.93	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
270	12927	25414	1.82	0.0E+00	X89772.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
278	12935		7.37	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
281	12947	25433	1.28	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
291	12947	25434	1.28	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
293	12949	25436	1.96	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC51250), mRNA
304	12959		2.01	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
305	12960	25449	2.17	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
305	12960	25450	2.17	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
308	12981		1.14	0.0E+00	AW845293.1	EST_HUMAN	IL2-CT0031-181199-020-B03 CT0031 Homo sapiens cDNA
315	12969	25457	6.39	0.0E+00	4557028	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
315	12969	25458	6.39	0.0E+00	4557028	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
326	12980	25468	8.1	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
327	12981	25469	4.44	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
328	15413		23.15	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
328	12982	25470	0.99	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, zyl8c06.11 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:753984 5'
330	12983		2.5	0.0E+00	AA480002.1	EST_HUMAN	zyl8c06.11 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:753984 5'
331	12984	25471	18.8	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
332	12984	25471	19.33	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
336	12988	25475	3.18	0.0E+00	AF114488.1	NT	Homo sapiens intercalin short isoform (ITSN) mRNA, complete cds
348	13000	25484	1.84	0.0E+00	Q14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
349	13000	25485	1.84	0.0E+00	Q14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
350	13001	25486	3.83	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
351	13001	25486	1.41	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
366	13015	25498	5.41	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLT4) mRNA
367	13016	25499	1.14	0.0E+00	4505258	NT	Homo sapiens moesin (MSN), mRNA
370	13019	25503	20.33	0.0E+00	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
373	13022	25508	1.49	0.0E+00	U71600.1	NT	Human zinc finger protein zfp31 (zfp31) mRNA, partial cds
378	13026	25512	2.59	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
378	13028	25513	2.59	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
378	13028	25514	2.86	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
381	13028	25516	0.74	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
384	13031	25520	1.3	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
385	13032	25521	1.87	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
386	13032	25521	1.52	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
388	13034	25523	0.83	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
389	13043	25534	3.85	0.0E+00	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLAGE1000899 5'
410	13085	25537	8.92	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
411	13086	25579	2.03	0.0E+00	AI983014.1	EST_HUMAN	qy81h05.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb:X54199
416	13051	25541	2.36	0.0E+00	AW754180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (HUMAN);
419	13053	25544	1.95	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
420	13054	25545	2.21	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
420	13054	25546	2.21	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
421	13055	25547	1.1	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
422	13056	25548	1.46	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
422	13056	25549	1.46	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
423	13057	25550	0.95	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
424	13058	25551	2.9	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
425	13059	25552	1.17	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
426	13060	25553	1.66	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
426	13060	25554	1.66	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
427	13060	25554	2.78	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
431	13064	-	96.04	0.0E+00	4506608	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
445	12674	25130	1.11	0.0E+00	R17795.1	EST_HUMAN	y809a02.r1 Soares infant brain T1B Homo sapiens cDNA clone IMAGE:31652 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
453	13087	25580	1.82	0.0E+00	4503974	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminimidazole synthetase (GART) mRNA
454	13088		20.68	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
455	13089	25581	5.49	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
456	13090	25582	10.07	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
456	13090	25583	10.07	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
457	13091	25584	5.34	0.0E+00	AF193607.1	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
469	13102		0.81	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
471	13104	25597	2.96	0.0E+00	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
476	13109		0.92	0.0E+00	AA324262.1	EST_HUMAN	EST27054 Cerebellum II Homo sapiens cDNA 5' and
477	13110		1.1	0.0E+00	BE254447.1	EST_HUMAN	601111620F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3352348 5'
493	13126	25611	4.29	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
493	13128	25612	4.29	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
499	13131	25620	11.34	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
499	13131	25621	11.34	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
509	13142	25627	2.62	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
510	13143	25628	5.1	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
510	13143	25628	5.1	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
519	13151	25634	6.04	0.0E+00	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
521	13153	25636	2.12	0.0E+00	AU132898.1	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
529	13161	25642	6.27	0.0E+00	BE385144.1	EST_HUMAN	601274951F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615756 5'
530	15417	25643	1.89	0.0E+00	AW938825.1	EST_HUMAN	PMO-DT0065-130400-002-c06 DT0065 Homo sapiens cDNA
533	13164	25645	1.33	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
534	13165	25646	1.42	0.0E+00	8923955	NT	Homo sapiens PC328 protein (PC328), mRNA
538	13169		0.72	0.0E+00	BF373403.1	EST_HUMAN	IL2-FT0159-070800-120-F07 FT0159 Homo sapiens cDNA
545	13176	25656	4.88	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
552	15418	25660	1.31	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-H05 BT0635 Homo sapiens cDNA
556	13187	25665	1.27	0.0E+00	BF028005.1	EST_HUMAN	601794859F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3986998 5'
562	13193	25672	1.12	0.0E+00	AS040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
565	13196	25675	14.24	0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
566	13197	25676	4.05	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
568	13197	25677	4.05	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
568	13199	25679	1.36	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
569	13200	25680	0.96	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
569	13200	25681	0.86	0.0E+00	8923631	NT	Homo sapiens enilin (LOC54443), mRNA
574	13204		4.55	0.0E+00	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
582	13212	25680	1.45	0.0E+00	AW135324.1	EST_HUMAN	UI-H-B1-acb-h-04-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
592	13222		6.6	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
612	13240	25715	4.68	0.0E+00	5174742	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCF1), nuclear gene encoding mitochondrial protein, mRNA
625	13252		6.05	0.0E+00	J04066.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
628	13255	25729	2.19	0.0E+00	BF104898.1	EST_HUMAN	60182627F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
630	13257	25731	1.6	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
630	13257	25732	1.6	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
631	13257	25731	1.74	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
631	13257	25732	1.74	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
632	13257	25731	1.81	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
632	13257	25732	1.81	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
637	13260	25735	0.88	0.0E+00	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
642	13265	25741	0.94	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
642	13265	25742	0.94	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
650	13273	25750	3.63	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
652	13276	25753	0.89	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
654	13277	25754	1.8	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
655	13278	25755	2.31	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
655	13278	25756	2.31	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
656	13278	25757	0.73	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
658	13279	25758	0.73	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
663	13287	25768	1.2	0.0E+00	AA309486.1	EST_HUMAN	zh60c07.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:726732 5'
667	13291	25772	6.55	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
671	13295	25775	48.91	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
671	13295	25776	48.91	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
674	13298		3.09	0.0E+00	4885526	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
681	13305	25788	2.98	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
683	13307	25791	1.7	0.0E+00	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
686	13310	25795	1.77	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
690	13314	25798	0.9	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
690	13314	25799	0.9	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
696	13319	25804	4.78	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
696	13319	25805	4.78	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
702	15421		1.23	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV6)
711	13332	25819	21.02	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA
716	13337	25823	5.36	0.0E+00	AB029012.1	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
726	13346	25838	7.22	0.0E+00	7657488	NT	np49d01.a1 NCI CGAP Br.1.1 Homo sapiens cDNA clone IMAGE:1129633 3' similar to gb:X57352
738	13358	25852	87.91	0.0E+00	AA614537.1	EST_HUMAN	INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);
742	13362	25856	4.31	0.0E+00	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
742	13362	25857	4.31	0.0E+00	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
752	13372	25868	1.46	0.0E+00	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
758	13377	25872	4.75	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
758	13377	25873	4.75	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
760	13379	25876	11.52	0.0E+00	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
766	13385	25884	2.52	0.0E+00	BE241577.1	EST_HUMAN	TCAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Bayor-HGSC project=TCAA Homo
766	13404	25908	1.47	0.0E+00	AF226990.2	NT	sapiens cDNA clone TCAAP0779
768	13404	25909	1.47	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
767	13405	25910	0.72	0.0E+00	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
780	13408	25913	19.87	0.0E+00	J03784.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
790	13408	25914	19.87	0.0E+00	J03784.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
793	13411	25915	1.09	0.0E+00	AB037780.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
794	13412	25916	1.82	0.0E+00	6912749	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
796	15425	25918	2.4	0.0E+00	D30612.1	NT	Homo sapiens mRNA for repressor protein, partial cds
797	13414	25919	3.29	0.0E+00	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
801	13418	25923	2.87	0.0E+00	R48915.1	EST_HUMAN	y68908.r1 Soares breast 2NHBst Homo sapiens cDNA clone IMAGE:154046 5'
802	13419	25924	4.63	0.0E+00	5032086	NT	Homo sapiens splicing factor 3a, subunit 1, 120KD (SF3A1), mRNA
811	13428	25933	1.72	0.0E+00	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
814	13432	25937	3.26	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
825	13442	25949	1.15	0.0E+00	D90006.1	NT	Human mRNA for KIAA0184 gene, partial cds
825	13442	25950	1.15	0.0E+00	D90006.1	NT	Human mRNA for KIAA0184 gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
830	13447	25954	2.88	0.0E+00	X89772.1	NT	H.sapiens mRNA for interferon alpha/beta receptor (long form)
834	13451	25958	2.77	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
834	13451	25959	2.77	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
839	13455	25985	9.17	0.0E+00	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
840	13456		8.31	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
857	13473	25986	1.71	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
858	13474	25987	2.81	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
860	13476	25989	2.3	0.0E+00	4557686	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNE1) mRNA
866	13481	25995	1.58	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
866	13481	25996	1.58	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
867	13482	25997	0.95	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
872	13487	26002	2.8	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
876	13490	26007	1.86	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
876	13490	26008	1.98	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
883	13497		1.72	0.0E+00	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
887	13501	26019	6	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
887	13501	26020	6	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
888	13502	26021	12.68	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
889	13503	26022	6.37	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
890	13504	26023	15.55	0.0E+00	4508728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
894	13508	26026	1.64	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
894	13508	26027	1.64	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
895	13509	26028	2.12	0.0E+00	AA533272.1	EST_HUMAN	Homo sapiens mRNA for KIAA0910 protein, partial cds
895	13509	26028	2.12	0.0E+00	AA533272.1	EST_HUMAN	Homo sapiens mRNA for KIAA0910 protein, partial cds
896	13510		6.29	0.0E+00	BF677694.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:4249915 5'
900	13514	26030	1.67	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
900	13514	26031	1.67	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
901	13515	26032	2.03	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
901	13515	26033	2.03	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
924	13537	26056	0.95	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
931	13544	26061	1.84	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
931	13544	26062	1.84	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
941	13554	26071	2.92	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
951	13563		32.19	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
954	13568	26079	6.19	0.0E+00	U35464.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
954	13568	26080	6.19	0.0E+00	U35464.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
956	13563		27.9	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (87kD, ribosomal protein SA) (LAMR1), mRNA
957	13568	26082	269.29	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antichymotrypsin precursor, mRNA, partial cds
958	13569	26083	16.83	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
958	13569	26084	16.83	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
958	13569	26085	16.83	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
959	13570	26086	12.58	0.0E+00	L28101.1	NT	Homo sapiens kallistatin (Pl4) gene, exons 1-4, complete cds
985	13598	26111	0.9	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
987	13599	26112	8.4	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
988	13600	26113	0.6	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
989	13601	26114	1.26	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
989	13601	26115	1.26	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
997	15430	26122	6.65	0.0E+00	A1001948.1	EST_HUMAN	cs98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
997	15430	26123	6.65	0.0E+00	A1001948.1	EST_HUMAN	cs98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
999	13610	26125	8.95	0.0E+00	7657268	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1010	13620	26135	2.35	0.0E+00	AB030566.1	NT	Homo sapiens mRNA for PSP24, complete cds
1019	13629	26142	1.58	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1019	13629	26143	1.58	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1019	13629	26144	1.58	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1021	13631	26147	2.54	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1021	13631	26148	2.54	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1030	13640	26155	2.14	0.0E+00	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
1042	13651	26163	1.69	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1043	13652	26164	31.97	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1044	13652	26164	15.2	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1047	13655		5.72	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1048	13655		7.75	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1052	13659	26170	1.8	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1053	13659	26170	2.85	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1054	13659	26170	2.84	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1055	13660	26171	2.67	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1058	13663	26174	1.69	0.0E+00	7661885	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1062	13667	26178	3.66	0.0E+00	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1063	13668		2.66	0.0E+00	AA458680.1	EST_HUMAN	aa86g07.s1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838236 3' similar to SW_PRS8_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8;
1069	13671	26182	0.94	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1066	13671	26183	0.94	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 5124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1067	13672	26184	2.11	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1067	13672	26185	2.11	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1071	13676		2.98	0.0E+00	8922933	NT	Homo sapiens hypothetical protein FLJ11196 (FLJ11196), mRNA
1085	13690	26200	5.51	0.0E+00	4758569	NT	Homo sapiens heat shock 70kD protein 98 (mortalin-2) (HSPA9B) mRNA
1103	13707	26215	2.09	0.0E+00	4826872	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1103	13707	26216	2.09	0.0E+00	4826872	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1107	13711	26220	3.31	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1107	13711	26221	3.31	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1108	13712	26222	72.04	0.0E+00	AJ245022.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1110	13714		1.08	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1112	13716	26226	4.16	0.0E+00	5174384	NT	Homo sapiens alkylation repair, alkB homolog (ABH), mRNA
1121	13724	26237	4.88	0.0E+00	4758117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1135	13738	26247	2.88	0.0E+00	BE005208.1	EST_HUMAN	MRO-BN0115-200300-003-H08 BN0115 Homo sapiens cDNA
1158	13761	26271	4.25	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1158	13761	26272	4.25	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1171	13773	26282	1.29	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1171	13773	26283	1.29	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1172	13774	26284	23.49	0.0E+00	4506712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1174	13776	26288	1.24	0.0E+00	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1177	13779	26289	15.95	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1179	13781	26290	37.33	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1180	13782	26291	6.32	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1180	13782	26292	6.32	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1184	13785	26295	2.19	0.0E+00	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51728), mRNA
1185	13786	26296	1.92	0.0E+00	X95826.1	NT	H. sapiens ART4 gene
1185	13786	26297	1.92	0.0E+00	X95826.1	NT	H. sapiens ART4 gene
1186	13787	26298	2.16	0.0E+00	AI147650.1	EST_HUMAN	qb22d10.x1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:1697011 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1188	13789	26300	1.59	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1197	13788	26309	0.7	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1197	13788	26310	0.7	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1198	13789	26311	1	0.0E+00	986844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
1210	13810	26323	3.09	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1210	13810	26324	3.09	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1213	13813	26327	1.78	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1220	13820	26336	8.63	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1251	13848		0.83	0.0E+00	7657336	NT	Homo sapiens mult. (E. coli) homolog 3 (MLH3), mRNA
1265	13862	26379	0.63	0.0E+00	8922593	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
1269	13866	26383	2.13	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1269	13866	26384	2.13	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1270	13867	26385	2.51	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1271	15436	26386	2.03	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1289	13884	26409	6.85	0.0E+00	AF109718.1	NT	Homo sapiens:chromosome 3 subtelomeric region
1280	13885	26410	1.33	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanome-associated) (CSPG4), mRNA
1300	13894	26416	0.83	0.0E+00	4505740	NT	Homo sapiens prefoldin 4 (PFDN4) mRNA
1309	13903		2.3	0.0E+00	Y18000.1	NT	Homo sapiens NF2 gene
1317	13911	26431	160.44	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1324	13918	26440	3.36	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSOR8) mRNA, complete cds
1331	13925	26445	1.6	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1331	13925	26446	1.6	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1343	13938	26459	2.36	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1343	13938	26460	2.36	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1343	13938	26461	2.36	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1344	13939		2.81	0.0E+00	AF086156.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1354	15438	26473	2.05	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1354	15438	26474	2.05	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1360	13954	26480	4.79	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1361	13955	26481	1.2	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1363	13957	26482	0.97	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1364	13958	26483	4.9	0.0E+00	5803146	NT	Homo sapiens ring finger protein 8 (RNF8), mRNA
1365	13959	26484	1.23	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1367	13961	26486	3.51	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1368	13982	26487	2.76	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1369	13963	26488	4.67	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1370	13964	26489	4.11	0.0E+00	8587387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1370	13964	26490	4.11	0.0E+00	8587387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1382	13975	26503	1	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1442	14035	26563	0.96	0.0E+00	BE257855.1	EST_HUMAN	601109792F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350471 5'
1442	14035	26564	0.96	0.0E+00	BE257855.1	EST_HUMAN	601109792F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5'
1454	14048	26578	0.92	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cyndromatosis cyd gene
1482	14054	26587	1.2	0.0E+00	AJ208756.1	EST_HUMAN	qg38b06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837427 3' similar to WP:T27A1.5
1463	14055	26588	11.41	0.0E+00	6042208	NT	RAN, member RAS oncogene family/Homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1472	14064	26589	1	0.0E+00	4505646	NT	Homo sapiens protein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1472	14064	26600	1	0.0E+00	4505646	NT	Homo sapiens protein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1474	14068	26603	3.26	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1474	14068	26604	3.26	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1477	14069	26606	7.19	0.0E+00	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1488	14081	26620	3.54	0.0E+00	AF038280.1	NT	Homo sapiens alpha1-6fucosyltransferase (alpha1-6FucT) gene, exon 7
1510	14102	26638	3.27	0.0E+00	AL132989.1	NT	Novel human gene on chromosome 20
1512	14104	26638	1.4	0.0E+00	AL137784.1	NT	Novel human gene mapping to chromosome 1
1516	14108	26644	1.45	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1518	14111	26647	9.86	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1521	14113	26649	2.74	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1558	14150	26682	2.74	0.0E+00	7706434	NT	Homo sapiens hHDC for homolog of Drosophila headcase (LOC51696), mRNA
1573	14168	26697	1.46	0.0E+00	AA481172.1	EST_HUMAN	aa34803.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815118 5'
1578	14172	26701	23.67	0.0E+00	AF023880.1	NT	Carcopithecus aethiops cyclophilin A mRNA, complete cds
1578	14172	26702	23.67	0.0E+00	AF023880.1	NT	Carcopithecus aethiops cyclophilin A mRNA, complete cds
1581	14174	26705	1.2	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGE resequences, MAGN Homo sapiens cDNA
1581	14174	26706	1.2	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGE resequences, MAGN Homo sapiens cDNA
1582	14175	26707	1.02	0.0E+00	D10884.1	NT	Bovine mRNA for neurocalcin
1584	14177		3.69	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1585	14178	26710	1.89	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1595	14178	26711	1.89	0.0E+00	4503404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1596	14179	26712	3.3	0.0E+00	7682405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1597	14180		8.59	0.0E+00	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1593	14188	26718	8.96	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1596	15445		25.62	0.0E+00	4508654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1597	14189	26720	28.65	0.0E+00	M14199.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1609	14202	26735	11.52	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1617	14210		1.58	0.0E+00	D00333.1	NT	human c-yes-2 gene
1624	14217	26749	10.11	0.0E+00	Z83738.1	NT	H. sapiens HH2B/le gene
1625	14218	26750	2.24	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1625	14218	26751	2.24	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1626	14219	26752	7.63	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1628	14219	26753	7.63	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1628	15446	26754	2.78	0.0E+00	AB040905.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1632	14224	26755	1.01	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1634	14226	26758	3.22	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1634	14228	26759	3.22	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1636	14228	26760	37.34	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1636	14228	26761	37.34	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1638	14230	26763	0.87	0.0E+00	M91803.1	NT	Human sodium channel mRNA
1652	14244	26778	7.35	0.0E+00	H26973.1	EST_HUMAN	yo76c05.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:183848 3'
1661	14254	26789	1.46	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1661	14254	26790	1.46	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1680	14272	26805	0.9	0.0E+00	AW444637.1	EST_HUMAN	UI-H-B13-ajw-c-04-0-UJ.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
1708	14301	26838	0.91	0.0E+00	A1768104.1	EST_HUMAN	wg81b07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2733294 3'
1709	14302	26839	2.5	0.0E+00	AF057177.1	NT	TR:Q62788 Q62788 CY52HIS2 ZINC FINGER PROTEIN. ;
1713	14305	26843	1.38	0.0E+00	M29580.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1713	14305	26844	1.38	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1715	14307	26846	6.78	0.0E+00	4557887	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1716	14308	26847	0.95	0.0E+00	7657065	NT	Homo sapiens keratin 18 (KRT18) mRNA
1720	14312	26850	0.95	0.0E+00	BE222374.1	EST_HUMAN	Homo sapiens v-bis avian erythroblastosis virus E26 oncogene related (ERG), mRNA hu11d05.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1720	14312	26851	0.95	0.0E+00	BE222374.1	EST_HUMAN	hu11005.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1723	14314	26855	3.69	0.0E+00	H30132.1	EST_HUMAN	y559e08.r1 Soares breast 3NBHBS1 Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1723	14314	26856	3.69	0.0E+00	H30132.1	EST_HUMAN	y559e08.r1 Soares breast 3NBHBS1 Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1725	14316	26858	6.58	0.0E+00	Z80780.1	NT	H sapiens H2B/h gene
1725	14316	26859	6.58	0.0E+00	Z80780.1	NT	H sapiens H2B/h gene
1728	14318		20.47	0.0E+00	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1737	14327	26871	4.35	0.0E+00	8923841	NT	Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA
1742	14332	26877	0.92	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1742	14332	26878	0.92	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1745	14335	26882	1.17	0.0E+00	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1), mRNA
1751	14341	26889	3.79	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1753	14343		3.16	0.0E+00	S94400.1	NT	TCR zeta [human, Genem/mRNA, 365 nt, segment 1 of 8]
1762	14352	26898	1.05	0.0E+00	4557538	NT	Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2), mRNA
1781	14371	26916	2.35	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1820	15450		35.11	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
1825	14414	26960	1.31	0.0E+00		NT	Homo sapiens E1A binding protein p300 (EP300), mRNA
1825	14414	26961	1.31	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300), mRNA
1828	14417	26965	1.47	0.0E+00	U63963.1	NT	Human GSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1831	15451	26969	5.45	0.0E+00	4505332	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP), mRNA
1843	14431	26984	13.62	0.0E+00	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
1845	14433	26987	7.44	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
1846	14434	26988	9.59	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4), mRNA
1846	14434	26989	9.59	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4), mRNA
1846	14434	26990	9.59	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4), mRNA
1857	14445	27001	1.57	0.0E+00	4505328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1), mRNA
1863	14450	27009	1.38	0.0E+00	4504828	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA, and translated products
1863	14450	27010	1.38	0.0E+00	4504826	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA, and translated products
1874	14460	27018	7.62	0.0E+00	6005855	NT	Homo sapiens Retine-derived POU-domain factor-1 (RPF-1), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1874	14460	27017	7.62	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1884	14470	27027	0.93	0.0E+00	AB032878.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1884	14470	27028	0.93	0.0E+00	AB032878.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1888	14473	27030	5	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1888	14473	27031	5	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1889	14474	27032	8.6	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1889	14474	27033	8.6	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1892	14477	27036	1.32	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B11-afn-f07-0-U1 st NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1892	14477	27037	1.32	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B11-afn-f07-0-U1 st NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1916	14501	27056	3.38	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1916	14501	27057	3.38	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1939	14523	27079	1.77	0.0E+00	BE008292.1	EST_HUMAN	RC2-BN0126-200300-012-B04 BN0126 Homo sapiens cDNA
1967	14551	27106	2.92	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1967	14551	27107	2.92	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1976	14559		1.84	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1976	14555	27116	2.72	0.0E+00	M89478.1	NT	Human transglutaminase mRNA, complete cds
1976	14555	27117	2.72	0.0E+00	M89478.1	NT	Human transglutaminase mRNA, complete cds
1981	14564	27124	1.69	0.0E+00	4507484	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1981	14564	27125	1.69	0.0E+00	4507484	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1985	14567		5.68	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1990	14572		5.14	0.0E+00	M55632.1	NT	Human topoisomerase I pseudogene 1
1998	14581	27139	3.45	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1998	14581	27140	3.45	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
2009	14591		0.99	0.0E+00	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
2011	14593	27153	1.13	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
2011	14593	27154	1.13	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
2012	14594	27155	2.07	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
2012	14594	27156	2.07	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
2024	14606	27171	1.03	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2024	14606	27172	1.03	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2030	14612	27176	1.43	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2030	14812	27177	1.43	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
2032	14814	27178	0.89	0.0E+00	AW193024.1	EST_HUMAN	x69b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2878913 3'
2032	14814	27179	0.89	0.0E+00	AW193024.1	EST_HUMAN	x69b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2878913 3'
2033	14815	27180	7.94	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2033	14815	27181	7.94	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2035	14817	27183	0.88	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2036	14818	27184	0.92	0.0E+00	Z47558.1	NT	H. sapiens genes for semenogelin I and semenogelin II
2036	14818	27185	0.92	0.0E+00	Z47558.1	NT	H. sapiens genes for semenogelin I and semenogelin II
2043	14825	27194	2.25	0.0E+00	AB040846.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
2097	14878	27245	0.94	0.0E+00	7706742	NT	Homo sapiens TP53TG3a (TP53TG3a), mRNA
2102	14881	27249	2.71	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2102	14881	27250	2.71	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2104	14883	27251	1.39	0.0E+00	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9), mRNA
2105	14884	27252	3.79	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone IMAGE:4000321 5'
2106	14068	26603	1.97	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2106	14066	26604	1.97	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2108	14888	27254	1.59	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2108	14888	27255	1.59	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2110	14888		1.75	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2112	14890		1.76	0.0E+00	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2114	14892		2.2	0.0E+00	A1244247.1	EST_HUMAN	q60f08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive element
2119	14897	27266	2.72	0.0E+00	BE877225.1	EST_HUMAN	601485146F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5'
2121	14899	27268	1.8	0.0E+00	BF315325.1	EST_HUMAN	601902804F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2121	14899	27269	1.8	0.0E+00	BF315325.1	EST_HUMAN	601902804F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2126	14704	27275	2.31	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-410 CT0413 Homo sapiens cDNA
2128	14704	27278	2.31	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-410 CT0413 Homo sapiens cDNA
2133	14711	27283	2.79	0.0E+00	L00820.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2133	14711	27284	2.79	0.0E+00	L00820.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2134	14712	27285	1.61	0.0E+00	A1297709.1	NT	Homo sapiens mRNA for CDC2L5 protein kinase, (CDC2L5 gene), isoform 1
2139	14717	27289	1.28	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2143	14721	27292	34.67	0.0E+00	BE500995.1	EST_HUMAN	7634c02.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:3220610 3' similar to SW:DTD_HUMAN P50443 SULFATE TRANSPORTER;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2160	14737		2.08	0.0E+00	BE767964.1	EST_HUMAN	QV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA
2161	14738		1.9	0.0E+00	AF018983.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLRST1) gene, exon 8 and complete cds
2163	14740	27310	3.84	0.0E+00	BF027562.1	EST_HUMAN	601672066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2165	14742	27311	0.98	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2166	14743	27312	1.35	0.0E+00	AW752708.1	EST_HUMAN	IL3-CT0219-271099-022-G10 CT0219 Homo sapiens cDNA
2168	14745	27314	6.51	0.0E+00	AI904840.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2168	14745	27315	6.51	0.0E+00	AI904840.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2202	14778		0.97	0.0E+00	7657252	NT	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCMB3L), mRNA
2224	14799		1.37	0.0E+00	L14787.1	NT	Human DNA-binding protein mRNA, 3' end
2230	14805	27377	10.57	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2230	14805	27378	10.57	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2232	14807	27380	1.12	0.0E+00	AA931691.1	EST_HUMAN	cc32601.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567898 3'
2234	14809		7.75	0.0E+00	MT9828.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 22 through 28
2236	14811	27383	10.88	0.0E+00	BF344434.1	EST_HUMAN	602014828F1 NCL_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4150734 5'
2237	14812	27384	20.34	0.0E+00	BE748896.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
2240	14815	27387	2.59	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2240	14815	27388	2.59	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2244	15481	27393	2.04	0.0E+00	BF313617.1	EST_HUMAN	601900281F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129622 5'
2247	14821	27396	1.56	0.0E+00	BE018750.1	EST_HUMAN	b584e02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;
2248	14822	27397	0.94	0.0E+00	AA042813.1	EST_HUMAN	z53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFATORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN);
2248	14822	27398	0.94	0.0E+00	AA042813.1	EST_HUMAN	z53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFATORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN);
2256	14830	27406	2.87	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2256	14830	27407	2.87	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2257	14831	27408	0.98	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2257	14831	27409	0.98	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2262	14836		1.58	0.0E+00	U39294.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
2263	14837	27414	0.91	0.0E+00	AA282281.1	EST_HUMAN	z12b10.1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712891 5'
2270	14844	27420	0.92	0.0E+00	BE697487.1	EST_HUMAN	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
2271	14845		4.79	0.0E+00	M20903.1	NT	Human apolipoprotein C-I pseudogene, complete cds

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2282	14856	27433	6.28	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
2288	14862	27437	1.15	0.0E+00	7692401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2295	14869	27445	1.05	0.0E+00	BE895281.1	EST_HUMAN	601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918607 5'
2299	14872	27448	1.26	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2339	14910	27482	3.84	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2339	14910	27483	3.84	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2340	14911	27484	2.06	0.0E+00	AI078404.1	EST_HUMAN	oz09c07.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2342	14913	27486	1.81	0.0E+00	AA429001.1	EST_HUMAN	z78a11.1.1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2342	14913	27487	1.81	0.0E+00	AA429001.1	EST_HUMAN	z78a11.1.1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2344	14915	27489	1.98	0.0E+00	AA680387.1	EST_HUMAN	z11e12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430510 3'
2345	14916	27490	3.65	0.0E+00	BF347039.1	EST_HUMAN	602021846F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157339 5'
2350	14921	27496	3.07	0.0E+00	L02840.1	NT	Homo sapiens potassium channel Kv2.1 mRNA, complete cds
2351	14922	27497	1.6	0.0E+00	6325468	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2358	14929	27503	1.17	0.0E+00	BE676095.1	EST_HUMAN	7f22a02.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3295370 3' similar to TR:094939 094939 KIAA0857 PROTEIN ;
2360	14931	27504	5.89	0.0E+00	AF044571.1	NT	Homo sapiens phosphotyrosine kinase alpha subunit (PHKA2) gene, exon 32
2361	14932	27505	2.94	0.0E+00	AI625542.1	EST_HUMAN	y57c08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2283182 3'
2366	14937	27509	1.72	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2366	14937	27510	1.72	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2377	14946	27520	0.99	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2377	14946	27521	0.99	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2378	14947		1.07	0.0E+00	4557521	NT	Homo sapiens deiodinase, iodothyronine, type I (DIO1) mRNA
2387	14956	27527	2.83	0.0E+00	5174678	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2391	14959	27531	1.95	0.0E+00	AU131142.1	EST_HUMAN	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002064 5'
2392	14960		8.95	0.0E+00	BE794026.1	EST_HUMAN	601586843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'
2393	14961	27532	0.98	0.0E+00	AW867076.1	EST_HUMAN	MR1-SND033-120400-002-a04 SND033 Homo sapiens cDNA
2394	14962	27533	5.08	0.0E+00	7662017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2395	14963	27534	1.69	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2395	14963	27535	1.69	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2396	14964		3.28	0.0E+00	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2398	14966	27537	10.16	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2398	14966	27538	10.16	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'

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2398	14966	27539	10.16	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2458	15025	27595	4.3	0.0E+00	AU119592.1	EST_HUMAN	AU119592 HEMBA1 Homo sapiens cDNA clone HEMBA1008155 5'
2459	15026		3.3	0.0E+00	AI042035.1	EST_HUMAN	ox60b02.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1660683 3' similar to TR:O08662 O08662 230KDA PHOSPHATIDYLINOSITOL 4-KINASE ;
2460	15027	27598	1.06	0.0E+00	8923820	NT	Homo sapiens hypothetical protein FLJ20693 (FLJ20693), mRNA xv15f07.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2813221 3' similar to TR:O54824 O54924 EXO84 ;
2463	15030	27598	1.3	0.0E+00	AW303988.1	EST_HUMAN	601432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2465	15032		1.28	0.0E+00	BE95605.1	EST_HUMAN	AB005622 HeLa cDNA (T.Noma) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2476	15043		1.17	0.0E+00	AB005622.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2480	15048	27615	8.35	0.0E+00	6006002	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2484	15049	27619	1.84	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2484	15049	27620	1.94	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2491	15058	27629	3.24	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2498	15063	27638	3.07	0.0E+00	5729777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2507	15071	27644	4.18	0.0E+00	BF569144.1	EST_HUMAN	802184558T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3'
2518	15082	27655	2.85	0.0E+00	AW468922.1	EST_HUMAN	h04104.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3'
2520	15084	27656	2.91	0.0E+00	AW501010.1	EST_HUMAN	UIHF-BP0p-ais-c-07-Q-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2529	15093		1.39	0.0E+00	AI287878.1	EST_HUMAN	q23f06.x1 NCL_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MIR repetitive element ;
2537	15101	27674	1.54	0.0E+00	5453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2537	15101	27675	1.54	0.0E+00	5453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2548	15112		1.81	0.0E+00	AW813853.1	EST_HUMAN	RC3-ST0197-300300-016-c04 ST0197 Homo sapiens cDNA
2552	15118	27686	9.72	0.0E+00	BE795542.1	EST_HUMAN	801592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5'
2553	15117	27687	1.32	0.0E+00	BF509482.1	EST_HUMAN	UI-H-BI4-eoz-b-08-Q-UI.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2555	15119	27689	1.52	0.0E+00	Z32684.2	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2557	15121		3.57	0.0E+00	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
2559	15123	27682	0.89	0.0E+00	BE910378.1	EST_HUMAN	601503356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5'
2560	15124	27693	3.1	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2561	15125	27694	3.58	0.0E+00	BE150885.1	EST_HUMAN	RC4-H10276-160200-013-405 HT0276 Homo sapiens cDNA
2562	15126	27695	1.24	0.0E+00	8923340	NT	Homo sapiens hypothetical protein FLJ20366 (FLJ20366), mRNA
2563	15127	27696	3	0.0E+00	U93239.1	NT	Human Sec62 (Sec62) mRNA, complete cds
2568	15132	27700	1.34	0.0E+00	BE886490.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909866 5'
2571	15134	27704	4.84	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2571	15134	27705	4.84	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'

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2587	15150	27714	0.9	0.0E+00	BE536921.1	EST_HUMAN	601064738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2592	15154	27721	9.34	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001873 5'
2592	15154	27721	9.34	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001873 5'
2593	15155	27723	0.9	0.0E+00	BE292896.1	EST_HUMAN	601106312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955 5'
2593	15155	27723	0.9	0.0E+00	BE292896.1	EST_HUMAN	601106312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955 5'
2598	15158	27728	8.62	0.0E+00	AF245505.1	NT	Homo sapiens adican mRNA, complete cds
2633	15402	27766	1.76	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2633	15402	27767	1.76	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2634	15104		3.12	0.0E+00	BF513835.1	EST_HUMAN	U1-HBW1-amp-f-12-0-U1 s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2643	15202	27775	1.24	0.0E+00	AE71737.1	EST_HUMAN	In19b08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2168055 3' similar to gb:L20977
							CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN);
							Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kD (TAF21)
2644	15203	27778	2.08	0.0E+00	5032150	NT	mRNA
2647	15206	27779	6.91	0.0E+00	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
2648	15207	27780	0.99	0.0E+00	BE795445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2648	15207	27781	0.99	0.0E+00	BE795445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2651	15210	27782	1.16	0.0E+00	BE293328.1	EST_HUMAN	601143722F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051389 5'
2655	15214		5.98	0.0E+00	BE792472.1	EST_HUMAN	601584930F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'
2663	15221	27783	1.73	0.0E+00	4504686	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
							Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein
2671	15229		1.65	0.0E+00	U78027.1	NT	(L44L) and FTP3 (FTP3) genes, complete cds
2672	15230	27800	6.98	0.0E+00	AF173227.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2678	15234	27801	2.15	0.0E+00	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
2680	15238	27805	1.01	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2680	15238	27806	1.01	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2682	15240	27808	1.22	0.0E+00	AW887016.1	EST_HUMAN	RC1-OT0086-220300-011-407 OT0086 Homo sapiens cDNA
2685	15243	27811	3.43	0.0E+00	BE383165.1	EST_HUMAN	601268714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5'
2686	15244		2.17	0.0E+00	BE531263.1	EST_HUMAN	601278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610267 5'
2712	15269	27837	1.4	0.0E+00	8922843	NT	Homo sapiens hypothetical protein FLJ11052 (FLJ11052), mRNA
							EST189414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal
2748	15303		9.58	0.0E+00	AA316723.1	EST_HUMAN	protein L29
2749	15304	27868	12.57	0.0E+00	BE794884.1	EST_HUMAN	601589625F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 5'
2755	15310	27878	2.37	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2757	15312	27878	0.97	0.0E+00	7689517	NT	Homo sapiens neurogranin 1 (NRG1), transcript variant SMDF, mRNA

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2758	15313	27878	1.42	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2760	15319	27881	1.23	0.0E+00	AB051826.1	NT	Homo sapiens hG28K mRNA for GTP-binding protein like 1, complete cds
2765	15319	27885	20.41	0.0E+00	BE798376.1	EST_HUMAN	601591991F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2766	15320	27886	2.11	0.0E+00	BF680632.1	EST_HUMAN	602155923F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287132 5'
2769	15476	27890	14.33	0.0E+00	BE563433.1	EST_HUMAN	601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689564 5'
2770	15323		1.77	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBBYE09 5'
2772	15325	27893	2.47	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2772	15325	27894	2.47	0.0E+00	5174488	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2773	15326	27895	1.25	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2773	15326	27896	1.25	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2774	15327	27897	2.27	0.0E+00	AF290195.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2775	15328		131.05	0.0E+00	AV651086.1	EST_HUMAN	AV651086 GLC Homo sapiens cDNA clone GLCCLD07 3'
2776	15329	27898	4.94	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-808 TN0141 Homo sapiens cDNA
2776	15329	27899	4.94	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-808 TN0141 Homo sapiens cDNA
2780	15333	27902	7.42	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2780	15333	27903	7.42	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2784	15337	27908	3.11	0.0E+00	BE747193.1	EST_HUMAN	601580903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5'
2786	15349		0.98	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2797	15350	27919	2.76	0.0E+00	BF514110.1	EST_HUMAN	UI-H-BW1-aww-e-07-0-JJ.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'
2804	15356		0.89	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2808	15361	27928	1.76	0.0E+00	7705275	NT	Homo sapiens angiopoietin-3 (ANG-3), mRNA
2808	15361	27929	1.76	0.0E+00	7705275	NT	Homo sapiens angiopoietin-3 (ANG-3), mRNA
2810	15362	27930	4.3	0.0E+00	BF877694.1	EST_HUMAN	602085578F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248815 5'
2814	15366	27936	1.1	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, I (PTPRT), mRNA
2817	15369	27938	17.28	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2817	15369	27939	17.28	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2819	15371		9.44	0.0E+00	AB78163.1	EST_HUMAN	au55d04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to
2822	15374	27944	1.69	0.0E+00	BF530661.1	EST_HUMAN	SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A :
2823	15375	27945	7.68	0.0E+00	BE872768.1	EST_HUMAN	602071657F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4214679 5'
2825	15377	27946	1.55	0.0E+00	AU131494.1	EST_HUMAN	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854642 5'
2825	15377	27947	1.55	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002872 5'
2826	15378	27948	34.11	0.0E+00	BE300344.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002872 5'
2826	15378	27949	34.11	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'

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2832	12881	25345	7.88	0.0E+00	S76830.1	NT	glycoprotein D=Duffy group antigen [human, blood, Genomic DNA, 3068 nt]
2835	15385		1.75	0.0E+00	AB033281.1	NT	Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2841	13382	25881	1.88	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2841	13382	25882	1.88	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2846	13682	26192	3.33	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2846	13682		3.33	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2861	15480	27856	4.7	0.0E+00	X85980.1	NT	H. sapiens serine hydroxymethyltransferase pseudogene
2862	15481		2.28	0.0E+00	AF068824.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds
2863	15482		1.63	0.0E+00	AB040960.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2870	15488		1.06	0.0E+00	AJ238852.1	NT	Homo sapiens partial rp13 gene for ribosomal protein L3, U82 snRNA, U83a snRNA and U83b snRNA genes
2871	15489	27960	2.43	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2875	15493	27963	1.55	0.0E+00	M80602.1	NT	Human AHNK nucleoprotein mRNA, 5' end
2877	15495	27965	1.25	0.0E+00	BE154504.1	EST_HUMAN	PM0-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA
2877	15495	27966	1.25	0.0E+00	BE154504.1	EST_HUMAN	PM0-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA
2879	15497		1	0.0E+00	X73428.1	NT	H. sapiens l33 gene for HLH type transcription factor
2881	15499		2.76	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2882	15500	27969	1.01	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2882	15500	27970	1.01	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2882	15500	27971	1.01	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2884	15502	27972	2.39	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
2888	15505	27975	15.68	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2888	15505	27976	15.68	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2891	15508	27979	1.95	0.0E+00	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2892	15509		7.43	0.0E+00	Y10658.1	NT	H. sapiens mRNA for nuclear DNA helicase II
2893	15510		1.17	0.0E+00	AF152303.1	NT	Homo sapiens protodactherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2894	15511	27980	112.87	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2894	15511	27981	112.87	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2904	15521	27991	2.68	0.0E+00	4507280	NT	Homo sapiens serine/threonine kinase 9 (STK9) mRNA
2907	15524	27995	1.03	0.0E+00	AL047590.1	EST_HUMAN	DKFZp586G0821_r1 586 (synonym: huler) Homo sapiens cDNA clone DKFZp586G0821
2908	15525	27996	1.64	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2908	15525	27997	1.64	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2909	15526		2.8	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2912	15529	27999	6.04	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2912	15529	28000	6.04	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2918	15535	28008	0.71	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2918	15535	28008	0.71	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2921	15538	28013	2.25	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2921	15538	28014	2.25	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2922	15539	28015	1.29	0.0E+00	AA215579.1	EST_HUMAN	z96b11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683517 3' similar to contains Alu repetitive element
2929	15545		4.1	0.0E+00	Y19210.1	NT	Homo sapiens Hb5 gene for hair keratin, exons 1 to 9
2932	15548	28024	1.24	0.0E+00	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
2934	15550	28027	41.84	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2936	15552	28029	1.65	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
2937	15553	28030	1.25	0.0E+00	AF152338.1	NT	Homo sapiens protocadherin gamma C4 (PCCD-gamma-C4) mRNA, complete cds
2946	15562	28037	0.92	0.0E+00	AI209084.1	EST_HUMAN	qg4904.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1838527 3' similar to SW/GB20_HUMAN P52298 20 KD NUCLEAR CAP BINDING PROTEIN
2954	15570	28045	1.78	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2954	15570	28046	1.78	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2955	15571	28047	6.84	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2955	15571	28048	6.84	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2958	15574	28051	3.14	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2958	15574	28052	3.14	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2959	15575	28053	3.48	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2959	15575	28054	3.48	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2964	15579	28058	1.12	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1
2964	15579	28059	1.12	0.0E+00	BF110702.1	EST_HUMAN	Q9VLN1 CG17283 PROTEIN
2972	15588	28070	2.98	0.0E+00	4505084	NT	7n40d03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1
2972	15588	28071	2.98	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2981	15597	28077	1.82	0.0E+00	4758827	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2985	15601	28080	1.33	0.0E+00	X15309.1	NT	Homo sapiens neurxin III (NRXN3) mRNA
2985	15601	28080	1.33	0.0E+00	X15309.1	NT	H. sapiens NF-H gene, exon 4

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2985	15601	28081	1.33	0.0E+00	X15309.1	NT	H sapiens NF-H gene, exon 4
2987	15603	28083	9.28	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
3001	15617		1.28	0.0E+00	AI149880.1	EST_HUMAN	g43f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'
3009	15625	28103	0.72	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3009	15625	28104	0.72	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3010	15628	28105	1.24	0.0E+00	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
3011	15627	28106	2.29	0.0E+00	AB004884.1	NT	Homo sapiens mRNA for PKU-alpha, partial cds
3023	15639	28118	1.93	0.0E+00	7692273	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
3025	15641	28119	2.52	0.0E+00	5728755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3025	15641	28119	2.52	0.0E+00	5728755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3038	15652	28130	1.45	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3038	15652	28131	1.45	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3080	15678		0.73	0.0E+00	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3062	15678	28152	1.4	0.0E+00	MT4098.1	NT	Human displacement protein (GCAAT) mRNA
3072	15687	28159	0.72	0.0E+00	4506882	NT	Homo sapiens semenogelin 1 (SEMG1) mRNA
3075	15690	28163	0.68	0.0E+00	AW078268.1	EST_HUMAN	EST388375 MAGE resequences, MAGN Homo sapiens cDNA
3080	15695		3.98	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3083	15698	28171	20.17	0.0E+00	5578469	NT	Homo sapiens heat shock 70KD protein 1 (HSPA1A), mRNA
3083	15698	28172	20.17	0.0E+00	5578469	NT	Homo sapiens heat shock 70KD protein 1 (HSPA1A), mRNA
3085	15700		7.12	0.0E+00	AL359403.1	NT	isoform 2 of a novel human mRNA from chromosome 22
3089	15704	28178	2.79	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
3092	15707		2.39	0.0E+00	AF198779.1	NT	Homo sapiens transcription factor IGCHM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel alpha
3112	15727	28198	3.45	0.0E+00	X03528.1	NT	Human germline gene 16.1 for Ig lambda L-chain C region (Ig-LC16.1)
3118	15732		1.69	0.0E+00	AF199355.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3122	15738	28205	1.74	0.0E+00	AF084589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3140	15754	28221	3.58	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3141	15755	28222	5.25	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3146	15760	28228	4.35	0.0E+00	7682139	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA
3147	15761	28227	1.46	0.0E+00	AF042075.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3175	15788	28260	3.49	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3185	15797	28269	48.14	0.0E+00	L20941.1	NT	Human ferritin heavy chain mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3188	15800	28272	2.08	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3188	15800	28273	2.08	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3188	15808	28281	18.48	0.0E+00	T94870.1	EST_HUMAN	ye32603.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP:S28539
3210	15822	28298	1.23	0.0E+00	BF243336.1	EST_HUMAN	S28539 BASIC PROTEIN, 23K -
3211	15823	28299	1.28	0.0E+00	AI968086.1	EST_HUMAN	601878507F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107433 5'
3216	15828	28308	4.69	0.0E+00	X98922.1	NT	wu12h10.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2516803 3'
3216	15828	28307	4.69	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
3218	15830	28309	0.63	0.0E+00	AI985950.1	EST_HUMAN	H. sapiens mRNA for gamma-glutamyltransferase
3226	15838	28317	1.57	0.0E+00	4758827	NT	tu35g09.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2253376 3' similar to SW:RASD_DICDI
3226	15838	28318	1.57	0.0E+00	4758927	NT	P03987 RAS-LIKE PROTEIN RASD -
3233	15845	28325	10.75	0.0E+00	4504658	NT	Homo sapiens neurexin III (NRXN3) mRNA
3234	15846	28326	0.82	0.0E+00	4507720	NT	Homo sapiens neurexin III (NRXN3) mRNA
3234	15846	28327	0.92	0.0E+00	4507720	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
3245	15857	28340	1	0.0E+00	AJ277892.1	NT	Homo sapiens titin (TTN) mRNA
3253	15865	28346	2.89	0.0E+00	M28699.1	NT	Homo sapiens titin (TTN) mRNA
3257	15869	28349	2.27	0.0E+00	4502098	NT	Homo sapiens partial TTN gene for titin
3263	15876	28367	0.96	0.0E+00	4758055	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3263	15875	28358	0.96	0.0E+00	4758055	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
3265	15877	28359	4.57	0.0E+00	AA774783.1	EST_HUMAN	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3273	15885	28367	4.14	0.0E+00	AF286598.1	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3273	15885	28368	4.14	0.0E+00	AF286598.1	NT	aa87b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3285	15896	28374	1.44	0.0E+00	4557590	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3292	15903	28383	1.09	0.0E+00	4507720	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3300	15911		0.86	0.0E+00	M65189.1	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
						NT	Homo sapiens titin (TTN) mRNA
						NT	Human connexin 43 processed pseudogene
3301	15912	28390	1.7	0.0E+00	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
3303	15914	28392	4.47	0.0E+00	AF055084.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3313	18001	28400	2.26	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3313	18001	28401	2.26	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3328	15939	28415	2.57	0.0E+00	AF285208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3330	15940	28416	1.66	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
3355	15963	28440	1.02	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3368	15974	28451	5.9	0.0E+00	AI689264.1	EST_HUMAN	U59108.X2 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:222535 3' similar to SW:RL11_RAT
3369	15977	28454	1.4	0.0E+00	AW955400.1	EST_HUMAN	P25121 60S RIBOSOMAL PROTEIN L11, contains Alu repetitive element;
3374	15983	28460	2.28	0.0E+00	AF128893.1	NT	EST367470 MAGE resequences, MAGD Homo sapiens cDNA
3374	15983	28461	2.28	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
3375	15984	28462	0.91	0.0E+00	7657213	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
3375	15984	28463	0.91	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3378	15987	28465	1.23	0.0E+00	4502582	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3378	15987	28466	1.23	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3382	15991	28469	13.03	0.0E+00	AF111163.1	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3384	15993	28471	0.89	0.0E+00	AB040940.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
3403	16012	28491	1.08	0.0E+00	AI632569.1	EST_HUMAN	Homo sapiens mRNA for KIAA1507 protein, partial cds
3443	16051	28528	3.18	0.0E+00	AI123884.1	EST_HUMAN	wt0704.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2305279 3' similar to TR:Q91928 Q91929
3450	16057	28532	0.94	0.0E+00	7363436	NT	ZINC FINGER PROTEIN ;
3450	16057	28533	0.94	0.0E+00	7363436	NT	AU123664 NT2RM2 Homo sapiens cDNA clone NT2RM200735 5'
3453	16060	28535	1.88	0.0E+00	7706239	NT	Homo sapiens offactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3454	16061	28536	1.04	0.0E+00	AF211189.1	NT	Homo sapiens offactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3458	16065		1.03	0.0E+00	AW967015.1	EST_HUMAN	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
3471	16077	28560	1.28	0.0E+00	7662401	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA1I), mRNA, complete cds
3471	16077	28551	1.28	0.0E+00	7662401	NT	MR1-SN0033-100400-001-c08 SN0033 Homo sapiens cDNA
3472	16078	28552	1.05	0.0E+00	4502398	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3475	16081	28554	1.72	0.0E+00	5803087	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3484	15313	27879	1.56	0.0E+00	AF110763.1	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3489	16094	28567	2.36	0.0E+00	7657038	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3490	16095	28568	0.97	0.0E+00	5453985	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3490	16095	28569	0.97	0.0E+00	5453985	NT	Homo sapiens death receptor 6 (DR6), mRNA
3493	16098	28573	5.92	0.0E+00	K02380.1	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
3495	16100	28575	1.2	0.0E+00	7427522	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA

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3497	16102	28577	1	0.0E+00	4557746	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET) mRNA
3501	16106	28581	3.89	0.0E+00	A1935159.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2484819 3' similar to TR:O73634 O73634
3501	16106	28582	3.89	0.0E+00	A1935159.1	EST_HUMAN	NEURAL CELL ADHESION MOLECULE ;
3505	16110	28587	2.13	0.0E+00	AJ278120.1	NT	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2484819 3' similar to TR:O73634 O73634
3506	16111	28588	1.12	0.0E+00	7706378	NT	NEURAL CELL ADHESION MOLECULE ;
3512	16117	28596	2.09	0.0E+00	6552332	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3512	16117	28597	2.09	0.0E+00	6552332	NT	Homo sapiens ASB-4 protein (LOC51666), mRNA
3518	16123	28603	1.4	0.0E+00	M14123.1	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3523	16128	28608	8.45	0.0E+00	U43293.1	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3528	16133	28612	0.94	0.0E+00	9558718	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3528	16133	28613	0.94	0.0E+00	9558718	NT	Human endogenous retrovirus HERV-K10
3532	16137	28616	2.45	0.0E+00	AF045452.1	NT	Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds
3532	16137	28619	2.45	0.0E+00	AF045452.1	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3540	16145	28628	1.19	0.0E+00	AF231922.1	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3547	16151	28631	0.95	0.0E+00	AA626877.1	EST_HUMAN	Homo sapiens cell-line K562 transcriptional regulatory protein p54 mRNA, complete cds
3547	16151	28632	0.95	0.0E+00	AA626877.1	EST_HUMAN	Homo sapiens cell-line K562 transcriptional regulatory protein p54 mRNA, complete cds
3547	16151	28633	0.95	0.0E+00	AA626877.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
3553	16157	28639	1.53	0.0E+00	BE304791.1	EST_HUMAN	ab51112.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3553	16157	28640	1.53	0.0E+00	BE304791.1	EST_HUMAN	ab51112.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
							601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
							601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
							Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
3556	16160	28643	2.51	0.0E+00	4503848	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
3557	16161	28644	1.08	0.0E+00	4826795	NT	TRANSCRIPTION REGULATORY PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3560	16164	28647	1.58	0.0E+00	O14897	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3565	16169	28651	0.93	0.0E+00	A1384007.1	EST_HUMAN	1a35g12.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:O00488
3568	16172	28654	1.52	0.0E+00	M10976.1	NT	O00488 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN ;
3565	16189	28672	0.74	0.0E+00	AA456282.1	EST_HUMAN	Human endogenous retroviral DNA (4-1), complete retroviral segment
3565	16189	28673	0.74	0.0E+00	AA456282.1	EST_HUMAN	z889h04.1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5'
3594	16198	28681	1	0.0E+00	AV701869.1	EST_HUMAN	z889h04.1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5'
3595	16199	28682	0.73	0.0E+00	4506884	NT	AV701869 ADB Homo sapiens cDNA clone ADBDAH06 5'
3597	16201		1.47	0.0E+00	AF078868.1	NT	Homo sapiens semenogelin II (SEMG2) mRNA
3606	16210	28690	1.07	0.0E+00	AL193204.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
							Novel human gene mapping to chromosome X

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3610	16213	28693	0.89	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3622	16225	28703	1.1	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
3633	16236	28711	1.16	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3633	16236	28712	1.16	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3634	16237		1.14	0.0E+00	A1081907.1	EST_HUMAN	α77c11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1662356 3' similar to WP.T19B4.4
3636	16239	28715	1.26	0.0E+00	6325463	NT	CE13742;
3641	16244		5.41	0.0E+00	AW852217.1	EST_HUMAN	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA
3645	16248	28724	1.06	0.0E+00	4504294	NT	QV0-CT0225-230300-169-601 CT0225 Homo sapiens cDNA
3648	16252		1.74	0.0E+00	AF118846.1	NT	Homo sapiens H3 histone family, member K (H3FK), mRNA
3650	16253	28725	8.35	0.0E+00	BF670393.1	EST_HUMAN	Homo sapiens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cds
3653	16256		0.98	0.0E+00	AA988715.1	EST_HUMAN	602084583F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248596 5'
3663	16265	28737	0.9	0.0E+00	AW837977.1	EST_HUMAN	α984h08.e1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1594043 3' similar to contains MER29.b2
3675	16276	28743	0.8	0.0E+00	BF672054.1	EST_HUMAN	MER29 repetitive element;
3675	16276	28744	0.8	0.0E+00	BF672054.1	EST_HUMAN	QV0-DT0047-170200-123-g01 DT0047 Homo sapiens cDNA
3676	16277		1.3	0.0E+00	4826987	NT	QV0-DT0047-170200-123-g01 DT0047 Homo sapiens cDNA clone IMAGE:4293645 5'
3678	16278	28748	0.98	0.0E+00	AW664693.1	EST_HUMAN	602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'
3678	16278	28747	0.98	0.0E+00	AW664693.1	EST_HUMAN	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
3682	16283	28751	0.8	0.0E+00	4826763	NT	Homo sapiens NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2876024 3'
3684	16285	28754	0.91	0.0E+00		NT	h184g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2876024 3'
3692	16293	28762	0.72	0.0E+00	4557752	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA
3692	16293	28763	0.72	0.0E+00	4557752	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
3709	16310	28777	1.47	0.0E+00	D87327.1	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1), mRNA
3712	16313		20.4	0.0E+00	7669491	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1), mRNA
3730	16331	28797	2.49	0.0E+00	AB026542.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3732	16333	28799	0.93	0.0E+00	AB007866.2	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3734	16335	28800	2.62	0.0E+00	AF124250.1	NT	Homo sapiens WAVE2 mRNA for WASP family protein, complete cds
3734	16335	28801	2.62	0.0E+00	AF124250.1	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
						NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
						NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3739	16340	28807	2.63	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3739	16340	28808	2.63	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3743	16344	28811	1.66	0.0E+00	AL183204.2	NT	Homo sapiens chromosome 21 segment HS21C004

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3743	16344	28812	1.68	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3748	16347	28815	1.08	0.0E+00	AW851714.1	EST_HUMAN	MR2-CT0222-281099-005-005 CT0222 Homo sapiens cDNA
3748	16349	28817	1.4	0.0E+00	5729928	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3750	16351	28819	1.23	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, partial cds
3752	16353	28821	1.56	0.0E+00	Q14897	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3754	16355	28823	0.83	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3754	16355	28824	0.83	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3767	16368	28833	4.72	0.0E+00	AW298134.1	EST_HUMAN	UIH-BWO-ajls-e-12-0-UJ.s1 NC1_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3767	16368	28834	4.72	0.0E+00	AW298134.1	EST_HUMAN	UIH-BWO-ajls-e-12-0-UJ.s1 NC1_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3792	16392	28857	1.08	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen a1 chain, exon 6
3793	16393	28858	0.87	0.0E+00	AA463659.1	EST_HUMAN	aa0601.1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:812496 5' similar to SW:KRB4_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIB4. [1];
3798	16398	28863	1.04	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3801	16401	28866	4.05	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA.
3810	16409	28874	0.95	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3823	16423	28885	7.87	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3828	16428	28888	23.27	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3834	16433	28894	1.04	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3834	16433	28895	1.04	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3873	16471	28935	0.92	0.0E+00	7661867	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
3873	16471	28936	0.92	0.0E+00	7661867	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
3892	16491	28951	2.65	0.0E+00	AF179733.1	NT	Pan troglodytes olfactory receptor (PTR208) gene, partial cds
3896	16495	28956	1.55	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3898	16495	28957	1.55	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3900	16498	28962	1.35	0.0E+00	A1377699.1	EST_HUMAN	168210.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3901	16500		1.09	0.0E+00	AF152496.1	NT	Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds
3902	16501	28963	2.32	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
3905	16504	28966	10.94	0.0E+00	S78885.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ8/BIR1) gene, complete cds
3908	16505	28967	2.15	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA
3907	16506	28968	2.89	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3910	16509	28970	1.1	0.0E+00	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3910	16509	28971	1.1	0.0E+00	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3916	16514	28977	0.84	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3921	16519	28985	6.15	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3921	16519	28986	6.15	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3923	16521	28989	4.15	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3924	16522	28990	32.21	0.0E+00	AF114498.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3927	16525	28992	1.46	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3930	16528	28995	1.1	0.0E+00	AF012615.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3931	16529	28998	1.93	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129) mRNA
3933	16531	28998	1.09	0.0E+00	AF099117.1	NT	Homo sapiens amphiphysin gene, partial cds
3944	16542	29009	2.45	0.0E+00	AI864727.1	EST_HUMAN	wk01f01.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411085 3' similar to TR:O43340
3947	16545	29013	16.56	0.0E+00	4506742	NT	O43340 R28830_2; contains element PTR7 repetitive element;
3952	16550	29019	1.8	0.0E+00	AL040338.1	EST_HUMAN	Homo sapiens ribosomal protein S8 (RPS8) mRNA
3957	16555	29025	1.03	0.0E+00	6005887	NT	DKFZp434N0413_1 434 (synonym: hsa3) Homo sapiens cDNA clone DKFZp434N0413 5'
3957	16555	29026	1.03	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1) mRNA
3958	16556	29027	2.86	0.0E+00	4504138	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
3960	16558		2.2	0.0E+00	4505078	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
3964	16562	29031	1.02	0.0E+00	AF149412.1	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
3975	16573	29043	1.92	0.0E+00	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
3978	16577	29047	1.81	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIA0412) mRNA
3988	16586	29057	1.88	0.0E+00	BF355295.1	EST_HUMAN	RC3-H10860-011-a12 HT0860 Homo sapiens cDNA
							MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996726 similar to MXRA5
3990	16588	29059	1.04	0.0E+00	AW888221.1	EST_HUMAN	Matrix remodeling associated gene 5
							MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996726 similar to MXRA5
3990	16588	29060	1.04	0.0E+00	AW888221.1	EST_HUMAN	Matrix remodeling associated gene 5
3998	16596	29068	2.64	0.0E+00	AF129533.1	NT	Homo sapiens F-box protein Fb3b (FBL3B) mRNA, partial cds
4001	16599	29071	1.06	0.0E+00	U96281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
4001	16599	29072	1.06	0.0E+00	U96281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
4006	16604	29078	4.1	0.0E+00	BE378602.1	EST_HUMAN	601236966F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5'
4014	16612	29085	1.28	0.0E+00	AW580740.1	EST_HUMAN	PM3-L70031-100100-003-P09 L70031 Homo sapiens cDNA
4047	16644	29110	13.52	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4047	16644	29111	13.52	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4057	16654		4.5	0.0E+00	M23910.1	NT	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
4059	16656		6.04	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4065	16662	28124	1.23	0.0E+00	AL118494.1	NT	Novel human gene mapping to chromosome 20
4069	16665	28126	3.49	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4077	16673	28134	2.12	0.0E+00	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
4090	16686		60.86	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4098	16693	28150	1.89	0.0E+00	U09366.1	NT	Human zinc finger protein ZNF133
4120	16713	28169	10.72	0.0E+00	AB015610.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
4130	16722		3.27	0.0E+00	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (RNA48 gene)
4140	16732	28185	1.61	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4141	16733	28188	2.96	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rape-2 (rapa gene)
4141	16733	28187	2.96	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rape-2 (rapa gene)
4148	16740	28193	8.52	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4148	16740	28194	8.52	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4158	16750	28203	0.98	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylmethylimidazole synthetase (GART) mRNA
4164	16755	28207	7.55	0.0E+00	4885306	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
4165	16756	28208	4.94	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4168	16759	28209	0.68	0.0E+00	4759807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
4169	16760	28210	6.82	0.0E+00	11419297	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
4170	16761	28211	2.88	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4171	16762		1.11	0.0E+00	AA018975.1	EST_HUMAN	2855609.r1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:362920 5' similar to contains Alu repetitive element
4178	16769	28218	3.61	0.0E+00	AF165527.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
4189	13773	28282	0.76	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4189	13773	28283	0.76	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4195	16785	28233	2.14	0.0E+00	5501905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
4196	16786	28234	1.21	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4196	16786	28235	1.21	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4198	16189	28682	0.57	0.0E+00	4506884	NT	Homo sapiens semenogelin II (SEMG2) mRNA
4200	16789	28237	1.35	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4200	16789	28238	1.35	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4208	16795	28242	0.59	0.0E+00	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
4213	16802	28251	18.39	0.0E+00	A1982597.1	EST_HUMAN	w004d04.x1 NCI CGAP_G06 Homo sapiens cDNA clone IMAGE:2515975 3'
4213	16802	28252	18.39	0.0E+00	A1982597.1	EST_HUMAN	w004d04.x1 NCI CGAP_G06 Homo sapiens cDNA clone IMAGE:2515975 3'
4216	16804	28254	1.08	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-e02 HT0707 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4216	16804	29255	1.08	0.0E+00	BE184958.1	EST_HUMAN	MR1-HIT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4221	16809		3.97	0.0E+00	BE274217.1	EST_HUMAN	6011207779F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5'
4227	16815	29282	1.12	0.0E+00	AB032951.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4227	16815	29283	1.12	0.0E+00	AB032951.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4229	16817	29265	2.51	0.0E+00	5729725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3) mRNA
4236	16824		5.9	0.0E+00	AW675599.1	EST_HUMAN	ba5104.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800095 3' similar to SW.TH12_BOVIN Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR ;
4241	16829	29279	1.14	0.0E+00	AW408788.1	EST_HUMAN	UI-HF-BMO-adv-c-02-Q-UJ.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5'
4242	16830	29280	1.64	0.0E+00	8922466	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498). mRNA
4242	16830	29281	1.64	0.0E+00	8922466	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498). mRNA
4251	16839		2.08	0.0E+00	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
4263	16849	29297	1.08	0.0E+00	AB037739.1	NT	Homo sapiens mRNA for KIAA1318 protein, partial cds
4270	16856	29303	10.06	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element ;
4270	16856	29304	10.06	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element ;
4273	16859	29308	1.01	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4286	16872	29319	1.02	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4286	16872	29320	1.02	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4301	16887	29331	1.09	0.0E+00	7661989	NT	Homo sapiens KIAA0173 gene product (KIAA0173). mRNA
4305	16891	29333	1.6	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
4305	16891	29334	1.6	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
4314	16900		0.72	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4344	16931	29372	1.17	0.0E+00	AJ003145.1	NT	Homo sapiens mRNA for olfactory receptor protein, pseudogene
4346	16933	29374	0.98	0.0E+00	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
4360	16947	29389	17.92	0.0E+00	J02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds
4375	16962	29408	0.84	0.0E+00	AW936693.1	EST_HUMAN	PM2-DT0023-080300-004-a08 DT0023 Homo sapiens cDNA
4381	16968	29415	0.59	0.0E+00	4826827	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4381	16968	29416	0.59	0.0E+00	4826827	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4383	16970	29418	4.39	0.0E+00	AF174590.1	NT	Homo sapiens F-box protein Fb14 (FBL4) mRNA, partial cds
4391	16977		2.19	0.0E+00	AI189844.1	EST_HUMAN	qd23f08.x1 Soares_placenta_8to9weeks_2NhrP8t9SW Homo sapiens cDNA clone IMAGE:1724579 3' similar to contains MER20.b2 MER20 repetitive element ;
4395	16980		4.49	0.0E+00	U14520.1	NT	Human CBFA3 (Cbfa3) gene, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4399	16984	29429	0.84	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24;q24) translocated to, 4 (MLLT4) mRNA
4418	17003	29446	0.9	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4418	17003	29447	0.9	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4425	17010	29453	1.16	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4425	17010	29454	1.16	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4433	17019	29459	11.1	0.0E+00	6912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4451	17037		1.13	0.0E+00	AF153047.2	NT	Homo sapiens gap junction protein connexin-36 (CX36) gene, complete cds
4460	17046	29489	4.6	0.0E+00	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4464	17050	29494	5.78	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4484	17050	29495	5.78	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4470	17056	29501	1.97	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4470	17056	29502	1.97	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4475	17060	29508	10.17	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4475	17060	29509	10.17	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4484	17069	29519	1.11	0.0E+00	X82338.1	NT	Homo sapiens Menkes disease gene, exon 4
4487	17072	29523	16.07	0.0E+00	4885126	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4488	17073	29524	1.73	0.0E+00	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4491	17076	29528	1.14	0.0E+00	AB037781.1	NT	Homo sapiens mRNA for KIAA1360 protein, partial cds
4526	17110	29554	1.43	0.0E+00	7019456	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4537	17121		7.31	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4545	17129	29572	1.27	0.0E+00	AJ249785.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4545	17129	29573	1.27	0.0E+00	AJ249785.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4549	17132	29579	0.58	0.0E+00	W26176.1	EST_HUMAN	24q7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4549	17132	29580	0.58	0.0E+00	W26176.1	EST_HUMAN	24q7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4555	17138	29585	6.07	0.0E+00	4506792	NT	Homo sapiens spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1) (SCA1), mRNA
4555	17138	29586	6.07	0.0E+00	4506792	NT	Homo sapiens spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1) (SCA1), mRNA
4567	17150		2.3	0.0E+00	AF200628.1	NT	Homo sapiens HPS1 gene, intron 5
4585	17168	29611	0.59	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA Cot8-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F205 5'
4585	17168	29612	0.59	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA Cot8-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F205 5'
4588	17171		0.65	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4589	17172	28618	1.48	0.0E+00	AA228126.1	EST_HUMAN	z58c04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
4589	17172	28617	1.48	0.0E+00	AA228126.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
4589	17183	28630	6.46	0.0E+00	AW084964.1	EST_HUMAN	z58c04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
4601	18007		2.1	0.0E+00	8051819	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
4603	17186	28633	0.92	0.0E+00	AI696998.1	EST_HUMAN	xc68e08.x1 NCL_CGAP_Es62 Homo sapiens cDNA clone IMAGE:2589446 3' similar to SW:AHNK_HUMAN
4607	17190		8.58	0.0E+00	AL163207.2	NT	Q09606 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK. ;
4609	17192	28638	2.41	0.0E+00	AW381570.1	EST_HUMAN	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4615	17188	28645	1.43	0.0E+00	AJ278120.1	NT	wc56b02.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2322603 3' similar to contains MER22.b2
4615	17198	28646	1.43	0.0E+00	AJ278120.1	NT	PTR5 repetitive element ;
4617	17200	28648	2.01	0.0E+00	4758467	NT	Homo sapiens chromosome 21 segment HS21C007
4618	17201	28649	3.28	0.0E+00	AF106830.1	NT	PM1-HT0305-101199-002-003 HT0305 Homo sapiens cDNA
4623	17206	28655	1.19	0.0E+00	4506952	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4628	17211	28661	1.16	0.0E+00	AF111163.1	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4628	17211	28662	1.16	0.0E+00	AF111163.1	NT	Homo sapiens sialyltransferase 8 (alpha-N-acetylneuraminase; alpha-2,8-sialyltransferase, GD3 synthase) (SIAT8) mRNA
4637	18008	28673	2.92	0.0E+00	6005973	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4642	17224	28678	4.04	0.0E+00	AF208161.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4647	17229	28685	1.66	0.0E+00	AF152337.1	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4650	17232	28689	1.5	0.0E+00	5454175	NT	Homo sapiens syncytin precursor, mRNA, complete cds
4662	17244	28698	32.6	0.0E+00	4503470	NT	Homo sapiens protocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4671	17253	28705	0.79	0.0E+00	4505016	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4675	17257	28708	1.02	0.0E+00	4503098	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4678	17261	28713	1.14	0.0E+00	4502556	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4684	17266	28716	3.03	0.0E+00	L35485.1	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4686	17268	28717	6.75	0.0E+00	7682091	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4686	17268	28717	6.75	0.0E+00	7682091	NT	Homo sapiens iduronate sulphate sulphatase (IDS) gene, complete cds
4707	17289	28733	3.17	0.0E+00	AF143314.1	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4710	17292	28736	11.37	0.0E+00	AJ245418.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
							Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4710	17292	29737	11.37	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4712	17294	29738	0.64	0.0E+00	AB018338.1	NT	Homo sapiens mRNA for KIAA0795 protein, partial cds
4718	17299		0.65	0.0E+00	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4730	17311		1.68	0.0E+00	AA174072.1	EST_HUMAN	z18g08.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3'
4732	17313		1.97	0.0E+00	7657410	NT	Homo sapiens odz (odd Ozfen-m, Drosophila) homolog 1 (ODZ1), mRNA
4734	17315		2.45	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4735	17316	29758	1.69	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4736	17317	29759	5.45	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4737	17318		1.94	0.0E+00	AB037521.1	NT	Homo sapiens gene for natriuretic protein, partial cds
4739	17320	29760	0.82	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4747	17328	29770	8.77	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4747	17328	29771	8.77	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4748	17329	29772	1.57	0.0E+00	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4757	17338	29783	1.13	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4757	17338	29784	1.13	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4763	17344	29792	12.17	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4772	17353	29805	1.21	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0035-160400-142-h05 BT0035 Homo sapiens cDNA
4773	17354	29806	1.04	0.0E+00	AA418246.1	EST_HUMAN	z98b07.s1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:767605 3'
4779	17360		2.04	0.0E+00	AF066841.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4785	17365	29816	1.09	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4785	17366	29817	1.09	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4786	17368	29818	2.54	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4786	17366	29819	2.54	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4787	17367	29820	2.04	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
4792	17371	29824	2	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4792	17371	29825	2	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4794	12809	25297	1.8	0.0E+00	T56945.1	EST_HUMAN	ye83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
4794	12809	25298	1.8	0.0E+00	T56945.1	EST_HUMAN	ye83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
4797	17375		1.1	0.0E+00	BE278730.1	EST_HUMAN	6011588935F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505521 5'
4803	17381	29831	0.64	0.0E+00	BE360050.1	EST_HUMAN	601285246F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607087 5'
4818	17398	29849	0.93	0.0E+00	5729817	NT	Homo sapiens ecotropic viral integration site 2B (EVI2B), mRNA
4818	17398	29850	0.93	0.0E+00	5729817	NT	Homo sapiens ecotropic viral integration site 2B (EVI2B), mRNA

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4819	17397	29851	1.01	0.0E+00	U56651.1	NT	Mus musculus neuraxophilin 1 (Nxph1) gene, large exon and 3' end of the intron, and partial cds
4823	17401	29854	5.32	0.0E+00	M80902.1	NT	Human AHNK nucleoprotein mRNA, 5' end
4826	17404	29857	133.49	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4828	17404	29858	133.49	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4829	17407	29861	1.32	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4832	17410	29863	1.26	0.0E+00	7662181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4851	17429		1.08	0.0E+00	X58487.1	NT	Human CYP2D7AP pseudogene for cytochrome P450 2D8
4861	17439	29888	0.83	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4861	17439	29889	0.83	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4873	17448	29899	1.3	0.0E+00	AF026801.1	NT	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-26
4876	17451	29902	0.91	0.0E+00	6677700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4876	17451	29903	0.91	0.0E+00	6677700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4879	17454	29906	0.83	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (AD013), mRNA
4879	17454	29907	0.83	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (AD013), mRNA
4900	17475	29931	1.81	0.0E+00	AW444637.1	EST_HUMAN	UI-H-B19-gly-c-04-0-UI.st NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
4907	17482	29940	1.36	0.0E+00	AF0303134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4910	17485		1.51	0.0E+00	AF083242.1	NT	Homo sapiens HSPC024-iso mRNA, complete cds
4923	17498		0.59	0.0E+00	AW339253.1	EST_HUMAN	xz89d06.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2871371 3'
4968	17542		3.81	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4971	17545	29887	1.76	0.0E+00	X87205.1	NT	M.fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa
4973	17547	29889	1.19	0.0E+00	AF084478.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSR9) mRNA, complete cds
4974	17548	29890	1.36	0.0E+00	AF097416.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4975	17549	29891	4.69	0.0E+00	4503766	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4977	17551	29893	12.25	0.0E+00	4685048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4978	17552	29894	1.19	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
4980	17554	29896	1.7	0.0E+00	8922180	NT	Homo sapiens hypothetical protein DKFZp762E1312 (DKFZp762E1312), mRNA
4983	17557	30000	5.09	0.0E+00	8923080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4987	17561	30004	1.8	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4987	17561	30005	1.8	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4989	17563	30007	1.78	0.0E+00	X94628.1	NT	H. sapiens MeCP-2 gene
4989	17563	30008	1.78	0.0E+00	X94628.1	NT	H. sapiens MeCP-2 gene

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4892	17566	30011	2.79	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4894	17566	30012	0.98	0.0E+00	7708604	NT	Homo sapiens MAGE-C2 (MAGEC2), mRNA
5005	17578	30022	0.96	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kD (TAF2I) mRNA
5015	17589	30032	1.75	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
5016	17590	30033	0.64	0.0E+00	AB037864.1	NT	Homo sapiens mRNA for KIAA1443 protein, partial cds
5017	17591	30034	1.32	0.0E+00	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
5018	17592	30035	2.53	0.0E+00	6677648	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zik1), mRNA
5019	17593	30036	2.01	0.0E+00	5174560	NT	Homo sapiens meningo-expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA
5021	17595	30038	2.81	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
5023	17597	30040	0.98	0.0E+00	Y16723.1	NT	Homo sapiens gene encoding filensin, exon 8
5024	17598	30041	1.26	0.0E+00	5174560	NT	Homo sapiens meningo-expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA
5024	17598	30042	1.26	0.0E+00	5174560	NT	Homo sapiens meningo-expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA
5026	17600	30045	16.3	0.0E+00	AF055068.1	NT	Homo sapiens MHC class 1 region
5028	17602		2.87	0.0E+00	4505508	NT	Homo sapiens oploid receptor, delta 1 (OPRD1) mRNA
5029	17603	30048	3.33	0.0E+00	AF091711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
5041	17614	30058	2.27	0.0E+00	4503984	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDPS) mRNA
5043	17616	30060	3.9	0.0E+00	4557472	NT	Homo sapiens chloride channel 5 (nephrolithiasis 2, X-linked, Dent disease) (CLCN5) mRNA
5043	17616	30061	3.9	0.0E+00	4557472	NT	Homo sapiens chloride channel 5 (nephrolithiasis 2, X-linked, Dent disease) (CLCN5) mRNA
5058	17631		0.58	0.0E+00	AI291129.1	EST_HUMAN	q11505.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881921 3' similar to TR:Q61632
5061	17634	30078	2.85	0.0E+00	AB006625.1	NT	EN-2/LACZ FUSION PROTEIN :
5061	17634	30077	2.85	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
5072	17645	30087	0.92	0.0E+00	AB028988.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5088	17661	30101	1.38	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5093	17666	30105	0.57	0.0E+00	7662319	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
5103	17675	30115	2.12	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
5108	17680		7.33	0.0E+00	U14867.1	NT	Human ribosomal protein L21 mRNA, complete cds
5118	17690	30128	1.25	0.0E+00	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
5121	17693		2.86	0.0E+00	BE408863.1	EST_HUMAN	601303729F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 5'
5124	17696	30133	3.82	0.0E+00	4758189	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
5135	17707	30139	1.19	0.0E+00	AB028966.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5152	17722	30152	1.89	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5152	17722	30153	1.89	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5170	17738	30165	1.07	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN;
5170	17738	30166	1.07	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN;
5170	17738	30167	1.07	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN;
5172	17739	30168	0.96	0.0E+00	AF161463.1	NT	Homo sapiens HSPC114 mRNA, complete cds
5172	17739	30169	0.96	0.0E+00	AF161463.1	NT	Homo sapiens HSPC114 mRNA, complete cds
5183	12887	25374	0.58	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5188	17753		1.72	0.0E+00	4758225	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5199	17764	30189	0.94	0.0E+00	AF016705.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 3
5204	17769	30192	0.87	0.0E+00	U53588.1	NT	Homo sapiens MHC class 1 region
5211	17776		1.3	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5214	17779		29.82	0.0E+00	D50857.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
5245	17809	30231	3.36	0.0E+00	X52988.1	NT	Bacillus amyloqueliciens sacB gene for levansucrase (EC 2.4.1.10)
5266	17828	30252	1.23	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5266	17828	30253	1.23	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5287	17829	30254	0.96	0.0E+00	5454153	NT	Homo sapiens cyclophilin (USA-CYP) mRNA
5282	17844	30271	0.95	0.0E+00	6677700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
5298	17860	30285	0.77	0.0E+00	5902055	NT	Homo sapiens ring finger protein (RNF), mRNA
5300	17882	30286	1.03	0.0E+00	M10905.1	NT	Human cellular fibronectin mRNA
5300	17882	30287	1.03	0.0E+00	M10905.1	NT	Human cellular fibronectin mRNA
5301	17863	30288	0.93	0.0E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP73) gene, complete cds
5308	17870	30282	0.84	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
5326	17888	30304	0.67	0.0E+00	5602091	NT	Homo sapiens solute carrier family 5 (inositol transporters), member 3 (SLC5A3), mRNA
5333	17894	30308	1.1	0.0E+00	L35475.1	NT	Human olfactory receptor-like gene, complete cds
5333	17894	30309	1.1	0.0E+00	L35475.1	NT	Human olfactory receptor-like gene, complete cds
5340	17901	30318	0.81	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5340	17901	30317	0.81	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5341	17902	30318	0.6	0.0E+00	7662421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5347	17907	30322	25.99	0.0E+00	J02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds
5355	17919	30330	0.99	0.0E+00	U71801.1	NT	Human zinc finger protein zfp47 (zf47) mRNA, partial cds
5357	17917	30332	1.05	0.0E+00	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
5365	17925	30339	9.37	0.0E+00	M19928.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 22 through 29
5373	17932	30346	11.28	0.0E+00	5360213	NT	Homo sapiens glypican 3 (GPC3) mRNA
5374	17933	30347	1.1	0.0E+00	4826777	NT	Homo sapiens jumani (mouse) homolog (JMU) mRNA
5377	17936	30349	0.98	0.0E+00	AE000327.1	NT	Escherichia coli K-12 MG1655 section 217 of 400 of the complete genome
5385	17944	30357	8.06	0.0E+00	4502152	NT	Homo sapiens apolipoprotein B (including Ag(x) antigen) (APOB) mRNA
5399	17957	30368	1.01	0.0E+00	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
5430	17987	30391	1.58	0.0E+00	4826977	NT	Homo sapiens reelin (RELN) mRNA
5451	18020		3.55	0.0E+00	AF03093.1	NT	Homo sapiens acetylase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15
5459	18094	30411	2.28	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5459	18094	30412	2.28	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5478	18112	30521	1.27	0.0E+00	AI934964.1	EST_HUMAN	wp08g08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA IMAGE:2464094 3'
5481	18115	30524	2.18	0.0E+00	9256579	NT	Homo sapiens protocadherin alpha 13 (PCDH13), mRNA
5495	18129	30537	3.75	0.0E+00	BE931080.1	EST_HUMAN	RC3-GN0076-310800-013-803 GN0076 Homo sapiens cDNA
5499	18133	30541	3.31	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5499	18133	30542	3.31	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5506	18139	30550	2.06	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5506	18139	30551	2.06	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5584	18215	30684	5.94	0.0E+00	BE075488.1	EST_HUMAN	710c06.x1 NCI_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:3294250 3'
5585	18216				h169a02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3165104 3' similar to SW.Y054_HUMAN		
5585	18216	30665	1.67	0.0E+00	BE220763.1	EST_HUMAN	P42694 HYPOTHETICAL PROTEIN KIAA0054 ;
5588	18217	30666	1.58	0.0E+00	BE704412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5588	18217	30667	1.58	0.0E+00	BE704412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5589	18220	30670	7.35	0.0E+00	M29908.1	NT	Homo sapiens eosinophil peroxidase (EPP) gene, exon 7
5600	24746	30678	4.43	0.0E+00	11421038	NT	Homo sapiens Sp4 transcription factor (SP4), mRNA
5609	18238				BF665992.1	EST_HUMAN	602118928F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4276254 5'
5614	18243	30694	0.8	0.0E+00	BE538857.1	EST_HUMAN	601061489F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447839 5'
5622	18251	30719	1.49	0.0E+00	BE292784.1	EST_HUMAN	601105891F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2986310 5'
5626	18255	30724	2.5	0.0E+00	BF526328.1	EST_HUMAN	602071372F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4214272 5'
5626	18255	30725	2.5	0.0E+00	BF526328.1	EST_HUMAN	602071372F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4214272 5'
5645	19506	32325	2.91	0.0E+00	4557364	NT	Homo sapiens Bloom syndrome (BLM) mRNA
5648	18276	30751	0.9	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5848	18276	30752	0.9	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
5852	18278	30756	4.93	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5852	18279	30757	4.93	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5865	18292	30771	1.42	0.0E+00	D26535.1	NT	Human gene for dihydrodipicolinate succinyltransferase, complete cds (exon 1-15)
5865	18292	30772	1.42	0.0E+00	D26535.1	NT	Human gene for dihydrodipicolinate succinyltransferase, complete cds (exon 1-15)
5860	18307	30803	1.88	0.0E+00	11420819	NT	Homo sapiens ciliary receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5866	18312	30809	0.86	0.0E+00	Z38133.1	NT	H. sapiens mRNA for myosin
5704	18330	30833	0.89	0.0E+00	D61564.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05
5704	18330	30834	0.89	0.0E+00	D61564.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05
5707	18333	30838	5.12	0.0E+00	BF529831.1	EST_HUMAN	602042322F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4178988 5'
5707	18333	30839	5.12	0.0E+00	BF529831.1	EST_HUMAN	602042322F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4178988 5'
5712	18338	30843	2.7	0.0E+00	BF513139.1	EST_HUMAN	601897658F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5'
5723	18349	31052	4.03	0.0E+00	11434392	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
5753	18379	31090	1.48	0.0E+00	BE260777.1	EST_HUMAN	601150262F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502809 5'
5762	18398		4.66	0.0E+00	AW897316.1	EST_HUMAN	MRO-SN0037-030400-001-h07 SN0037 Homo sapiens cDNA
5775	18400	31114	2.42	0.0E+00	BE292889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987803 5'
5775	18400	31115	2.42	0.0E+00	BE292889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987803 5'
5783	18418	31133	1.67	0.0E+00	11420819	NT	Homo sapiens ciliary receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5793	18418	31134	1.67	0.0E+00	11420819	NT	Homo sapiens ciliary receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5800	18425	31142	4.39	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5800	18425	31143	4.39	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5806	18431	31151	2.56	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5806	18431	31152	2.56	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5833	18457	31176	0.72	0.0E+00	A1195515.1	EST_HUMAN	q984g10.x1 Soares_placenta_8to9weeks_2NBHP8b6W Homo sapiens cDNA clone IMAGE:1757730 3'
5837	18461	31184	6.38	0.0E+00	M85719.1	EST_HUMAN	similar to SW:CADC_HUMAN P55289 BRAIN-CADHERIN PRECURSOR ;
5844	18468	31193	6.29	0.0E+00	AW405472.1	EST_HUMAN	EST02238 Fetal brain, Stralagene (cat#930206) Homo sapiens cDNA clone HFBM48
5856	18479	31202	1.35	0.0E+00	Z26269.1	NT	UHF-BLO-ath-4-02-0-JL1.1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061658 5'
5866	18486	31212	1.78	0.0E+00	AW361877.1	EST_HUMAN	H. sapiens isoform 1 gene for L-type calcium channel, exon 14 and 15
5866	18488	31213	1.78	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091289-007-h05 CT0263 Homo sapiens cDNA
5866	18488	31214	1.78	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091289-007-h05 CT0263 Homo sapiens cDNA
5870	18492	31219	1.91	0.0E+00	U36281.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 13

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5897	18519	31244	1.02	0.0E+00	AB046881.1	NT	Homo sapiens mRNA for KIAA1641 protein, partial cds
5951	18573	31305	1.46	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5951	18573	31306	1.46	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5958	18580	31316	1.29	0.0E+00	AI207816.1	EST_HUMAN	HA2981 Human fetal liver cDNA library Homo sapiens cDNA
5975	18595	31330	4.89	0.0E+00	11416801	NT	Homo sapiens protocadherin beta 2 (PCDH2), mRNA
5980	18600	31333	1.09	0.0E+00	BE791173.1	EST_HUMAN	601584032F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938551 5'
5987	18607	31341	1.29	0.0E+00	9998943	NT	Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), mRNA
5988	18608	31342	6.36	0.0E+00	BE560082.1	EST_HUMAN	601345141F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677843 5'
5989	18609	31343	1.48	0.0E+00	10048478	NT	Mus musculus aczonin (Acz), mRNA
5990	18610	31344	3.25	0.0E+00	U86961.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5990	18610	31345	3.25	0.0E+00	U86961.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
6008	18628	31363	2.23	0.0E+00	BF338835.1	EST_HUMAN	602036272F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4184321 5'
6010	18630	31365	0.86	0.0E+00	AF142821.1	NT	Homo sapiens calcium channel gamma 5 subunit (CACNG5) gene, exon 4 and complete cds
6011	18631	31368	3.17	0.0E+00	BE273983.1	EST_HUMAN	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
6020	18639	31379	1.22	0.0E+00	BE503098.1	EST_HUMAN	h283411.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214581 3' similar to TR:Q62084 Q62084
6024	18643	31385	2.27	0.0E+00	BF569905.1	EST_HUMAN	PHOSPHOLIPASE C NEIGHBORING 1
6028	18647	31388	1.14	0.0E+00	AA454642.1	EST_HUMAN	z699d06.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811883 3'
6050	18677	31419	3.11	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6062	18678	31421	2.35	0.0E+00	BE826144.1	EST_HUMAN	RC5-ET0027-210600-022-G10 ET0027 Homo sapiens cDNA
6066	18683	31425	1.25	0.0E+00	BE956636.1	EST_HUMAN	601645287F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930453 5'
6083	18700	31447	0.9	0.0E+00	AW278760.1	EST_HUMAN	xp65f03.x1 NCI_CGAP_Ov69 Homo sapiens cDNA clone IMAGE:2745245 3' similar to TR:P78335 P78335
6093	18709	31457	0.96	0.0E+00	BF031742.1	EST_HUMAN	GUANYLATE KINASE ASSOCIATED PROTEIN 1
6093	18709	31458	0.96	0.0E+00	BF031742.1	EST_HUMAN	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6104	18720	31473	1.03	0.0E+00	AW470846.1	EST_HUMAN	ha34406.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875595 3' similar to TR:Q9Z1N3
6115	18731	31483	1.1	0.0E+00	BF155670.1	EST_HUMAN	QV4-HT0894-290900-399-a10 HT0894 Homo sapiens cDNA
6115	18731	31484	1.1	0.0E+00	BF155670.1	EST_HUMAN	QV4-HT0894-290900-399-a10 HT0894 Homo sapiens cDNA
6123	18738	31490	1.38	0.0E+00	W33069.1	EST_HUMAN	zc08h06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
6123	18738	31491	1.38	0.0E+00	W33069.1	EST_HUMAN	zc08h06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
6124	18739		2.2	0.0E+00	AF012618.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6127	18742	31495	3.14	0.0E+00	BE280197.1	EST_HUMAN	601158315F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505323 5'
6133	18747	31503	1.88	0.0E+00	BE889610.1	EST_HUMAN	601512630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5'
6148	18761	31520	1.46	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6148	18761	31521	1.46	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6149	18762	31522	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6149	18762	31523	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6149	18762	31524	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6164	24758	31540	10.16	0.0E+00	9789986	NT	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA
6167	18779	31543	1.38	0.0E+00	AA193506.1	EST_HUMAN	z40h01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:663905 5' similar to SW:YY05_HUMAN P42894 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
6167	18779	31544	1.38	0.0E+00	AA193506.1	EST_HUMAN	z40h01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:663905 5' similar to SW:YY05_HUMAN P42894 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
6189	18789	31568	12.83	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6189	18789	31569	12.83	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6229	18838	31611	1.35	0.0E+00	BE258330.1	EST_HUMAN	601114823F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355585 5'
6238	18847	31618	1.64	0.0E+00	BE156561.1	EST_HUMAN	QV0-HT0368-090200-099-e09 HT0368 Homo sapiens cDNA
6280	18888	31657	1.54	0.0E+00	BE378007.1	EST_HUMAN	601236276F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608490 5'
6288	18894	31663	1.23	0.0E+00	AU137772.1	EST_HUMAN	AU137772 PLACE1 Homo sapiens cDNA clone PLACE1007201 5'
6306	18913	31687	3.42	0.0E+00	U45982.1	NT	Human G protein-coupled receptor GPR-9-6 gene, complete cds
6334	18940	31717	4.13	0.0E+00	AA204740.1	EST_HUMAN	zq81d03.r1 Stratagene INT neuron (#937233) Homo sapiens cDNA clone IMAGE:648005 5' similar to TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN. ;
6335	18941	31718	3.66	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6335	18941	31719	3.66	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6354	18959	31737	0.7	0.0E+00	U07223.1	NT	Human beta2-chimerin mRNA, complete cds
6371	18975	31753	1.87	0.0E+00	11426367	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8), mRNA
6375	18979	31758	3.62	0.0E+00	BE257173.1	EST_HUMAN	601109532F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350622 5'
6388	18991		0.94	0.0E+00	AI886048.1	EST_HUMAN	tt911f10.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2248939 3' similar to TR:Q14839 Q14839 MI-2 PROTEIN. ;
6392	18995	31774	1.39	0.0E+00	L35930.1	NT	Human anion exchanger (AE1) gene, exons 1-20
6401	19004	31782	1.03	0.0E+00	BE797385.1	EST_HUMAN	601587971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6401	19004	31783	1.03	0.0E+00	BE797385.1	EST_HUMAN	601587971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6411	19014	31796	0.96	0.0E+00	BF357123.1	EST_HUMAN	MRO-HT0923-220800-102-b05 HT0923 Homo sapiens cDNA
6419	19022	31806	1.53	0.0E+00	11435630	NT	Homo sapiens peptide transporter 3 (LOC51296), mRNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6428	19031	31814	0.96	0.0E+00	D55949.1	NT	Human mRNA for alpha mannosidase II isozyme, complete cds
6442	19044	31832	1.11	0.0E+00	AW178142.1	EST_HUMAN	IL3-HT00082-010989-014-A04 HT0082 Homo sapiens cDNA
6462	19063	31848	0.78	0.0E+00	BE674544.1	EST_HUMAN	7602c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3281302 3' similar to SW:Y176_HUMAN
6466	19067	31853	0.96	0.0E+00	7682039	NT	Q14681 HYPOTHETICAL PROTEIN KIAA0176 ;
6480	19081		8.14	0.0E+00	AV650020.1	EST_HUMAN	Homo sapiens KIAA0285 gene product (KIAA0285), mRNA
6487	19088	31871	3.19	0.0E+00	AW575598.1	EST_HUMAN	AV650020 GLC Homo sapiens cDNA clone GLCAD09 3'
6490	19091	31874	5.26	0.0E+00	H01255.1	EST_HUMAN	UI-HF-BLO-acc-g-12-0-UI.t1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058751 3'
6501	19101	31886	3.3	0.0E+00	X15377.1	NT	y27b03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149933 5'
6503	19103	31888	1.02	0.0E+00	A1612841.1	EST_HUMAN	Human gene for the light and heavy chains of myeloperoxidase
6509	19109	31894	4.19	0.0E+00	BE735989.1	EST_HUMAN	b27d08.x1 NCI_CGAP_OV45 Homo sapiens cDNA clone IMAGE:2292887 3' similar to SW:NTCS_HUMAN
6509	19109	31895	4.19	0.0E+00	BE735989.1	EST_HUMAN	P53796 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 2 ;
6513	19113	31901	0.83	0.0E+00	AW748593.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
6513	19113	31902	0.83	0.0E+00	AW748593.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
6515	19115	31904	167.16	0.0E+00	AU119245.1	EST_HUMAN	MRO-BT0264-221199-002-f11 BT0264 Homo sapiens cDNA
6515	19115	31905	167.16	0.0E+00	AU119245.1	EST_HUMAN	MRO-BT0264-221199-002-f11 BT0264 Homo sapiens cDNA
6519	19119	31910	0.83	0.0E+00	BE780453.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
6520	19120	31911	0.89	0.0E+00	X92217.1	NT	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
6531	19131	31925	1.96	0.0E+00	A1899483.1	EST_HUMAN	601468712F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3871899 5'
6543	19142	31934	2.84	0.0E+00	BE283153.1	EST_HUMAN	H. sapiens germline immunoglobulin heavy chain, variable region, (13-2)
6543	19142	31935	2.84	0.0E+00	BE283153.1	EST_HUMAN	ws25c07.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2498220 3'
6606	19203	32009	1.05	0.0E+00	AW406348.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987963 5'
6606	19203	32010	1.05	0.0E+00	AW406348.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987963 5'
6634	19230	32034	5.36	0.0E+00	AV719444.1	EST_HUMAN	UI-HF-BLO-acc-h-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058931 5'
6642	19238	32040	1.02	0.0E+00	BE898340.1	EST_HUMAN	UI-HF-BLO-acc-h-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058931 5'
6642	19238	32041	1.02	0.0E+00	BE898340.1	EST_HUMAN	AV719444 GLC Homo sapiens cDNA clone GLOEHC08 5'
6645	19241	32044	2.16	0.0E+00	AF190860.1	NT	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6648	19244	32046	1.05	0.0E+00	11420658	NT	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6655	19251	32053	3.35	0.0E+00	AW163640.1	EST_HUMAN	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant CavT.1a (CACNA1G) mRNA, complete cds
6655	19251	32054	3.35	0.0E+00	AW163640.1	EST_HUMAN	Homo sapiens transformation/transcription domain-associated protein (TRRAP), mRNA
							au96h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206 ;
							au86h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206 ;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6659	19255	32057	0.97	0.0E+00	W37163.1	EST_HUMAN	zb20e06.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:302626 5' similar to SW:ZN45_HUMAN Q02386 ZINC FINGER PROTEIN 45;
6659	19255	32058	0.97	0.0E+00	W37163.1	EST_HUMAN	zb20e06.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:302626 5' similar to SW:ZN45_HUMAN Q02386 ZINC FINGER PROTEIN 45;
6671	19267	32071	1.08	0.0E+00	BE794853.1	EST_HUMAN	601589371F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943504 5'
6678	19274	32078	4.45	0.0E+00	BE799873.1	EST_HUMAN	601587561F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 5'
6682	19278	32081	7.35	0.0E+00	BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6682	19278	32082	7.35	0.0E+00	BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6689	19285	32088	3.81	0.0E+00	L24493.1	NT	Human antigen CD27 gene, exons 1-2
6694	19290	32092	2.03	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6694	19290	32093	2.03	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6700	19296	32100	3.54	0.0E+00	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
6703	19298	32102	3.88	0.0E+00	A1638412.1	EST_HUMAN	tt311f1.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE
6704	19299	32103	1.36	0.0E+00	L32832.1	NT	P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR. ;
6714	19308	32112	0.78	0.0E+00	AW505430.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A), mRNA, complete cds
6716	19310	32113	3.78	0.0E+00	AA434584.1	EST_HUMAN	UI-HF-BNO-ama-c-01-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081217 5'
6730	19324	32133	1.08	0.0E+00	BF217200.1	EST_HUMAN	zw52c03.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:773668 5'
6734	19328	32133	1.72	0.0E+00	BE925875.1	EST_HUMAN	601885317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103693 5'
6774	19366	32178	1.98	0.0E+00	AU125928.1	EST_HUMAN	QV3-BN0047-300800-278-c08 BN0047 Homo sapiens cDNA
6776	19368	32181	0.73	0.0E+00	BE701434.1	EST_HUMAN	AU125928 NT2RM4 Homo sapiens cDNA clone NT2RM4002430 5'
6776	19368	32181	0.73	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA
6795	19388	32202	1.28	0.0E+00	BE142363.1	EST_HUMAN	PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA
6815	19406	32222	0.91	0.0E+00	BE006012.1	EST_HUMAN	CM0-HT0143-270999-082-d08 HT0143 Homo sapiens cDNA
6815	19406	32223	0.91	0.0E+00	BE006012.1	EST_HUMAN	RCO-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
6835	19425	32241	7.25	0.0E+00	BE169131.1	EST_HUMAN	RCO-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
6837	19427	32243	1.62	0.0E+00	BF085667.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
6873	19607	32441	3.11	0.0E+00	AA190755.1	EST_HUMAN	IL5-GN0032-180900-145-d07 GN0032 Homo sapiens cDNA
6882	19617	32452	0.99	0.0E+00	U39573.1	NT	zp88e03.r1 Strategene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627292 5'
6885	19620	32454	0.72	0.0E+00	BE671987.1	EST_HUMAN	Human salivary peroxidase mRNA, complete cds
6892	19626	32482	6.2	0.0E+00	A1940621.1	EST_HUMAN	7a49b07.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3222037 3' similar to TR:Q9Z285 Q9Z285
6892	19626	32463	6.2	0.0E+00	A1940621.1	EST_HUMAN	TEKTN. ;
6902	19638	32474	2.67	0.0E+00	11435628	NT	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
							IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
							Homo sapiens CD6 antigen (CD6), mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6913	19572	32401	0.84	0.0E+00	AL042443.1	EST_HUMAN	DKFZp434D2021_11_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2021 5'
6916	19575	32404	0.84	0.0E+00	A168270.1	EST_HUMAN	co10d01.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1565761 3' similar to
6921	19580	32409	0.89	0.0E+00	BE734087.1	EST_HUMAN	TR:Q26623 Q26623 TEKIN C1.;
6936	18044	30466	1.22	0.0E+00	BE568381.1	EST_HUMAN	601567370F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842080 5'
6943	18051	30473	13.34	0.0E+00	BE667889.1	EST_HUMAN	601339977F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682287 5'
6943	18051	30473	13.34	0.0E+00	BE667889.1	EST_HUMAN	601443687F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
6943	18051	30474	13.34	0.0E+00	BE667889.1	EST_HUMAN	601443687F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
6948	19525	32347	1.75	0.0E+00	BE550162.1	EST_HUMAN	7b49f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95.;
6948	19525	32348	1.75	0.0E+00	BE550162.1	EST_HUMAN	7b49f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN
6970	19547	32371	2.55	0.0E+00	BF086376.1	EST_HUMAN	Q08379 GOLGIN-95.;
6977	19563	32378	2.01	0.0E+00	AA195106.1	EST_HUMAN	CM1-HT0877-060900-397-g11 HT0877 Homo sapiens cDNA
6984	19482		10.79	0.0E+00	11034910	NT	Z344g03.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665332 5'
6986	19484	32305	1.11	0.0E+00	11431474	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
7001	19499	32319	2.35	0.0E+00	BF569905.1	EST_HUMAN	Homo sapiens sodium channel, nonvoltage-gated 1, beta (Liddle syndrome)(SCNN1B), mRNA
7008	19506	32325	0.75	0.0E+00	4557384	NT	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7016	19514		2.49	0.0E+00	J03069.1	NT	Homo sapiens Bloom syndrome (BLM) mRNA
7024	19558	32383	4.16	0.0E+00	AF217289.1	NT	Human MYGL2 gene, complete cds
7024	19558	32384	4.16	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7025	19559	32385	1	0.0E+00	M38113.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7036	18056	30479	2.94	0.0E+00	11420775	NT	Human neurofibromatosis type 1 gene, exon x8
7039	18059	30481	0.69	0.0E+00	BE266708.1	EST_HUMAN	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA
7057	18076	30429	1.11	0.0E+00	AU118478.1	EST_HUMAN	601115515F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356330 5'
7059	18078	30432	4.93	0.0E+00	BE262941.1	EST_HUMAN	AU118479 HEMBA1 Homo sapiens cDNA clone HEMBA1003979 5'
7080	18079	30433	2.1	0.0E+00	Z37976.1	NT	601148954F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3501829 5'
7080	18079	30434	2.1	0.0E+00	Z37976.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7081	18080	30435	2.68	0.0E+00	AF257737.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7081	18080	30436	2.68	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7088	18085	30441	1.44	0.0E+00	AF310105.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7071	19643	32480	0.68	0.0E+00	BE762770.1	EST_HUMAN	Homo sapiens NALP1 mRNA, complete cds
7075	19647	32485	2.59	0.0E+00	BF569905.1	EST_HUMAN	QV3-NT0022-140600-223-f01 NT0022 Homo sapiens cDNA
7079	19651	32480	3.92	0.0E+00	L01978.1	NT	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
							Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7089	19660	32499	0.82	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D2211 5'
7089	19660	32500	0.82	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D2211 5'
7095	19666	32505	8.1	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7100	19670	32509	2.1	0.0E+00	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
7132	19472	32292	1.1	0.0E+00	AL049784.1	NT	Novel human gene mapping to chromosome 13
7167	19699	32546	0.89	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7167	19699	32547	0.89	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7173	19705	32553	1.43	0.0E+00	AW954806.1	EST_HUMAN	EST366876 MAGE resequences, MAGEC Homo sapiens cDNA
7174	19706	32554	1.08	0.0E+00	BE254103.1	EST_HUMAN	601113958F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3354566 5'
7187	19719	32566	1.23	0.0E+00	L01973.1	NT	Human type VI sodium channel alpha polypeptide (SCN4A) gene, exon 14
7195	19726	32576	0.71	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
7195	19726	32577	0.71	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
7201	19732	32584	1.97	0.0E+00	AU133213.1	EST_HUMAN	AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP4001556 5'
7216	19747	32603	0.86	0.0E+00	11428081	NT	Homo sapiens membrane protein CH1 (CH1), mRNA
7221	19752		2.39	0.0E+00	AU143706.1	EST_HUMAN	AU143706 Y79AA1 Homo sapiens cDNA clone Y79AA1002365 5'
7222	19753	32608	1.2	0.0E+00	4758839	NT	Homo sapiens netrin 1 (NTN1), mRNA
7231	19762	32617	1.83	0.0E+00	BE881286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7231	19762	32618	1.83	0.0E+00	BE881286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7252	18094	30411	2.27	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7252	18094	30412	2.27	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7263	19791	32646	0.78	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'
7263	19791	32647	0.78	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'
7274	19802	32659	4.67	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7274	19802	32660	4.67	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7302	19830	32688	28.85	0.0E+00	A1128344.1	EST_HUMAN	qc67a07.x1 Soares_placenta_8b9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW_ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR ; contains element HGR repetitive element
7302	19830	32689	28.85	0.0E+00	A1128344.1	EST_HUMAN	qc67a07.x1 Soares_placenta_8b9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW_ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR ; contains element HGR repetitive element
7304	19832	32691	4.05	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7304	19832	32692	4.05	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7307	19835		14.08	0.0E+00	BF337375.1	EST_HUMAN	602035089F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4182839 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7309	19837	32695	3.39	0.0E+00	AA128453.1	EST_HUMAN	zn60f09.r1 Stratigene muscle 937209 Homo sapiens cDNA clone IMAGE:582601 5' similar to TR:G806562 G806962 NEBULIN ;
7314	19841	32701	0.9	0.0E+00	AL078497.1	EST_HUMAN	DKFZp434B0226_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0226 5'
7314	19841	32702	0.9	0.0E+00	AL078497.1	EST_HUMAN	DKFZp434B0226_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0226 5'
7349	19875	32741	1.2	0.0E+00	BE295499.1	EST_HUMAN	601174576F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528784 5'
7351	19877	32742	0.86	0.0E+00	11427965	NT	Homo sapiens hypothetical protein (FLJ20281), mRNA
7354	19880		2.37	0.0E+00	AU118607.1	EST_HUMAN	AU118607 HEMBA1 Homo sapiens cDNA clone HEMBA1003989 5'
7355	19881	32745	1.77	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7355	19881	32746	1.77	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7365	19891	32754	0.99	0.0E+00	AF245505.1	NT	Homo sapiens adican mRNA, complete cds
7371	19897	32758	8.87	0.0E+00	X70172.1	NT	H. sapiens DNA for ZNGP2 pseudogene, exon 4
7373	19899	32760	8.18	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7373	19899	32761	8.18	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7385	19911	32775	0.98	0.0E+00	AW955503.1	EST_HUMAN	EST368573 MAGC resequences, MAGD Homo sapiens cDNA
7387	19913	32777	3.25	0.0E+00	AW950516.1	EST_HUMAN	EST362598 MAGC resequences, MAGA Homo sapiens cDNA
7408	19933	32797	1.04	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7408	19933	32798	1.04	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7408	19933	32799	1.04	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7425	19949		0.78	0.0E+00	M90354.1	NT	Human BTF3 protein homologue gene, complete cds
7426	19950	32815	0.71	0.0E+00	BE408293.1	EST_HUMAN	601302879F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3637434 5'
7451	19975		1.16	0.0E+00	R87430.1	EST_HUMAN	yn88h10.r1 Scores adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:160051 5'
7452	19978	32841	2.37	0.0E+00	AW239328.1	EST_HUMAN	xb39a03.y1 NCI_CGAP_Lu31 Homo sapiens cDNA clone IMAGE:2578640 5' similar to TR:Q08050 Q08050
7468	19990		1.19	0.0E+00	AU117553.1	EST_HUMAN	HNF3/FH TRANSCRIPTION FACTOR GENESIS ;
7470	19992	32855	3.61	0.0E+00	11427135	NT	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA
7482	20004	32869	0.88	0.0E+00	AA211663.1	EST_HUMAN	zn5802.r1 Stratigene muscle 937209 Homo sapiens cDNA clone IMAGE:582203 5' similar to gb:X03740
7488	20011	32877	0.82	0.0E+00	L32832.1	NT	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
7509	20030	32894	0.98	0.0E+00	BF306996.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
7509	20030	32895	0.98	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7517	20037	32905	1.48	0.0E+00	AU118767.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7561	20078	32952	4.53	0.0E+00	AI752561.1	EST_HUMAN	AU118767 HEMBA1 Homo sapiens cDNA clone HEMBA1004314 5'
							cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7561	20078	32853	4.53	0.0E+00	AI752561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
7631	20143	33023	1.45	0.0E+00	AF084205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7631	20143	33024	1.45	0.0E+00	AF084205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7639	20151	33035	1.03	0.0E+00	U74315.1	EST_HUMAN	HSU74315 Human chromosome 14 Homo sapiens cDNA clone 1-4
7653	20165	33052	0.87	0.0E+00	BE439545.1	EST_HUMAN	HTM1-183F1 HTM1 Homo sapiens cDNA
7654	20166	33053	1.08	0.0E+00	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
7681	20192	33081	2.91	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7687	20196	33084	1	0.0E+00	N76126.1	EST_HUMAN	za86d05.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299456 3'
7691	20200	33087	5.26	0.0E+00	BF217805.1	EST_HUMAN	60185465F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103728 5'
7699	20208	33095	4.27	0.0E+00	AU129622.1	EST_HUMAN	AU129622 NT2RP2 Homo sapiens cDNA clone NT2RP2005913 5'
7715	24789	33111	1.1	0.0E+00	AW068274.1	EST_HUMAN	cr42d09.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42d09 3'
7715	24789	33112	1.1	0.0E+00	AW068274.1	EST_HUMAN	cr42d09.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42d09 3'
7718	20226	33114	6.48	0.0E+00	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC-1), member 3 (ABCA3), mRNA
7725	20233	33121	1.01	0.0E+00	AV758467.1	EST_HUMAN	AV758467 BM Homo sapiens cDNA clone BMFBGG05 5'
7726	20234	33122	6.72	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
7728	20234	33123	6.72	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
7727	20235	33124	0.81	0.0E+00	6912461	NT	Homo sapiens atrophin-1 Interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
7727	20235	33125	0.81	0.0E+00	6912461	NT	Homo sapiens atrophin-1 Interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
7728	20238	33126	1.02	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
7728	20236	33127	1.02	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
7757	20265	33160	1.73	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
7757	20265	33161	1.73	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
7767	20275	33173	0.8	0.0E+00	AW402189.1	EST_HUMAN	U1-HF-BK0-aet-c-07-QJ1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3054733 5'
7776	20285	33182	0.9	0.0E+00	AW968044.1	EST_HUMAN	EST380119 IMAGE resequences, MAGJ Homo sapiens cDNA
7795	20338	33246	1.97	0.0E+00	AU133187.1	EST_HUMAN	AU133187 NT2RP4 Homo sapiens cDNA clone NT2RP4001507 5'
7840	20382		0.51	0.0E+00	BF217200.1	EST_HUMAN	60185317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103693 5'
7853	20395	33300	0.85	0.0E+00	BE313013.1	EST_HUMAN	601150347F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503050 5'
7864	20406	33313	1.18	0.0E+00	AA149791.1	EST_HUMAN	z001c06.r1 Stragene cdon (#937204) Homo sapiens cDNA clone IMAGE:566410 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7877	20419	33327	0.8	0.0E+00	BF026628.1	EST_HUMAN	601872310F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955131 5'
7890	20432	33341	0.51	0.0E+00	AA017021.1	EST_HUMAN	2a33h08.r1 Soares refina N2b4HR Homo sapiens cDNA clone IMAGE:360831 5'
7907	20449	33358	2.32	0.0E+00	BE736048.1	EST_HUMAN	601305658F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639903 5'
7923	20465	33372	3.32	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
7923	20465	33373	3.32	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
7953	20495	33404	0.77	0.0E+00	AW674581.1	EST_HUMAN	bb34d02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2985123 5' similar to TR:O64652 O64652
7953	20495	33405	0.77	0.0E+00	AW674581.1	EST_HUMAN	F17K2.26 PROTEIN.; F17K2.26 PROTEIN.;
7960	20502	33411	3.05	0.0E+00	AA397551.1	EST_HUMAN	z81b04.r1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
7962	20504	33412	0.83	0.0E+00	AW387131.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
7965	20507	33413	0.53	0.0E+00	AB020691.1	NT	MRO-ST0031-061099-003-e11 ST0031 Homo sapiens cDNA
7966	20508	33414	7.21	0.0E+00	AU142402.1	EST_HUMAN	Homo sapiens mRNA for KIAA0884 protein, partial cds
7970	20512	33418	0.87	0.0E+00	BE388421.1	EST_HUMAN	AU142402 Y79AA1 Homo sapiens cDNA clone Y79AA1000277 5'
7970	20512	33419	0.97	0.0E+00	BE388421.1	EST_HUMAN	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
7985	20527	33433	0.52	0.0E+00	7657276	NT	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
7987	20529	33435	0.87	0.0E+00	W95278.1	EST_HUMAN	Homo sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 (KIR2DS1), mRNA
7987	20529	33436	0.87	0.0E+00	W95278.1	EST_HUMAN	z805d01.r1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:358081 5'
7989	20531	33438	17.03	0.0E+00	BF673096.1	EST_HUMAN	z805d01.r1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:358081 5'
7993	20535	33453	1.38	0.0E+00	AU134114.1	EST_HUMAN	602153008F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294128 5'
8007	20549	33453	2.35	0.0E+00	BF525534.1	EST_HUMAN	AU134114 OVARC1 Homo sapiens cDNA clone OVARC1001296 5'
8037	20579	33484	1.88	0.0E+00	AL120124.1	EST_HUMAN	602069632F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4212727 5'
8037	20579	33485	1.88	0.0E+00	AL120124.1	EST_HUMAN	602069632F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4212727 5'
8077	20619	33550	1.82	0.0E+00	BE877693.1	EST_HUMAN	DKFZp761P092_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
8088	20639	33550	2.09	0.0E+00	AW500549.1	EST_HUMAN	DKFZp761P092_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
8106	20647	33558	11.19	0.0E+00	AW157233.1	EST_HUMAN	601483254F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887773 5'
8123	20664	33574	0.65	0.0E+00	AW072395.1	EST_HUMAN	U1HF-BNO-ak-f01-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077496 5'
8141	20682	33594	1.05	0.0E+00	11421722	NT	eu3b08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783799 3' similar to TR:O60463 O60463
8144	20685	33597	0.75	0.0E+00	W01616.1	EST_HUMAN	TR:O60463 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHODIOLASE. [1]; x807d12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567639 3' similar to contains element OFR repetitive element;
							Homo sapiens centrosomal protein 2 (CEP2), mRNA
							2a36d05.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:284633 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8148	20687	33589	1.55	0.0E+00	BE745597.1	EST_HUMAN	601578105F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'
8148	20687	33600	1.55	0.0E+00	BE745597.1	EST_HUMAN	601578105F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'
8168	20699	33613	1.32	0.0E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
8178	20719	33634	6.51	0.0E+00	D45032.1	NT	Human DNA for ceruloplasmin, exon 5
8198	20739	33651	1.47	0.0E+00	A367350.1	EST_HUMAN	q995g12.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:1889334 3' similar to TR:Q14873 Q14873
8211	20752	33666	3.14	0.0E+00	BE674157.1	EST_HUMAN	KIAA0164 PROTEIN. ; 7d76a04.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278862 3' similar to TR:O65793 O65793
8213	20764	33668	1.31	0.0E+00	A1885671.1	EST_HUMAN	wf80b10.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429275 3' similar to SW:COGT_HUMAN P50281 MATRIX METALLOPROTEINASE-14 PRECURSOR ;
8224	20765	33682	1.38	0.0E+00	BE563650.1	EST_HUMAN	601334780F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
8224	20765	33683	1.38	0.0E+00	BE563650.1	EST_HUMAN	601334780F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
8231	20772	33692	1.63	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8231	20772	33693	1.63	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8233	20774	33695	1.7	0.0E+00	AA403192.1	EST_HUMAN	z66f02.r1 Soares_tetol_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758619 5' similar to TR:G1304132 G1304132 TPRD. ;
8233	20774	33696	1.7	0.0E+00	AA403192.1	EST_HUMAN	z66f02.r1 Soares_tetol_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758619 5' similar to TR:G1304132 G1304132 TPRD. ;
8275	20816		4.36	0.0E+00	AA398511.1	EST_HUMAN	z73a08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727958 3' similar to gb:S85655 PROHIBITIN (HUMAN);
8283	20824	33745	0.5	0.0E+00	BE837593.1	EST_HUMAN	RC2-FN0084-120600-013-h07 FN0084 Homo sapiens cDNA
8284	20825	33746	1.22	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221289-046-c07 DT0045 Homo sapiens cDNA
8284	20825	33747	1.22	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221289-046-c07 DT0045 Homo sapiens cDNA
8303	20844	33766	1.24	0.0E+00	BE612586.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856179 5'
8303	20844	33767	1.24	0.0E+00	BE612586.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856179 5'
8318	20859	33784	1.28	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8318	20859	33785	1.26	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8326	20867	33790	0.78	0.0E+00	A1884477.1	EST_HUMAN	wm33a11.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437724 3' similar to TR:O75457 O75457
8333	20874	33786	0.93	0.0E+00	AA502294.1	EST_HUMAN	CYTOSOLIC PHOSPHOLIPASE A2-GAMMA. ; ne25d10.a.1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:882259 3' similar to TR:G1138434
8338	20879		0.64	0.0E+00	11416799	NT	G1138434 KIAA0187 PROTEIN. ;
8345	20886	33907	1.33	0.0E+00	A1580780.1	EST_HUMAN	Homo sapiens protocadherin beta 3 (PCDH13), mRNA
8348	20889		1.86	0.0E+00	BE890797.1	EST_HUMAN	ta04f11.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2043117 3' 601431238F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916568 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8374	20914	33833	0.61	0.0E+00	AW245765.1	EST_HUMAN	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'
8374	20914	33834	0.61	0.0E+00	AW245765.1	EST_HUMAN	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'
8375	20915	33835	2.27	0.0E+00	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8375	20915	33838	2.27	0.0E+00	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8378	20918	33838	0.6	0.0E+00	U88084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8378	20918	33839	0.6	0.0E+00	U88084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8443	20983	33898	0.7	0.0E+00	AJ251760.1	NT	Homo sapiens NESP55, GNAS1 antisense (partial) and XLaiphas (partial) genes
8448	20988	33904	3.77	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8448	20988	33905	3.77	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8448	20988	33908	3.77	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8483	21003	33920	1.07	0.0E+00	U82679.1	NT	Human immunoglobulin-like transcript-3 mRNA, complete cds
8502	21041	33962	0.88	0.0E+00	AF022655.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8502	21041	33963	0.88	0.0E+00	AF022655.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8505	21044	33965	0.89	0.0E+00	AU131671.1	EST_HUMAN	AU131671 NT2RP3 Homo sapiens cDNA clone NT2RP3003016 5'
8520	21059	33982	0.6	0.0E+00	11426372	NT	Homo sapiens immunoglobulin superfamily, member 2 (IGSF2), mRNA
8524	21063		1.64	0.0E+00	AW513513.1	EST_HUMAN	xc48601.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707032 3' similar to gb:M141423_cde4
8528	21065		0.84	0.0E+00	BE783232.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
8527	21066	33985	16.45	0.0E+00	D52650.1	EST_HUMAN	HUM084C02B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-084C02 5'
8557	21068	34017	3.98	0.0E+00	BE378495.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8563	21102	34021	2.84	0.0E+00	AA410545.1	EST_HUMAN	z32604.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724062 5'
8565	21104		2.44	0.0E+00	BF313946.1	EST_HUMAN	601900571F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129744 5'
8572	21111	34030	0.85	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
8576	21115	34034	1.28	0.0E+00	AW139673.1	EST_HUMAN	U1-H-B11-adr-12-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
8578	21115	34035	1.28	0.0E+00	AW139673.1	EST_HUMAN	U1-H-B11-adr-12-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
8581	21120		0.82	0.0E+00	AI640190.1	EST_HUMAN	w830b10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2299579 3' similar to TR:O15044
8600	21139	34053	1.78	0.0E+00	BF377897.1	EST_HUMAN	O15044 KIAA0335 ;
8608	21147	34063	0.55	0.0E+00	AL163301.2	NT	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
8614	21153	34067	2.14	0.0E+00	BE260272.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
8619	21158	34071	2.58	0.0E+00	BF700165.1	EST_HUMAN	601150051F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502836 5'
8619	21158	34072	2.58	0.0E+00	BF700165.1	EST_HUMAN	602127684F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284542 5'
8619	21158	34072	2.58	0.0E+00	BF700165.1	EST_HUMAN	602127684F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284542 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8619	21158	34073	2.58	0.0E+00	BF700165.1	EST_HUMAN	602127684F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
8633	21172	34080	0.63	0.0E+00	AI458722.1	EST_HUMAN	h13h11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2150949 3'
8660	21189	34117	2.45	0.0E+00	AL449770.1	EST_HUMAN	AL449770 Homo sapiens fetal brain (Stavrides GS) Homo sapiens cDNA
8687	21206	34123	18.43	0.0E+00	AA962527.1	EST_HUMAN	or80g02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602194 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
8673	21212	34131	4.87	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
8673	21212	34132	4.97	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
8697	21236	34159	1.28	0.0E+00	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
8699	21238	34161	1.76	0.0E+00	BE278917.1	EST_HUMAN	601156330F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139734 5'
8708	21247		4.02	0.0E+00	AV718377.1	EST_HUMAN	AV718377 FHTB Homo sapiens cDNA clone FHTBAAF11 5'
8715	21254	34175	3.11	0.0E+00	AW337277.1	EST_HUMAN	xv73c07.x1 NCI_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2833644 3' similar to gb:X53587 INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN);
8721	21260	34180	1.42	0.0E+00	AU124051.1	EST_HUMAN	AU124051 NT2RM2 Homo sapiens cDNA clone NT2RM2001575 5'
8766	21335	34260	0.9	0.0E+00	AU140704.1	EST_HUMAN	AU140704 PLACE4 Homo sapiens cDNA clone PLACE4000089 5'
8806	21345	34289	0.54	0.0E+00	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8810	21349	34272	0.6	0.0E+00	R17132.1	EST_HUMAN	y09e09.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31674 5'
8810	21349	34273	0.6	0.0E+00	R17132.1	EST_HUMAN	y09e09.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31674 5'
8814	21353	34275	3.95	0.0E+00	AW592233.1	EST_HUMAN	h148a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
8814	21353	34276	3.85	0.0E+00	AW592233.1	EST_HUMAN	h148a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
8849	21388	34311	0.5	0.0E+00	AU128804.1	EST_HUMAN	AU128804 NT2RP2 Homo sapiens cDNA clone NT2RP2004245 5'
8859	21398	34321	1.27	0.0E+00	AV714764.1	EST_HUMAN	AV714764 DCB Homo sapiens cDNA clone DCBAUA06 5'
8874	21413	34335	2.6	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C1814 3'
8874	21413	34336	2.6	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C1814 3'
8880	21418	34342	1.55	0.0E+00	AF133801.1	NT	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
8882	21420	34345	1.68	0.0E+00	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
8889	21427	34352	0.54	0.0E+00	BF875505.1	EST_HUMAN	602138483F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4274708 5'
8891	21429		0.97	0.0E+00	BF058289.1	EST_HUMAN	7k29b03.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476692 3' similar to TR:O36448 O36449 S GAG.;
8921	21469	34377	6.2	0.0E+00	11422857	NT	Homo sapiens tumor protein p73 (TP73), mRNA
8930	21468	34388	1.15	0.0E+00	K01241.1	NT	Human Ig rearranged H-chain epsilon-3 pseudogene, constant region
8937	21475	34395	4.14	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
8937	21475	34396	4.14	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
8942	21480	34402	1.61	0.0E+00	AB0660739.1	EST_HUMAN	AV660739 GLC Homo sapiens cDNA clone GLCGKG12 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8948	21486	34408	3.39	0.0E+00	7706638	NT	Homo sapiens polycystin-L (PKDL), mRNA
8953	21491	34413	2.58	0.0E+00	BE793328.1	EST_HUMAN	601588304F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942553 5'
8954	21492	34414	0.56	0.0E+00	AB033077.1	NT	Homo sapiens mRNA for KIAA1251 protein, partial cds
8954	21492	34415	0.56	0.0E+00	AB033077.1	NT	Homo sapiens mRNA for KIAA1251 protein, partial cds
8966	21504		1.07	0.0E+00	H73937.1	EST_HUMAN	yu03h08.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:232767 5'
8976	21514	34437	4.52	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
8976	21514	34438	4.52	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
8986	21524	34453	0.63	0.0E+00	BE612721.1	EST_HUMAN	601452582F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3856100 5'
8986	21524	34454	0.63	0.0E+00	BE612721.1	EST_HUMAN	601452582F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3856100 5'
8989	21527		0.58	0.0E+00	M89986.1	NT	Human polymorphic loci in Xq28
8991	21529	34458	1.84	0.0E+00	X14766.1	NT	Human mRNA for GABA-A receptor, alpha 1 subunit
9011	21548	34477	2.5	0.0E+00	A1061395.1	EST_HUMAN	ant29e04.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700094 3'
9016	21553	34481	1.82	0.0E+00	A1954607.1	EST_HUMAN	wc34e12.x1 NCI CGAP CGC8 Homo sapiens cDNA clone IMAGE:2473150 3' similar to SW:MGB3_HUMAN
9021	21558	34486	4.57	0.0E+00	9258595	NT	O15480 MELANOMA-ASSOCIATED ANTIGEN B3
9031	21568	34497	2.1	0.0E+00	AW858311.1	EST_HUMAN	Homo sapiens protocadherin alpha 8 (PCDH8), mRNA
9041	21578	34507	2.81	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
9056	21593	34523	1.13	0.0E+00	AU142662.1	EST_HUMAN	AU142682 Y79AA1 Homo sapiens cDNA clone Y79AA1000678 5'
9070	21607	34538	1.25	0.0E+00	11436995	NT	Homo sapiens MAP-kinase activating death domain (MADD), mRNA
9071	21608		0.9	0.0E+00	BE410768.1	EST_HUMAN	601301876F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636163 5'
9085	21621	34557	1.89	0.0E+00	BF002024.1	EST_HUMAN	7g97h12.x1 NCI CGAP Co16 Homo sapiens cDNA clone IMAGE:3314471 3' similar to TR:Q9UJH62
9099	21635	34573	0.83	0.0E+00	AB011150.1	NT	Q9UJH62 HYPOTHETICAL 42.5 KD PROTEIN
9100	21638	34574	7.17	0.0E+00	BE794823.1	EST_HUMAN	Homo sapiens mRNA for KIAA0578 protein, partial cds
9104	21640	34578	0.52	0.0E+00	BE810292.1	EST_HUMAN	601589284F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943463 5'
9104	21640	34580	0.52	0.0E+00	BE810292.1	EST_HUMAN	RC3-PT0151-290600-011-c05 PT0151 Homo sapiens cDNA
9107	21643	34583	1.17	0.0E+00	AU136228.1	EST_HUMAN	RC3-PT0151-290600-011-c05 PT0151 Homo sapiens cDNA
9112	21648	34588	1.18	0.0E+00	BE838343.1	EST_HUMAN	AU136228 PLACE1 Homo sapiens cDNA clone PLACE1003804 5'
9112	21648	34589	1.18	0.0E+00	BE838343.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
9130	21665	34605	0.78	0.0E+00	AB011166.1	NT	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
9133	21668	34609	1.84	0.0E+00	AA344601.1	EST_HUMAN	Homo sapiens mRNA for KIAA0594 protein, partial cds
9133	21668	34610	1.84	0.0E+00	AA344601.1	EST_HUMAN	EST50505 Gall bladder Homo sapiens cDNA 5' end
							EST50505 Gall bladder Homo sapiens cDNA 5' end
							be54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 6' similar to TR:O60275
9188	21705	34647	0.85	0.0E+00	AW673469.1	EST_HUMAN	KIAA0522 PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9188	21705	34848	0.95	0.0E+00	AW673469.1	EST_HUMAN	be54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN ;
9222	21738	34880	3.48	0.0E+00	BE207063.1	EST_HUMAN	be0905.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus Bcl-xL mRNA, complete cds (MOUSE);
9222	21738	34881	3.48	0.0E+00	BE207063.1	EST_HUMAN	be0905.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus Bcl-xL mRNA, complete cds (MOUSE);
9233	21955	34904	2.35	0.0E+00	BF348013.1	EST_HUMAN	602023150F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158300 5'
9268	21784	34743	2.8	0.0E+00	BE712515.1	EST_HUMAN	QV2-HT0698-250700-282-b08 HT0698 Homo sapiens cDNA
9289	21899	34846	0.98	0.0E+00	BF034377.1	EST_HUMAN	601455116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859035 5'
9299	21899	34847	0.98	0.0E+00	BF034377.1	EST_HUMAN	601455116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859035 5'
9305	21805	34854	0.53	0.0E+00	A1906351.1	EST_HUMAN	RC-BT108-040399-032 BT108 Homo sapiens cDNA
9308	21808	34856	1.54	0.0E+00	5803069	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9308	21908	34857	1.54	0.0E+00	5803069	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9317	21831	34782	1.96	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0120 5'
9352	21866	34816	2.17	0.0E+00	A1088043.1	EST_HUMAN	TR:Q14877 Q14877 KIAA0171 PROTEIN ;
9359	20298	33198	0.93	0.0E+00	BF309962.1	EST_HUMAN	601892245F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138066 5'
9361	20300	33189	2.28	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9361	20300	33200	2.28	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9363	20302	33203	18.79	0.0E+00	A1290909.1	EST_HUMAN	qim09a06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN
9363	20302	33204	18.79	0.0E+00	A1290909.1	EST_HUMAN	qim09a06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN
9364	20303	33205	6.56	0.0E+00	AW953836.1	EST_HUMAN	P29316 60S RIBOSOMAL PROTEIN L23A ;
9391	21814	34763	3.79	0.0E+00	AF153466.1	NT	P29316 60S RIBOSOMAL PROTEIN L23A ;
9394	21817	34767	0.81	0.0E+00	BE885128.1	EST_HUMAN	EST366026 MAGC resequences, MAGC Homo sapiens cDNA
9394	21817	34768	0.81	0.0E+00	BE885128.1	EST_HUMAN	Homo sapiens polycystic kidney disease 2-like protein (PKD2L) gene, exon 8
9403	21912		19.73	0.0E+00	BE255829.1	EST_HUMAN	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'
9408	21915	34864	1.36	0.0E+00	BE781382.1	EST_HUMAN	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'
9408	21915	34865	1.36	0.0E+00	BE781382.1	EST_HUMAN	601109942F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350722 5'
9408	21917	34866	29.88	0.0E+00	AW163779.1	EST_HUMAN	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
							601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
							au86c04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783142 5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9428	21937	34866	3	0.0E+00	BE283191.1	EST_HUMAN	601145054F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160477 5'
9446	21972	34922	4.5	0.0E+00	C08158.1	EST_HUMAN	C08158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9446	21972	34923	4.5	0.0E+00	C08158.1	EST_HUMAN	C08158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9448	21974	34926	2.7	0.0E+00	BE746215.1	EST_HUMAN	601578683F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927548 5'
9458	21984	34936	2.92	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9458	21984	34937	2.92	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9458	21984	34938	2.92	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9478	21877	34824	1.89	0.0E+00	BE800549.1	EST_HUMAN	601673425F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956238 5'
9496	21996	34952	0.76	0.0E+00	AV701829.1	EST_HUMAN	AV701829 ADB Homo sapiens cDNA clone ADBBYH01 5'
9508	22008	34965	2.38	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2e (KRT2E) gene, complete cds
9508	22008	34966	2.38	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2e (KRT2E) gene, complete cds
9540	22040	35001	1.32	0.0E+00	BE082977.1	EST_HUMAN	RC2-BT0642-130300-017-g01 BT0642 Homo sapiens cDNA
9559	22059	35021	1.86	0.0E+00	AW500293.1	EST_HUMAN	UI-HF-BNO-akg-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9559	22059	35022	1.86	0.0E+00	AW500293.1	EST_HUMAN	UI-HF-BNO-akg-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9568	22068	35028	1.75	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
9568	22068	35029	1.75	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
9570	22070	35030	0.72	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'
9570	22070	35031	0.72	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'
9578	22078	35043	1.14	0.0E+00	W56629.1	EST_HUMAN	zid16e11.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:340844 5'
9578	22078	35044	1.14	0.0E+00	W56629.1	EST_HUMAN	zid16e11.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:340844 5'
9591	22091	35055	1.05	0.0E+00	AB035358.1	NT	Homo sapiens mRNA for neurexin I-alpha protein, complete cds
9595	22095		0.64	0.0E+00	A1124780.1	EST_HUMAN	am56e11.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539548 3'
9597	22097	35060	2.65	0.0E+00	AW500528.1	EST_HUMAN	UI-HF-BNO-akg-c-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077364 5'
9840	22140	35107	1.48	0.0E+00	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
9866	22165	35138	2.21	0.0E+00	S78468.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9866	22165	35139	2.21	0.0E+00	S78468.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9869	22168	35144	2.54	0.0E+00	BE563320.1	EST_HUMAN	601334603F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3686880 5'
9869	22168	35161	1.5	0.0E+00	AW363135.1	EST_HUMAN	CM2-CT0311-301199-043-h11 CT0311 Homo sapiens cDNA
9708	22208	35179	0.91	0.0E+00	11436432	NT	Homo sapiens multimerin (MMRN), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9709	22207	35180	0.74	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
9718	22216	35190	0.83	0.0E+00	BE206710.1	EST_HUMAN	bb26c01.x1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:2864000 3'
9733	22231	35208	2.41	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
9733	22231	35209	2.41	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
9742	22240	35221	1.45	0.0E+00	AW500936.1	EST_HUMAN	UI-HF-BPOp-air-4-05-Q-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072897 5'
9748	22246	35227	19.68	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
9748	22246	35228	19.68	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
9761	22259	35242	2.32	0.0E+00	7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
9779	22277	35282	1.98	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0120 5'
9784	22282	35268	0.71	0.0E+00	AL041084.2	EST_HUMAN	DKFZp434B2416_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2416 5'
9794	22292	35275	2.32	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
9795	22293	35276	2.48	0.0E+00	AF152308.1	NT	Homo sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA, complete cds
9822	22320	35304	2.61	0.0E+00	AF009220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
9822	22320	35305	2.61	0.0E+00	AF009220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
9838	22336	35318	3.23	0.0E+00	BF092898.1	EST_HUMAN	MR4-TN0114-110900-101-e04 TN0114 Homo sapiens cDNA
9865	22362	35342	2.74	0.0E+00	BE280793.1	EST_HUMAN	601155227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138798 5'
9874	22371	35348	8.19	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'
9874	22371	35349	8.19	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'
9883	22380	35355	9.02	0.0E+00	AW236259.1	EST_HUMAN	xn72b01.x1 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2899977 3' similar to gb:X02152_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
9884	22381	35358	0.92	0.0E+00	AA341305.1	EST_HUMAN	EST46740 Fetal kidney II Homo sapiens cDNA 5' and
9893	22390	35368	0.5	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9916	22412	35387	0.79	0.0E+00	AW964113.1	EST_HUMAN	EST376188 MAGE resequences, MAGH Homo sapiens cDNA
9929	22425	35398	6.82	0.0E+00	AU143873.1	EST_HUMAN	AU143873 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'
9929	22425	35399	6.82	0.0E+00	AU143873.1	EST_HUMAN	AU143873 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'
9932	22428	35402	3.44	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
9935	22430	35404	2.52	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
9935	22430	35405	2.52	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
9968	22463	35447	3.55	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
9968	22463	35448	3.55	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
9984	22479	35462	2.1	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene
9984	22479	35463	2.1	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene
9989	22484	35470	0.92	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GK Homo sapiens cDNA clone GKCDX07 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9989	22484	35471	0.92	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GKC Homo sapiens cDNA clone GKDXA07 5'
9995	22490	35478	0.57	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
9997	22492	35481	2.78	0.0E+00	AA196387.1	EST_HUMAN	z097h11.11 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628197 5'
10020	22515	35508	1.61	0.0E+00	AA131248.1	EST_HUMAN	z31f01.1 Soares pregnant uterus NBHPU Homo sapiens cDNA clone IMAGE:503545 5'
10020	22515	35509	1.01	0.0E+00	AA131248.1	EST_HUMAN	z31f01.1 Soares pregnant uterus NBHPU Homo sapiens cDNA clone IMAGE:503545 5'
10061	22556	35551	1.56	0.0E+00	AF178308.1	NT	Homo sapiens KIF4 (KIF4) mRNA, complete cds
10102	22597	35590	0.75	0.0E+00	BE880658.1	EST_HUMAN	601491565F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3893657 5'
10113	22608	35598	11.65	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10113	22608	35599	11.65	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10118	22613	35603	1.05	0.0E+00	AU127403.1	EST_HUMAN	AU127403 NT2RP2 Homo sapiens cDNA clone NT2RP2001212 5'
10127	22622	35612	0.99	0.0E+00	BE958511.1	EST_HUMAN	601645134F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930177 5'
10127	22622	35613	0.99	0.0E+00	BE958511.1	EST_HUMAN	601645134F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930177 5'
10142	22637	35628	0.78	0.0E+00	BE897487.1	EST_HUMAN	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
10153	22648	35642	0.78	0.0E+00	AA311624.1	EST_HUMAN	EST182353 Jurkat T-cells VI Homo sapiens cDNA 5' end
10154	22649	35643	0.57	0.0E+00	4758827	NT	Homo sapiens neurixin III (NRXN3) mRNA
10187	22682	35657	0.81	0.0E+00	BE891113.1	EST_HUMAN	601432228F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917598 5'
10170	22685	35660	1.29	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10179	22674	35666	1.47	0.0E+00	AB029290.1	NT	Homo sapiens mRNA for actin binding protein ABP620, complete cds
10180	22675	35667	0.53	0.0E+00	BE304522.1	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987918 5'
10180	22675	35668	0.53	0.0E+00	BE304522.1	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987918 5'
10187	22682	35673	6.03	0.0E+00	AB008590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10187	22682	35674	6.03	0.0E+00	AB008590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10194	22689	35682	0.57	0.0E+00	AA194770.1	EST_HUMAN	zq06h11.11 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628985 5' similar to TR:G407097
10196	22691	35684	1.18	0.0E+00	AA704457.1	EST_HUMAN	z19b06.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:450707 3' similar to gb:M14123_cds1 RETROVIRUS-RELATED GAG POLYPROTEIN (HUMAN);
10198	22693	35685	1.31	0.0E+00	M22921.1	NT	Human beta 1,4-galactosyl-transferase mRNA, complete cds
10200	22695	35688	5.5	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4184939 5'
10200	22695	35689	5.5	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4184939 5'
10227	22722	35713	0.93	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10227	22722	35714	0.93	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10256	22751	35739	0.53	0.0E+00	AV716271.1	EST_HUMAN	AV716271 DCB Homo sapiens cDNA clone DCBDDC09 5'
10256	22751	35740	0.53	0.0E+00	AV716271.1	EST_HUMAN	AV716271 DCB Homo sapiens cDNA clone DCBDDC09 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10285	22780	35770	0.77	0.0E+00	AI631818.1	EST_HUMAN	wa36e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204 Q61204 NOTCH2-LIKE ;
10285	22780	35771	0.77	0.0E+00	AI631818.1	EST_HUMAN	wa36e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204 Q61204 NOTCH2-LIKE ;
10298	22792	35782	1.32	0.0E+00	T03078.1	EST_HUMAN	FB23A4 Fetal brain, Stratagene Homo sapiens cDNA clone FB23A4 3'end
10321	22815	35811	0.83	0.0E+00	AU122428.1	EST_HUMAN	AU122428 MAMMA1 Homo sapiens cDNA clone MAMMA1002388 5'
10348	22842	35838	2.69	0.0E+00	BF436218.1	EST_HUMAN	na45a12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3285271 3'
10349	22843		1.61	0.0E+00	AV654765.1	EST_HUMAN	AV654765 GLC Homo sapiens cDNA clone GLCZC07 3'
10387	22861	35854	3.53	0.0E+00	AW517860.1	EST_HUMAN	xu74b01.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:M69066 MOESIN (HUMAN);
10371	22865	35858	21.07	0.0E+00	BE549213.1	EST_HUMAN	601078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5'
10386	22880	35874	0.55	0.0E+00	11436005	NT	Homo sapiens hypothetical protein DKFZp781P1010 (DKFZp781P1010), mRNA
10410	22904	35901	1.22	0.0E+00	X89893.1	NT	H. sapiens mRNA for NK receptor (183 Act1)
10411	22905	35902	3	0.0E+00	BE781742.1	EST_HUMAN	601467419F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870700 5'
10430	22924	35929	2.88	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-403 BT0642 Homo sapiens cDNA
10430	22924	35930	2.88	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-403 BT0642 Homo sapiens cDNA
10437	22931	35938	0.6	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10443	22937	35947	0.68	0.0E+00	AI658890.1	EST_HUMAN	164607.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2244612 3'
10450	22944	35954	5.46	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
10450	22944	35955	5.46	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
10453	22947	35956	1.83	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845956 3'
10453	22947	35957	1.83	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845956 3'
10458	22952	35960	0.49	0.0E+00	D29954.1	NT	Human mRNA for KIAA0056 gene, partial cds
10458	22952	35961	0.49	0.0E+00	D29954.1	NT	Human mRNA for KIAA0056 gene, partial cds
10474	22968	35977	0.68	0.0E+00	H39805.1	EST_HUMAN	yp01a10.r1 Soares breast 3NHBst Homo sapiens cDNA clone IMAGE:186138 5'
10487	22981	35989	0.46	0.0E+00	AW748117.1	EST_HUMAN	QV0-BT0107-230799-007-c06 BT0107 Homo sapiens cDNA
10498	22980	35989	1.14	0.0E+00	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10508	23002	36010	0.8	0.0E+00	D29854.1	NT	Human mRNA for KIAA0056 gene, partial cds
10515	23053	36064	2.76	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'
10515	23053	36065	2.76	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'
10517	23055		6.05	0.0E+00	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-ab3 ST0197 Homo sapiens cDNA
10525	23062	36073	7.48	0.0E+00	AW963563.1	EST_HUMAN	EST1375636 MAGe resequences, MAGH Homo sapiens cDNA
10538	23075	36088	1.91	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
10538	23075	36089	1.91	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10540	23077	36091	1.82	0.0E+00	AW057621.1	EST_HUMAN	wy61f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2553065 3' similar to TR:Q60568 Q60568 VDX;
10549	23085	36099	2.28	0.0E+00	BE243270.1	EST_HUMAN	TCAAP3D0917 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0917
10550	23086	36100	2.73	0.0E+00	A1652239.1	EST_HUMAN	wb28a12.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element;
10550	23086	36101	2.73	0.0E+00	A1652239.1	EST_HUMAN	wb28a12.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element;
10561	23097	36110	4.31	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
10561	23097	36111	4.31	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
10576	23111	36124	1.88	0.0E+00	AW404795.1	EST_HUMAN	U1-HF-BLO-acm-4-04-0-U1.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059383 5'
10580	23115	36129	5.92	0.0E+00	11424829	NT	Homo sapiens hypothetical protein FLJ20079 (FLJ20079), mRNA
10581	23116	36130	10.05	0.0E+00	4504538	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA
10581	23116	36131	10.05	0.0E+00	4504538	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA
10582	23117	36132	2.9	0.0E+00	A1991827.1	EST_HUMAN	wu32b06.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2521715 3'
10585	23120	36136	2.57	0.0E+00	BE882109.1	EST_HUMAN	601505204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906865 5'
10589	23124	36138	15.86	0.0E+00	BE891630.1	EST_HUMAN	601434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919636 5'
10591	23126	36139	2.44	0.0E+00	8923839	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10591	23126	36140	2.44	0.0E+00	8923839	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10606	23140	36152	6.94	0.0E+00	BE903304.1	EST_HUMAN	601674332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5'
10609	18572	31304	2.31	0.0E+00	AA195905.1	EST_HUMAN	zp95b11.r1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
10630	23162	36174	1.99	0.0E+00	AA809080.1	EST_HUMAN	hm17c08.st NCI_CGAP_G080 Homo sapiens cDNA clone IMAGE:1240718 3' similar to gb:X57809 IG LAMBDA CHAIN C REGIONS (HUMAN);
10632	23164	36176	5.44	0.0E+00	BE793498.1	EST_HUMAN	601588829F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943015 5'
10640	23172	36183	19.41	0.0E+00	AV727382.1	EST_HUMAN	AV727382 HTC Homo sapiens cDNA clone HTCAQH06 5'
10640	23172	36184	19.41	0.0E+00	AV727382.1	EST_HUMAN	AV727382 HTC Homo sapiens cDNA clone HTCAQH06 5'
10654	23186	36202	18.4	0.0E+00	AW516055.1	EST_HUMAN	xy04g10.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852228 3' similar to gb:M60854 40S RIBOSOMAL PROTEIN S16 (HUMAN);
10660	23192	36207	3.16	0.0E+00	AU135741.1	EST_HUMAN	AU135741 PLACE1 Homo sapiens cDNA clone PLACE1002794 5'
10665	23197	36210	2.88	0.0E+00	AW593333.1	EST_HUMAN	hg13c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
10665	23197	36211	2.88	0.0E+00	AW593333.1	EST_HUMAN	hg13c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10685	23197	36212	2.88	0.0E+00	AW593333.1	EST_HUMAN	hg13402.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element:
10687	23198	36213	1.99	0.0E+00	Z34897.1	NT	H. sapiens mRNA for H1 histamine receptor
10688	23200	36214	3.18	0.0E+00	F13069.1	EST_HUMAN	HSC3C031 normalized infant brain cDNA Homo sapiens cDNA clone c-3ic03
10676	23208	36220	3.91	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
10676	23211	36222	33.46	0.0E+00	11425570	NT	Homo sapiens ryonodine receptor 1 (skaleia) (RYR1), mRNA
10695	23225	36239	3.59	0.0E+00	AW338094.1	EST_HUMAN	xw68f01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832985 3' similar to gb:X17115 IG MU CHAIN C REGION (HUMAN);
10696	23226	36240	5.84	0.0E+00	AW451230.1	EST_HUMAN	UIH-B13-elh-a-01-0-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736849 3'
10696	23226	36241	5.84	0.0E+00	AW451230.1	EST_HUMAN	UIH-B13-elh-a-01-0-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736849 3'
10699	12891		16.23	0.0E+00	4506832	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
10701	23230	36243	2.17	0.0E+00	AB014567.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
10714	23242	36259	2.28	0.0E+00	BE28848.1	EST_HUMAN	601119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029219 5'
10730	23256	36272	1.99	0.0E+00	AB011117.1	NT	Homo sapiens mRNA for KIAA0545 protein, partial cds
10746	23270	36286	2.18	0.0E+00	BE792155.1	EST_HUMAN	601582046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936539 5'
10747	23271		78.35	0.0E+00	BF684081.1	EST_HUMAN	602141405F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302432 5'
10749	23273	36288	4.66	0.0E+00	AU118386.1	EST_HUMAN	AU118386 HEMBA1 Homo sapiens cDNA clone HEMBA1003486 5'
10750	23274		8.15	0.0E+00	AW236269.1	EST_HUMAN	x072b01.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2669977 3' similar to gb:X02152_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
10755	23279	36282	7.25	0.0E+00	A1149809.1	EST_HUMAN	qf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
10755	23279	36283	7.25	0.0E+00	A1149809.1	EST_HUMAN	qf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
10756	23280	36284	3.47	0.0E+00	AW391837.1	EST_HUMAN	QV4-ST0234-121199-032-b08 ST0234 Homo sapiens cDNA
10768	23292		1.54	0.0E+00	AU116908.1	EST_HUMAN	AU116908 HEMBA1 Homo sapiens cDNA clone HEMBA1000255 5'
10771	23295	36301	20.86	0.0E+00	11424728	NT	Homo sapiens insulin receptor (INSR), mRNA
10771	23301	36307	1.89	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM0093-170400-191-406 UM0093 Homo sapiens cDNA
10777	23301	36308	1.89	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM0093-170400-191-406 UM0093 Homo sapiens cDNA
10776	23302	36309	2.04	0.0E+00	BF740308.1	EST_HUMAN	602037014F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184979 5'
10779	23303	36310	39.28	0.0E+00	BE281209.1	EST_HUMAN	601148357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310 5'
10780	23313	36321	3.78	0.0E+00	U50326.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17
10784	23317	36326	3.48	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-07 FT0134 Homo sapiens cDNA
10784	23317	36327	3.48	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-07 FT0134 Homo sapiens cDNA
10818	23337	36350	55.63	0.0E+00	AA740782.1	EST_HUMAN	cb32607.s1 NCI_CGAP_K1d5 Homo sapiens cDNA clone IMAGE:1325412 3' similar to contains element MSR1 repetitive element:
10822	23343	36358	3.04	0.0E+00	AF252303.1	NT	Homo sapiens signaling lymphocytic activation molecule (SLAM) gene, exon 2

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10835	23366	36371	1.92	0.0E+00	BE266478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538867 5'
10835	23356	36372	1.92	0.0E+00	BE266478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538867 5'
10838	23359	36374	6.99	0.0E+00	C05089	Human heart cDNA (YNeKamura)	Homo sapiens cDNA clone 3NHC4817
10845	23366	36382	2.16	0.0E+00	AA746376.1	EST_HUMAN	oa56h01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
10845	23366	36383	2.16	0.0E+00	AA746375.1	EST_HUMAN	oa56h01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
10856	23377	36395	8.08	0.0E+00	AL157608.1	EST_HUMAN	DKFZp761J2116_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J2116 5'
10868	23389	36404	12.82	0.0E+00	AU116988.1	EST_HUMAN	AU116988 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'
10881	23402	36419	2.07	0.0E+00	AV683656.1	EST_HUMAN	AV683656 GKC Homo sapiens cDNA clone GKCCNC03 5'
10913	23432	36453	3.17	0.0E+00	BE182360.1	EST_HUMAN	PM0-HT0845-060500-002-E05 HT0845 Homo sapiens cDNA
10913	23432	36454	3.17	0.0E+00	BE182360.1	EST_HUMAN	PM0-HT0845-060500-002-E05 HT0845 Homo sapiens cDNA
10914	23433		1.8	0.0E+00	AV701152.1	EST_HUMAN	AV701152 ADA Homo sapiens cDNA clone ADAAD06 5'
10928	23446	36467	3.19	0.0E+00	BE996423.1	EST_HUMAN	601439092F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5'
10935	23452	36474	1.69	0.0E+00	AW500307.1	EST_HUMAN	UI-HF-BNO-akg-d-02-q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
10935	23452	36475	1.69	0.0E+00	AW500307.1	EST_HUMAN	UI-HF-BNO-akg-d-02-q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
							bb78c04.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048486 5' similar to gb:Y00345_cds1 POLYADENYLATE-BINDING PROTEIN (HUMAN); gb:X65553 M.musculus mRNA for poly(A) binding protein (MOUSE);
10938	23455	36478	6.2	0.0E+00	BE018283.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
10972	23487	36518	5.22	0.0E+00	BE897953.1	EST_HUMAN	ea85g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
10973	23488	36517	1.99	0.0E+00	AI459545.1	EST_HUMAN	ea85g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
10973	23488	36518	1.99	0.0E+00	AI459545.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0120 5'
10986	23500	36530	1.82	0.0E+00	AL042278.1	EST_HUMAN	Homo sapiens neurexin III (NRXN3) mRNA
11018	23532	36568	3.57	0.0E+00	4758827	NT	
11019	23533	36569	8.71	0.0E+00	BF206561.1	EST_HUMAN	601870902F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4101433 5'
11023	23537	36573	20.4	0.0E+00	AW207734.1	EST_HUMAN	UI-H-BI2-egs-h-01-q-UJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724312 3'
11028	23542	36577	6.39	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11028	23542	36578	6.39	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
							ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B- 55KDA-ASSOCIATED PROTEIN ;
11029	23543	36579	3.28	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B- 55KDA-ASSOCIATED PROTEIN ;
11029	23543	36580	3.28	0.0E+00	BE206846.1	EST_HUMAN	55KDA-ASSOCIATED PROTEIN ;
11053	23566	36602	2.05	0.0E+00	BF083887.1	EST_HUMAN	QV0-UM0081-120900-365-b12 UM0081 Homo sapiens cDNA
11054	20011	32877	2.13	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
11057	23569	36604	3.38	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA
11057	23569	36605	3.38	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11092	23604	36644	5.37	0.0E+00	BF507876.1	EST_HUMAN	UI-H-BI4-eok-b-10-Q-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11092	23604	36645	5.37	0.0E+00	BF507876.1	EST_HUMAN	UI-H-BI4-eok-b-10-Q-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11101	23611	36651	3.82	0.0E+00	AU135170.1	EST_HUMAN	AU135170 PLACE1 Homo sapiens cDNA clone IMAGE:4271630 5'
11105	23615	36655	1.61	0.0E+00	BF576138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11105	23615	36656	1.61	0.0E+00	BF576138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11108	23616	36657	8.82	0.0E+00	BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3889207 5'
11108	23616	36658	8.82	0.0E+00	BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3889207 5'
11113	23623	36664	1.95	0.0E+00	DB7682.1	NT	Human mRNA for KIAA0241 gene, partial cds
11118	23628	36680	5.3	0.0E+00	BF240536.1	EST_HUMAN	601875630F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099710 5'
11132	23640	36680	3.05	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11132	23640	36681	3.05	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11137	23645	36685	3.57	0.0E+00	11430968	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11137	23645	36686	3.57	0.0E+00	11430968	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11154	23661	36708	9.12	0.0E+00	4503544	EST	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11162	23669	36714	1.68	0.0E+00	BF576267.1	EST_HUMAN	602134132F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289502 5'
11165	23672	36718	8.44	0.0E+00	AW328173.1	EST_HUMAN	602134132F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289502 5'
11168	23675	36725	46.81	0.0E+00	M55083.1	NT	Human gamma actin-like pseudogene, complete cds
11173	23680	36728	5.47	0.0E+00	BF306998.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11173	23680	36728	5.47	0.0E+00	BF306998.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11180	23686	36733	45.22	0.0E+00	BF362462.1	EST_HUMAN	QV2-NN0054-230800-333-e04 NN0054 Homo sapiens cDNA
11201	23708	36757	1.99	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11201	23708	36758	1.99	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11205	23710	36760	6.26	0.0E+00	BE897051.1	EST_HUMAN	601439805F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924577 5'
11208	23711	36774	1.61	0.0E+00	4503788	NT	Homo sapiens fyn-related kinase (FRK) mRNA
11217	23720	36774	2.82	0.0E+00	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11219	23722	36774	2.56	0.0E+00	BF207662.1	EST_HUMAN	601861947F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081715 5'
11220	23723	36774	7.59	0.0E+00	BE257744.1	EST_HUMAN	60116705F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357384 5'
11233	23764	36820	5.51	0.0E+00	BE206846.1	EST_HUMAN	55KDA-ASSOCIATED PROTEIN ;
11233	23764	36821	5.51	0.0E+00	BE206846.1	EST_HUMAN	55KDA-ASSOCIATED PROTEIN ;
11235	23766	36823	4.66	0.0E+00	AW753028.1	EST_HUMAN	QV0-CT0225-101289-071-f08 CT0225 Homo sapiens cDNA
11240	23771	36823	3.42	0.0E+00	AA558707.1	EST_HUMAN	ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11241	18112	30521	6.08	0.0E+00	AI934954.1	EST_HUMAN	wp06g08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2484094 3'
11242	23772	36829	9.55	0.0E+00	AW327895.1	EST_HUMAN	020208.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846919 5'
11260	24801	36847	1.56	0.0E+00	AW292776.1	EST_HUMAN	U1H-BW0-ell-d-07-0-UI.s1 NCL CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729509 3'
11266	23004	36012	2.1	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
11274	23727	36781	1.59	0.0E+00	BE95909.2	EST_HUMAN	601859088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11274	23727	36782	1.59	0.0E+00	BE95909.2	EST_HUMAN	601859088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11275	23728	36783	4.55	0.0E+00	BE185956.1	EST_HUMAN	IL5-HT0731-020500-077-03 HT0731 Homo sapiens cDNA
11288	23740	36796	5.82	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5'
11288	23740	36797	5.82	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5'
11298	23750	36807	18.85	0.0E+00	AI923116.1	EST_HUMAN	wn83g03.x1 NCL CGAP_UH Homo sapiens cDNA clone IMAGE:2452488 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
11301	23784	36851	7	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCL CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686
11301	23784	36852	7	0.0E+00	AA760913.1	EST_HUMAN	Q13686 ALKB HOMOLOG PROTEIN.1;
11306	23799	36858	2.02	0.0E+00	BE910548.1	EST_HUMAN	nz11c07.s1 NCL CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686
11314	23012	36021	7.16	0.0E+00	BE676347.1	EST_HUMAN	Q13686 ALKB HOMOLOG PROTEIN.1;
11323	23021	36030	1.89	0.0E+00	AV757420.1	EST_HUMAN	601501090F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902926 5'
11352	23806	36866	3.55	0.0E+00	L39891.1	NT	7127112.x1 NCL CGAP_G0B1 Homo sapiens cDNA clone IMAGE:3902926 5'
11352	23806	36866	3.55	0.0E+00	L39891.1	NT	CHECKPOINT SUPPRESSOR 1.1;
11368	23818	36879	4.02	0.0E+00	AU138211.1	EST_HUMAN	AV757420 BM Homo sapiens cDNA clone BMFAGH03 5'
11381	23833	36898	9.87	0.0E+00	BE622317.1	EST_HUMAN	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11386	23838	36900	11.61	0.0E+00	AI207425.1	EST_HUMAN	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11386	23838	36901	11.61	0.0E+00	AI207425.1	EST_HUMAN	601441096F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916270 5'
11415	23866	36927	36.86	0.0E+00	BE748899.1	EST_HUMAN	HA2787 Human fetal liver cDNA library Homo sapiens cDNA
11415	23866	36928	36.86	0.0E+00	BE748899.1	EST_HUMAN	HA2787 Human fetal liver cDNA library Homo sapiens cDNA
11425	23876	36940	2.19	0.0E+00	AU141882.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3833012 3'
11425	23876	36940	2.19	0.0E+00	AU141882.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3833012 3'
11428	23879	36944	2.52	0.0E+00	AW006022.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
11431	24802	36947	3.76	0.0E+00	BF002333.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
11450	23800	36867	3.81	0.0E+00	AW387776.1	EST_HUMAN	w291h01.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2566225 3' similar to WP:F53H10.2
11450	23800	36867	3.81	0.0E+00	AW387776.1	EST_HUMAN	CE11040 ZINC FINGER, C2H2 TYPE.1
11450	23800	36867	3.81	0.0E+00	AW387776.1	EST_HUMAN	7h22b10.x1 NCL CGAP_C016 Homo sapiens cDNA clone IMAGE:3316698 3' similar to TR:Q13458 Q13458 TRIO.1
11450	23800	36867	3.81	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261099-012-603 ST0118 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11450	23900	36988	3.81	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261089-012-b03 ST0118 Homo sapiens cDNA
11459	23909		2.48	0.0E+00	AW863777.1	EST_HUMAN	MR3-SN0010-310300-107-h03 SN0010 Homo sapiens cDNA
11471	23921	36990	3.38	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11471	23921	36991	3.38	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11476	23926	36997	7.44	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
11479	23929	36999	12.8	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
11479	23929	37000	12.8	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
11492	23941	37012	2.5	0.0E+00	BE794758.1	EST_HUMAN	601590588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
11493	23942	37013	115.56	0.0E+00	BE878633.1	EST_HUMAN	601481821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5'
11507	23956	37028	18.88	0.0E+00	BE409993.1	EST_HUMAN	601289403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629544 5'
11508	23957	37027	1.94	0.0E+00	BE148650.1	EST_HUMAN	MR0-HT0241-150500-011-02 HT0241 Homo sapiens cDNA
11509	23958	37028	3.08	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11509	23958	37029	3.08	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11510	23962	30771	1.77	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidin succinyltransferase, complete cds (exon 1-15)
11510	23962	30772	1.77	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidin succinyltransferase, complete cds (exon 1-15)
11518	23966	37038	2.03	0.0E+00	AU132940.1	EST_HUMAN	AU132940 NT2RP4 Homo sapiens cDNA clone NT2RP4000929 5'
11521	23969	37040	4.44	0.0E+00	BE903372.1	EST_HUMAN	601876357F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958935 5'
11533	23981	37051	1.84	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127089 5'
11533	23981	37052	1.84	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127089 5'
11535	23983	37054	3.01	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11535	23983	37055	3.01	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11544	23992		4.03	0.0E+00	BE906402.1	EST_HUMAN	601488553F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900396 5'
11560	24007	37078	1.74	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
11574	24803		23.39	0.0E+00	BF309120.1	EST_HUMAN	601890534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5'
11580	24026	37094	55.98	0.0E+00	BE297175.1	EST_HUMAN	601174074F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532968 5'
11589	24032	37102	7.09	0.0E+00	AL040783.1	EST_HUMAN	DKFZp434D0415.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D0415 5'
11652	25091	30499	6.23	0.0E+00	BE12542.1	EST_HUMAN	601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5'
11666	24925		1.78	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11668	24936		8.17	0.0E+00	AI190993.1	EST_HUMAN	qel7b12.x1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1739231 3'
11679	24097		3.67	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
11699	24112		4.16	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11701	24114		1.35	0.0E+00	AB016195.1	NT	Homo sapiens ELK1 pseudogene (ELK2) and immunoglobulin heavy chain gamma pseudogene (IGHGP)
11709	24120		3.59	0.0E+00	11417892	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
11728	24134		5.98	0.0E+00	5802873	NT	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA
11763	24697	30711	1.49	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11774	24908		4.78	0.0E+00	AL041931.1	EST_HUMAN	DKFZp434K0819_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434K0819 5'
11803	25056		4.26	0.0E+00	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
11812	24184		11.29	0.0E+00	AL049544.1	EST_HUMAN	DKFZp434G218_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G218 5'
11824	24941		2.62	0.0E+00	AI903497.1	EST_HUMAN	IL-BT030-271098-001 BT030 Homo sapiens cDNA
11862	25079		2.35	0.0E+00	N54484.1	EST_HUMAN	Y40608.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245222 3' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN ;
11877	24227		4.72	0.0E+00	AF106656.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
11880	13490	26007	5.48	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
11880	13490	26008	5.48	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
11889	24945		2.49	0.0E+00	10092587	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
11917	13204		3.24	0.0E+00	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
11955	24720	30870	4.32	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12017	24871	30708	24.38	0.0E+00	AW590882.1	EST_HUMAN	hg31e06.x1 NCI_CGAP_GCG Homo sapiens cDNA clone IMAGE:2847234 3' similar to contains Alu repetitive element/contains element MER22 repetitive element ;
12028	24926		1.5	0.0E+00	BE090210.1	EST_HUMAN	RC8-BT0711-280300-011-D05 BT0711 Homo sapiens cDNA
12073	24938		2	0.0E+00	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12112	24373		4.16	0.0E+00	8635487	NT	Human endogenous retrovirus, complete genome
12155	24931		1.93	0.0E+00	AI204914.1	EST_HUMAN	an05004.x1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'
12199	24927		1.52	0.0E+00	BE439792.1	EST_HUMAN	HTM1-654F HTM1 Homo sapiens cDNA
12244	14314	26855	4.92	0.0E+00	H30132.1	EST_HUMAN	y059c08.r1 Soares breast 3Nhb1st Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12244	14314	26856	4.92	0.0E+00	H30132.1	EST_HUMAN	y059c08.r1 Soares breast 3Nhb1st Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12256	24466		33.19	0.0E+00	D50659.1	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
12259	24469	30928	3.51	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12259	24469	30928	3.51	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12279	14717	27289	1.42	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
12318	24508		1.61	0.0E+00	AW664998.1	EST_HUMAN	h188g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979154 3'
12401	15963	28440	5.09	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
12409	18031	30492	2.86	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12412	24566		2.55	0.0E+00	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
12453	24587	30917	1.67	0.0E+00	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
12481	25102		2.92	0.0E+00	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
12488	13277	25754	2.02	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12573	24870	30876	1.55	0.0E+00	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12576	24872		2.54	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12580	24876		4.31	0.0E+00	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
12600	24686		2.35	0.0E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)

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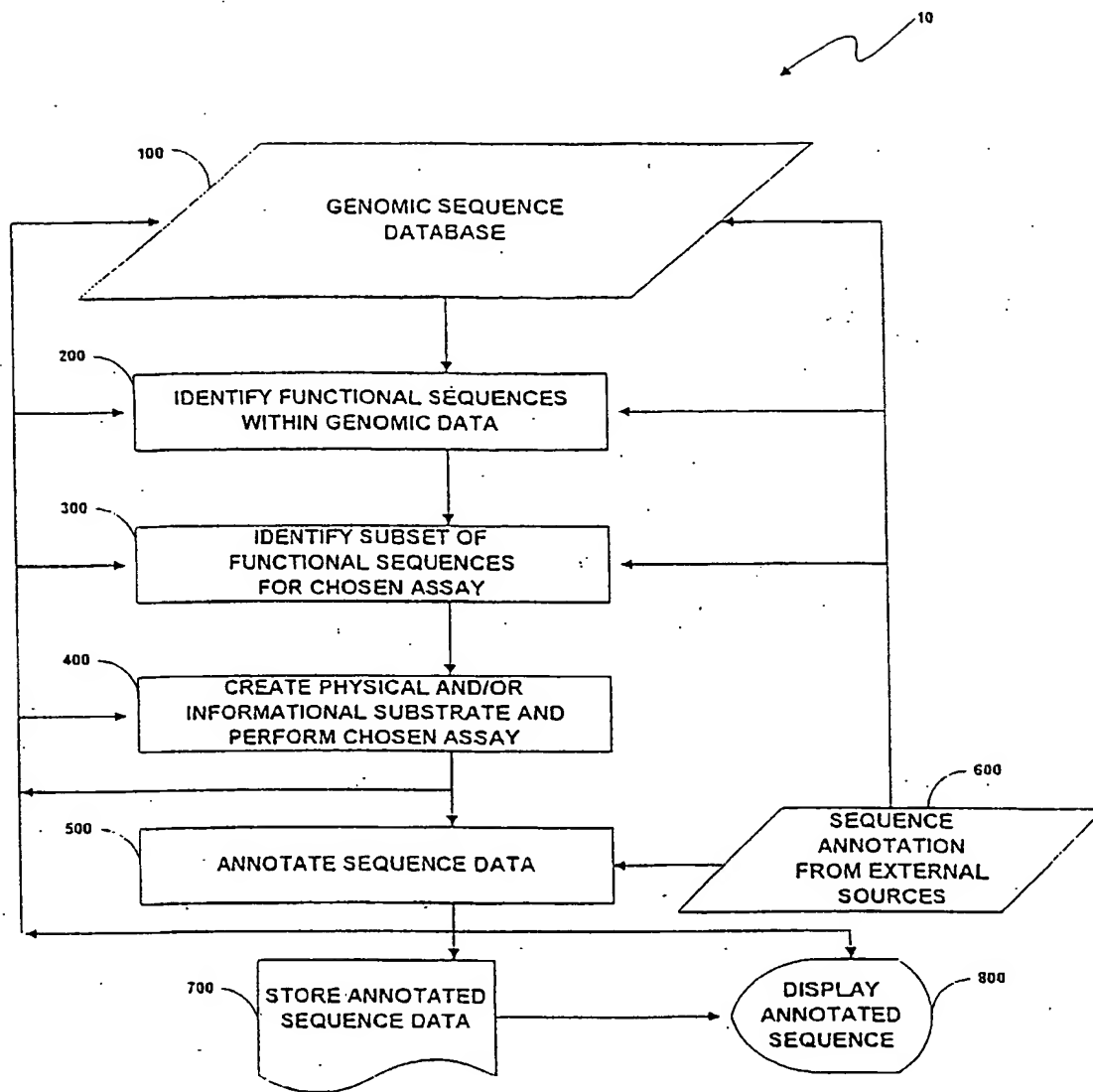


Fig. 1

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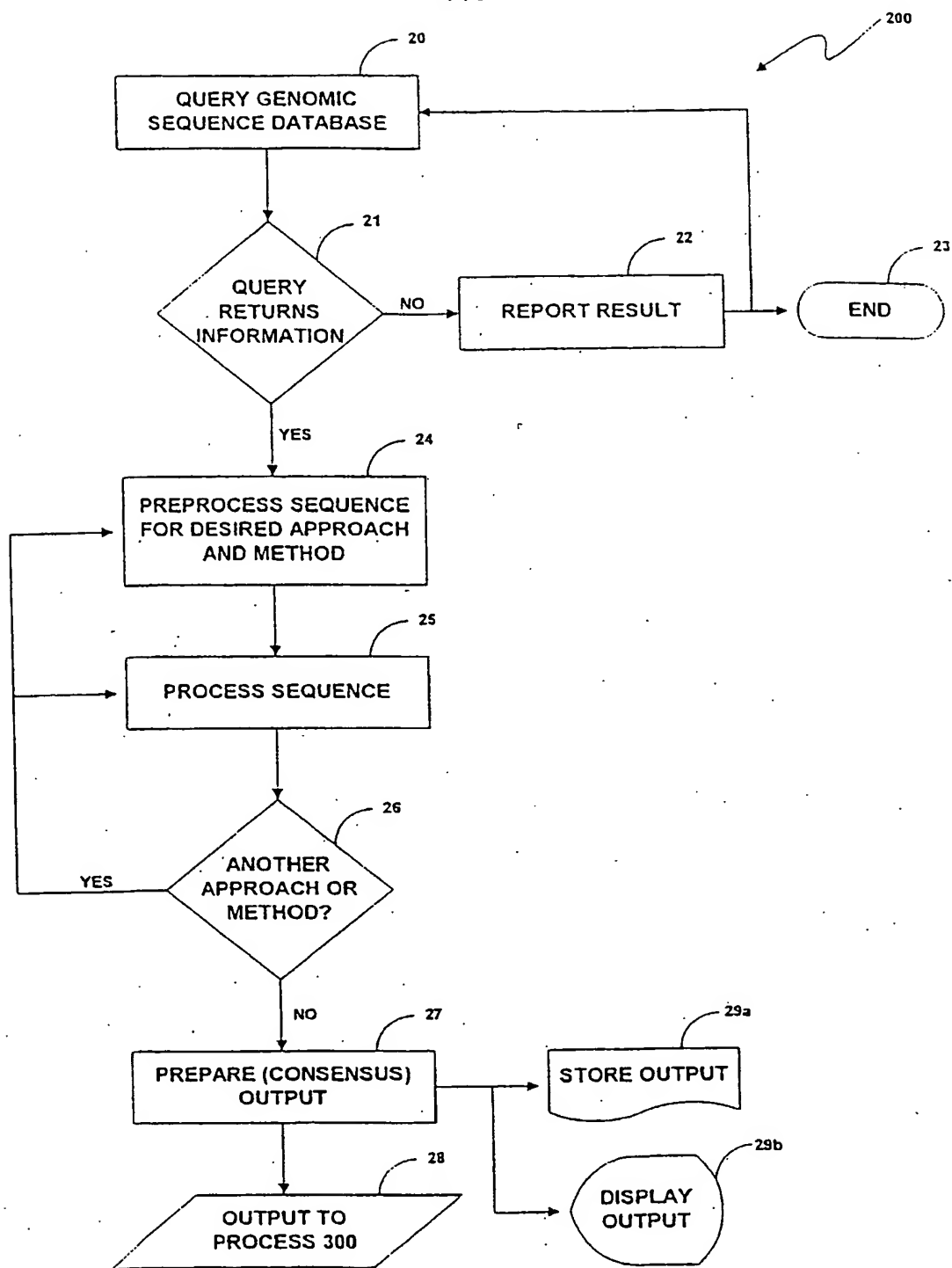
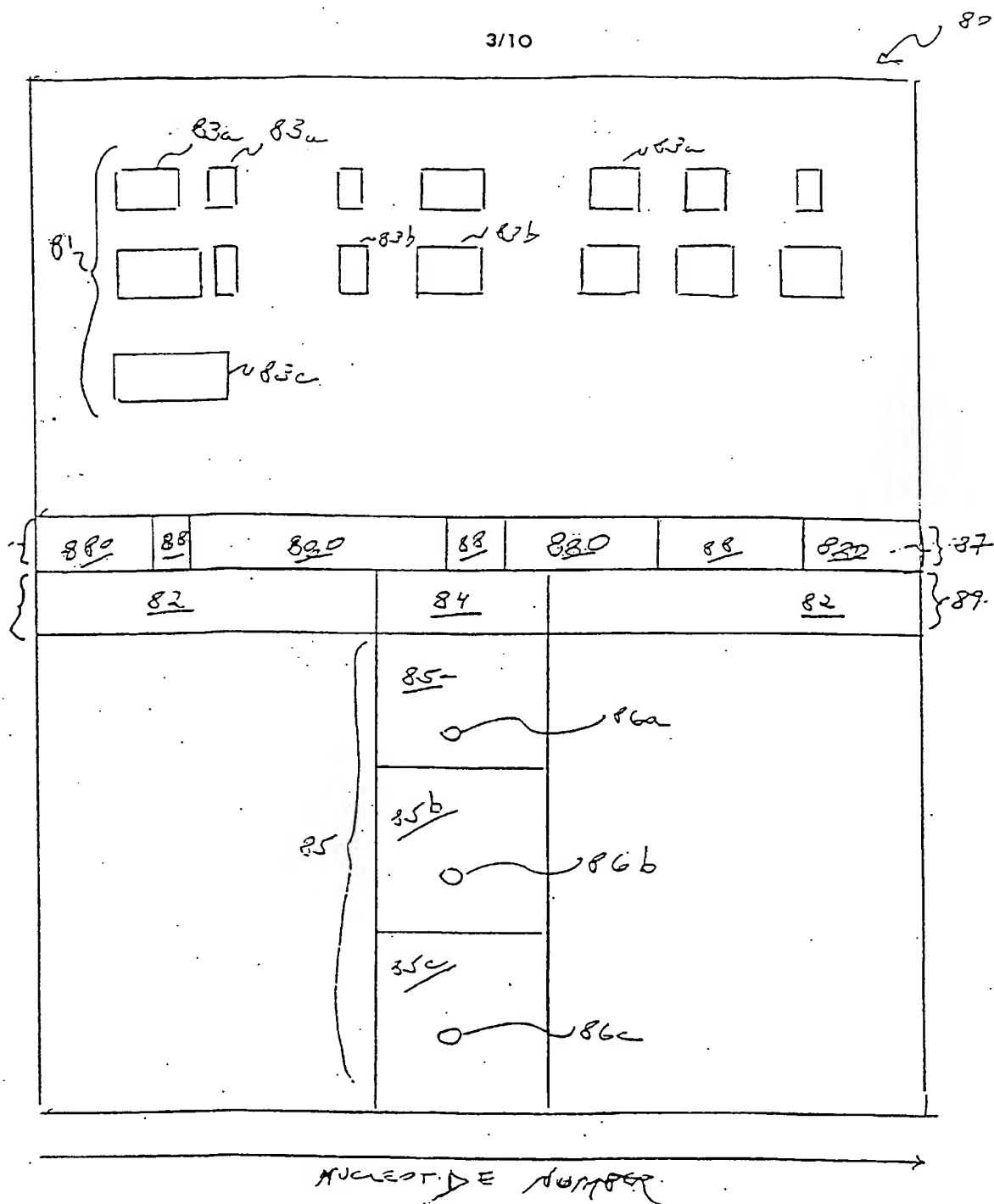


Fig. 2

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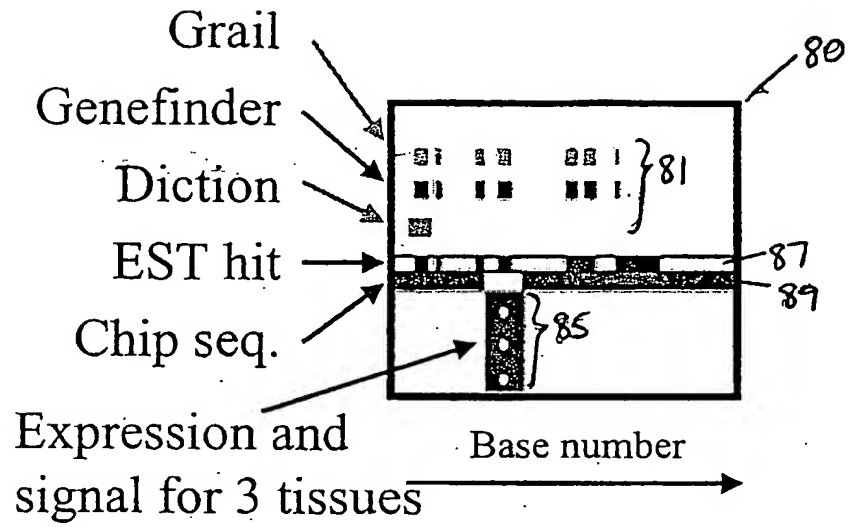


Fig. 4

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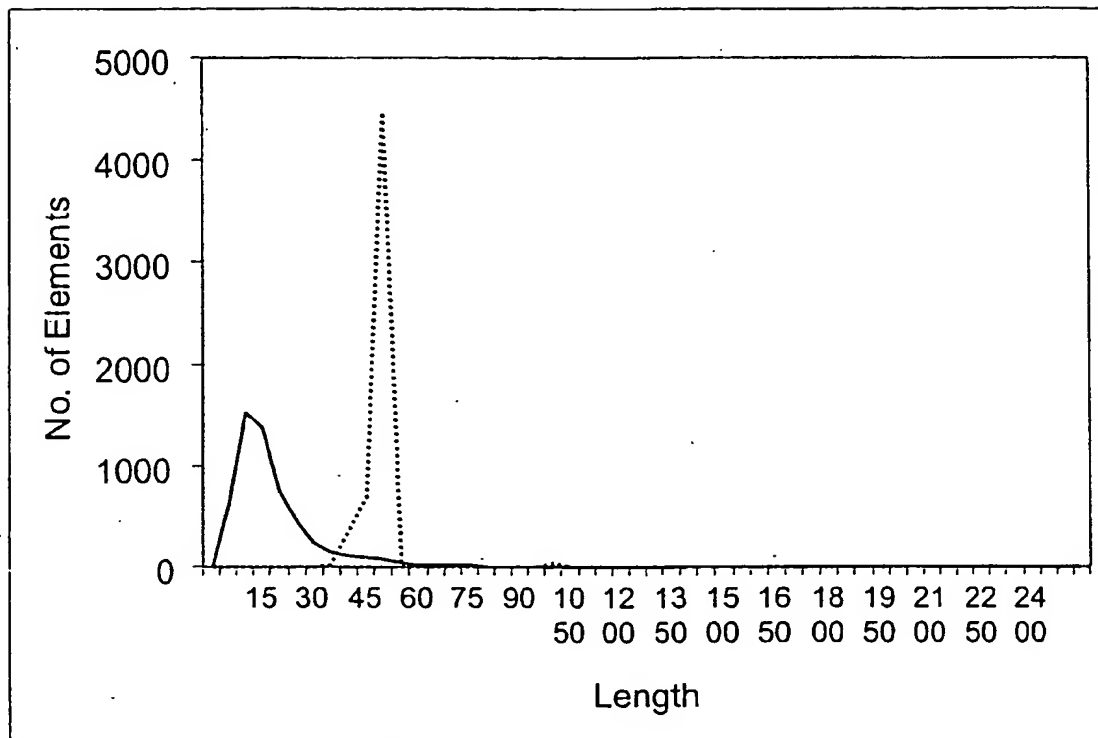


Fig. 5

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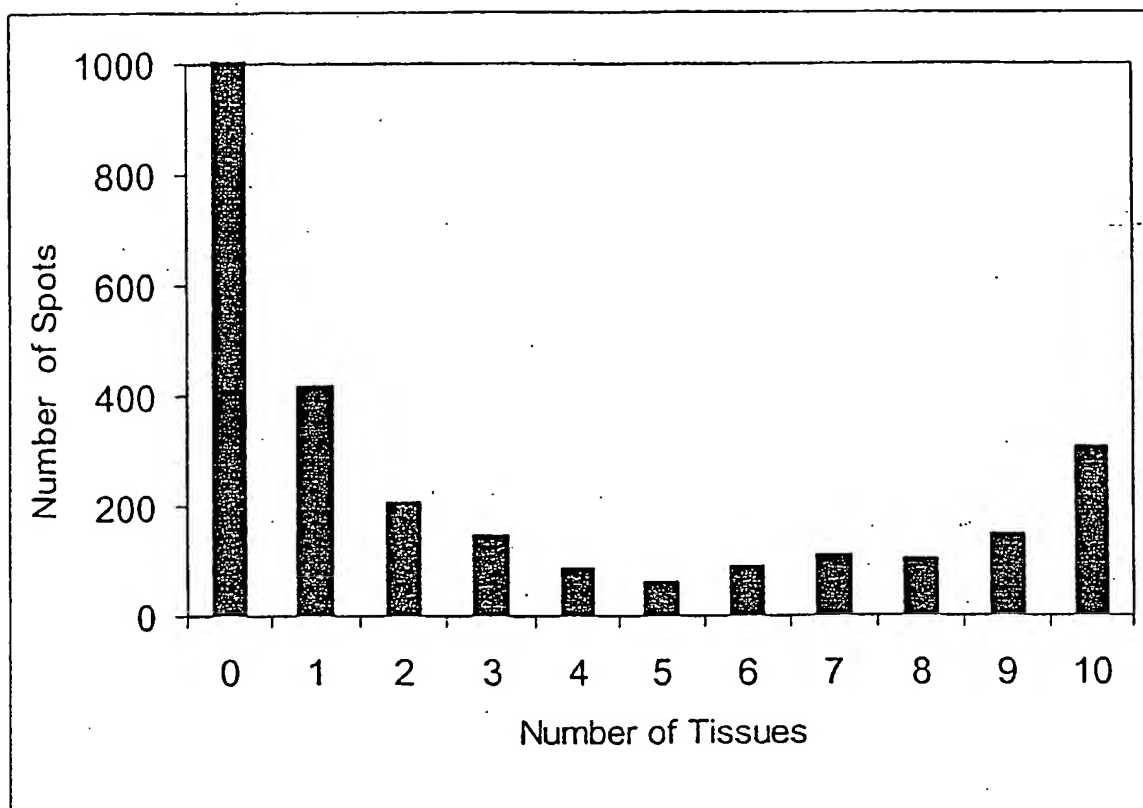
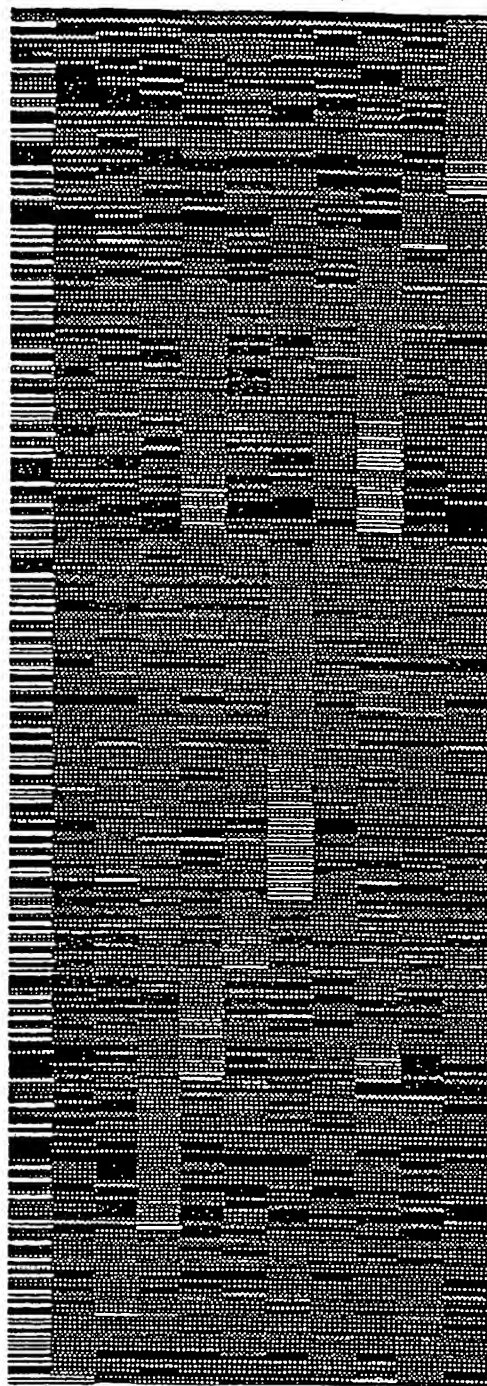


Fig. 6

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EST Hit
Bone Marrow
Brain
BT474
Fetal Liver
HBL100
Heart
Hela
Liver
Lung
Placenta

Fig. 7a

ratio legend

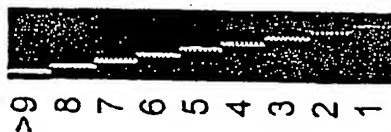


Fig. 7b

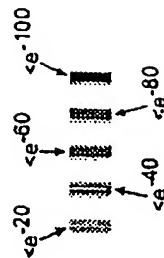


Fig. 7c

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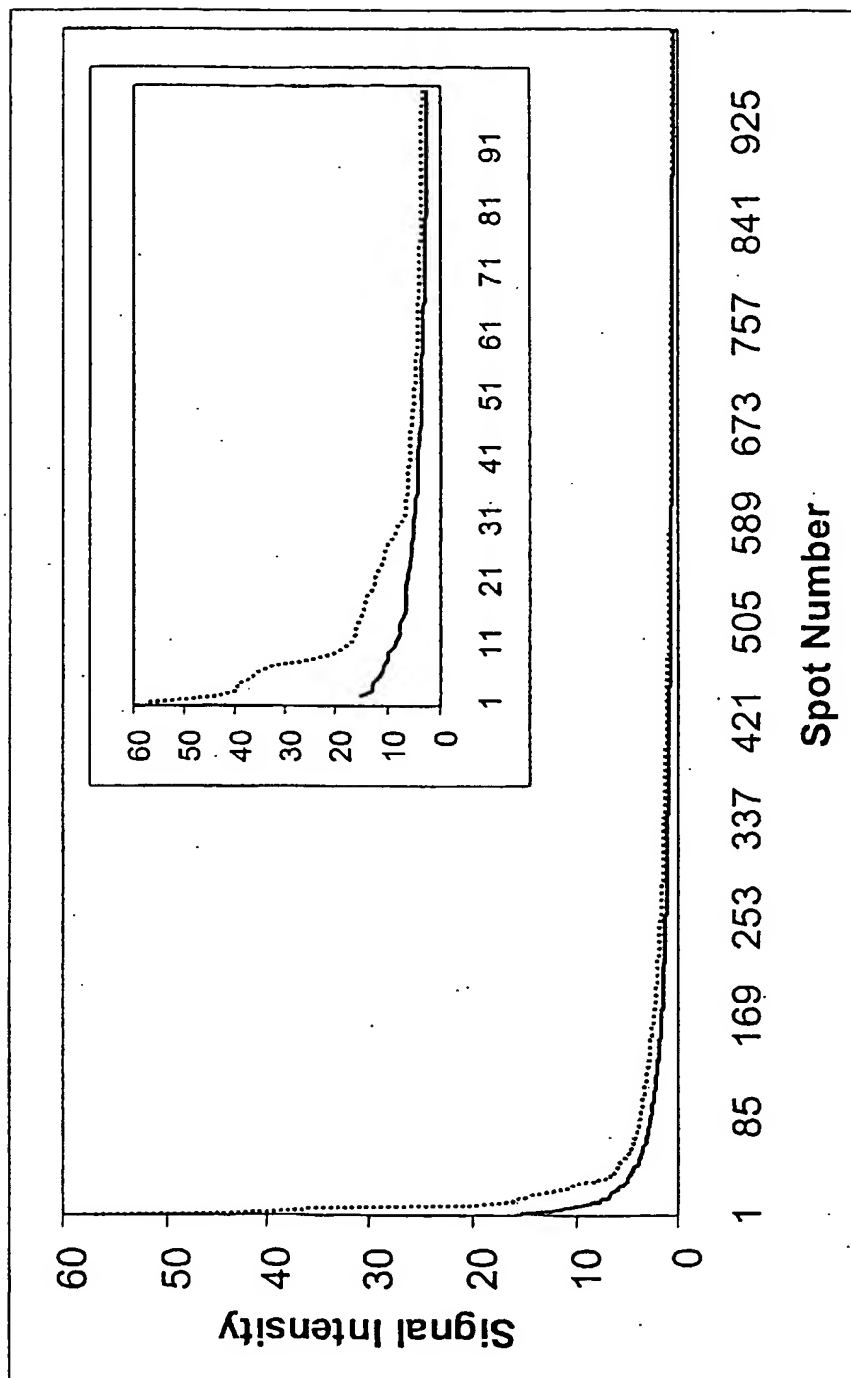


Fig. 8

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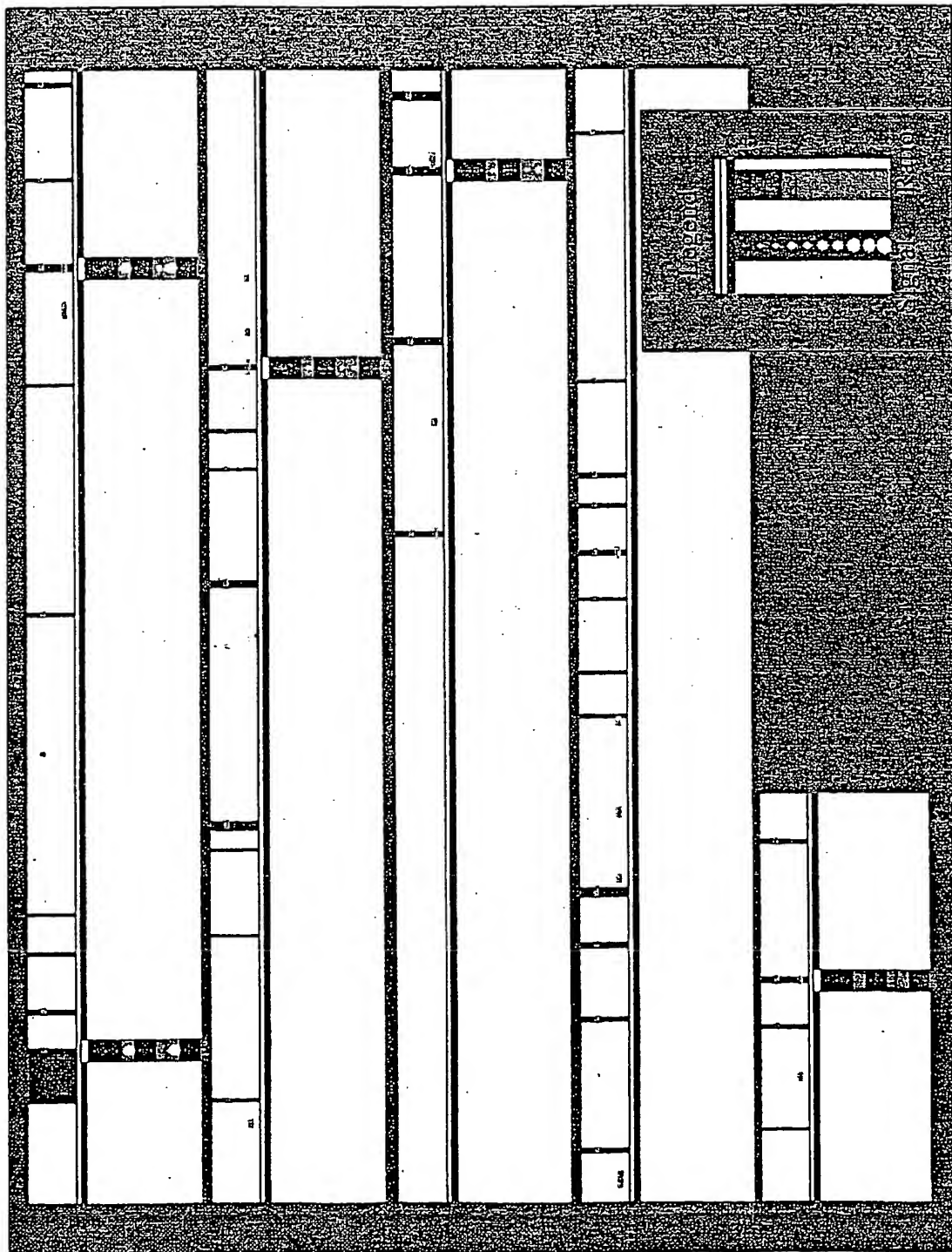
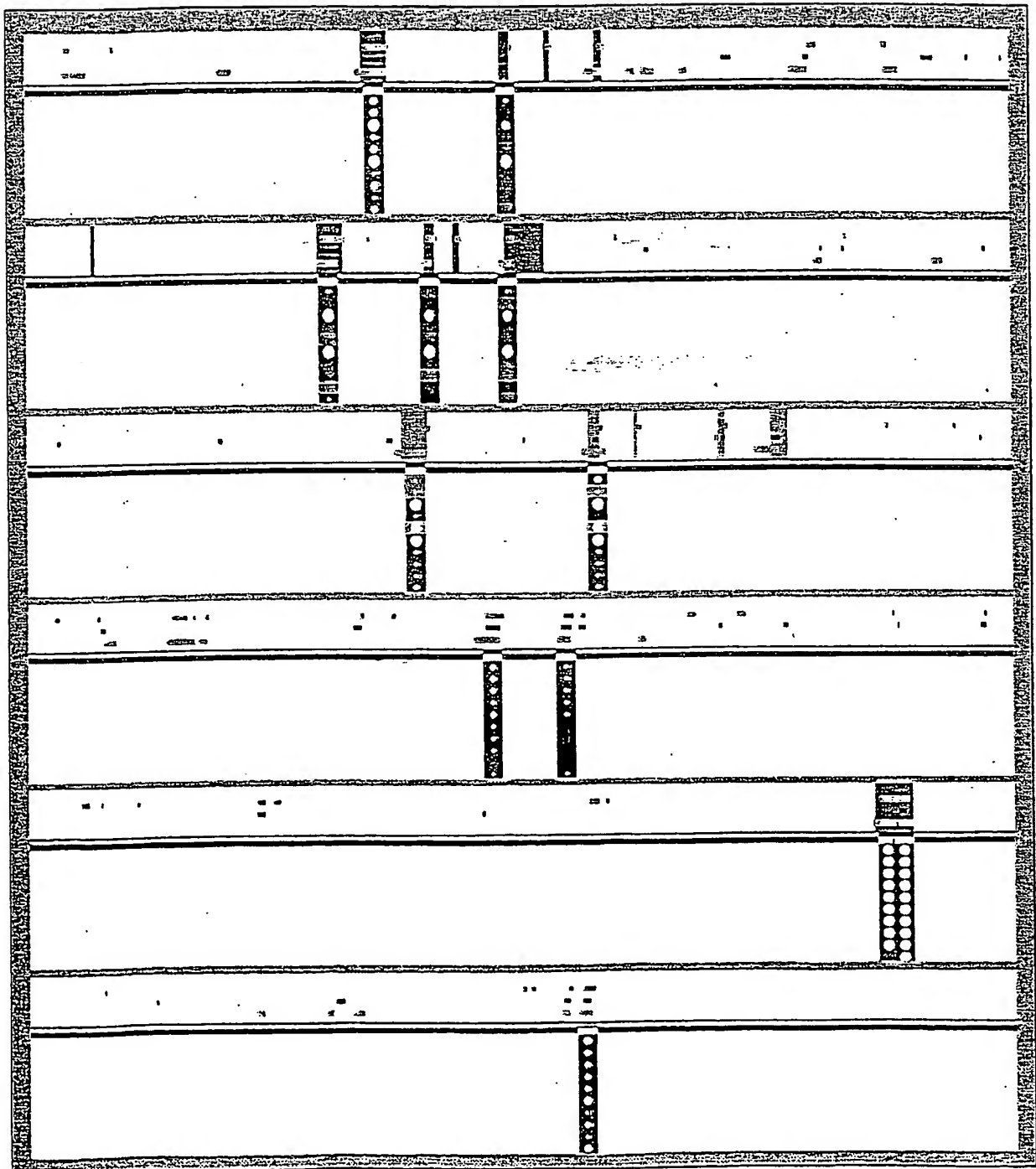


Fig. 9

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Fig. 10



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| 60/234,687 | 21 September 2000 (21.09.2000) | US |
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| 0024263.6 | 4 October 2000 (04.10.2000) | GB |
- (74) Agent: **RONNING, Royal, N., Jr.**; Amersham Pharmacia Biotech, Inc., 800 Centennial Avenue, Piscataway, NJ 08855 (US).
- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
- (71) Applicant (*for all designated States except US*): **AEOM-ICA, INC.** [—/US]; 928 East Arques Avenue, Sunnyvale, CA 94085 (US).
- (72) Inventors; and
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- Published:**
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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human Fetal liver is described. Also described are single exon nucleic acid probes expressed in the Fetal liver and their use in methods for detecting gene expression.



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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00669

A. CLASSIFICATION OF SUBJECT MATTER
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According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

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Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, WPI Data, EPO-Internal, SEQUENCE SEARCH, PAJ

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 23254 A (AFFYMETRIX INC ;NAIR ARCHANA (US); LOCKHART DAVID J (US); WARRINGT) 14 May 1999 (1999-05-14) the whole document	1-27
X	EP 0 321 362 A (PASTEUR INSTITUT) 21 June 1989 (1989-06-21) the whole document specially page 11, paragraph 1	1-27
X	PATENT ABSTRACTS OF JAPAN vol. 015, no. 373 (C-0869), 19 September 1991 (1991-09-19) & JP 03 147799 A (HOECHST JAPAN LTD), 24 June 1991 (1991-06-24) abstract	1-27
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T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

A document member of the same patent family

Date of the actual completion of the international search

11 July 2002

Date of mailing of the international search report

07.08.2002

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Molina Galan, E

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00669

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	DATABASE EBI 'Online! EMBL; Accession Number AC007372, 27 April 1999 (1999-04-27) DICKHOFF ET AL: "Sequencing of human chromosome 14q31 region" XP002182131 sequence ---	13
X	DATABASE EBI 'Online! EMBL; ROBINS ET AL.: "2006 expressed-sequence tags derived from human chromosome 7-enriched cDNA libraries" Database accession no. AA078318 XP002185755 Sequence ---	13
X	DATABASE SWISSPROT 'Online! EMBL; AN: 002711, 1 July 1997 (1997-07-01) BENIT ET AL.: "Cloning of a new murine endogenous retrovirus" XP002037954 the whole document ---	13
X	DATABASE EBI 'Online! embl; AN: AA414703, 9 May 1997 (1997-05-09) MARRA ET AL: "The Washu-HHMI mouse EST project" XP002205620 the whole document ---	13
A	US 5 618 671 A (LINDSTROEM PER) 8 April 1997 (1997-04-08) column 1, line 60 -column 2, line 19 column 4, line 36 -column 5, line 29; claims --- -/--	1-27

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00669

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	EISEN M B ET AL: "Cluster analysis and display of genome-wide expression patterns" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 95, December 1998 (1998-12), pages 14863-14868, XP002140966 ISSN: 0027-8424 the whole document	1,12
P,X	PENN S G ET AL: "Mining the human genome using microarrays of open reading frames." NATURE GENETICS, (2000 NOV) 26 (3) 315-8., XP002183793 the whole document	1

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 01/00669

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/00669

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 1-27 (partially)
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1-27 (partially)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 1-27 (partially)

The following statements about the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject matter for which a search has been performed and identified as the first and second inventions in form 206 PCT.

Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising Seq. Id. 1 or 2 as well as microarrays comprising said sets. In fact, the claims contain so many possible permutations that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search of the claims impossible. Consequently, the search for the sets of probes comprising Seq. Id. 1 or 2 has been limited to the Seq. Id. as such.

Claims 1-3, 5, 6, 8-15 and 18-24 relate to portions or fragments of nucleic acids defined by Seq. Id. 1 or 2. The length or other similar characterizing features of the portions or fragments is not disclosed, bringing the total number of possible prior art sequences to exceptionally high numbers. The shorter the length, the higher the possibility that an overflow of, in principle unrelated, sequences are retrieved, making the establishment of a meaningful International Search Report impossible. For this reason the search has been limited to portions or fragments of Seq. Id. 1 or 2 having a significant minimum length and being supported by the description, namely at least 15 contiguous nucleotides (see claim 16).

Claims 15-21 relate to an extremely large number of nucleic acid probes. The probes are defined solely by their potential to code for peptide Seq. Id. 25138. However, due to the degeneracy of the genetic code, every peptide is potentially coded by an extremely high number of nucleic acid sequences. In fact, the claims contain so many potential nucleic acid sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole scope of the claims impossible. The search has therefore been carried out for those parts of the claims which do appear to be clear and concise, namely the nucleic acid sequences disclosed in the application and identified as encoding the referred peptide in table 4 (Seq. Ids. 1 or 2 and 12682).

Likewise, claim 26, which refers to peptides encoded by Seq. Id. 1 or 2 and 12682, encompasses a high and undefined number of possible peptides. Besides three possible reading frames deriving from the encoding nucleic acid strand, as well as three additional reading frames deriving from the complementary nucleic acid strand, every possible fragment of these is being covered by the claim. This is due to the potential presence of stop codons within any of the six possible reading frames which can not be established a priori. Thus, claim 26 contains so many potential peptide sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search

FURTHER INFORMATION CONTINUED FROM PCT/SA/ 210

over the whole scope of the claim impossible. Consequently, the search has been carried out for those parts of the claim which do appear to be clear and concise, namely the peptide disclosed, identified by Seq. Id. 25138.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-27 (partially)

Invention 1

A nucleic acid probe comprising SEQ ID 1, complementary sequences or fragments thereof (in particular comprising Seq. Id. 12674). Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptides encoded by Seq. Id. 1 (in particular the one defined by Seq. Id. 25130).

2. Claims: 1-27 (partially)

Invention 2

A nucleic acid probe comprising SEQ ID 2, complementary sequences or fragments thereof (in particular comprising Seq. Id. 12682). Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptides encoded by Seq. Id. 1 (in particular the one defined by Seq. Id. 25138).

3. Claims: 1-27 (partially)

Inventions 3-12673

A nucleic acid probe comprising SEQ ID n (where n ranges from 3-12673 according to the invention number above), complementary sequences or fragments thereof, in particular comprising the SEQ ID no. which is listed in the column "Exon Seq. Id. no." in the same row that contains Seq. Id. n in table 4. Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptides encoded by Seq. Id. n, in particular the one defined by the Seq. Id. no. in the column "ORF Seq. Id. no." of the same row where Seq. Id. n is listed.